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“Role of *Salmonella enterica* serovar Typhimurium effectors proteins SopB and SifA in the intracellular survival and modification of the vacuolar compartment in *Dictyostelium discoideum*”

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TESIS DE DOCTORADO

Se informa a la Escuela de Postgrado de la Facultad de Ciencias que la Tesis de Doctorado presentada por la candidata.

CAMILA VALENZUELA MONTENEGRO

Ha sido aprobada por la comisión de Evaluación de la tesis como requisito para optar al grado de Doctor en Ciencias mención Microbiología, en el examen de Defensa Privada de Tesis rendido el día ………………………………………………………………………………………

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Dr. Francisco Chávez ....

Dr. Roberto Vidal ....

Dr. Mauricio Farfán ....

Hope is like the sun. If you only believe in it when you
can see it, you'll never make it through the night
– Leia Organa

This Thesis was conducted at Laboratorio de Microbiología, Facultad de Ciencias Químicas y Farmacéuticas, Universidad de Chile, under the supervision of Dr. Carlos Santiviago. Part of the work was done at the Dynamique des Interactions Hôte-Pathogène Unit at Institut Pasteur, Paris as part of an international collaboration with Dr. Jost Enninga.

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BIOGRAFÍA

Mi interés por la ciencia comenzó a temprana edad de pura curiosidad y amor por la lectura, que fueron fomentados por mi familia desde siempre. Durante el colegio me di cuenta que lo mio era la Bioquímica, título que obtuve el 2013. Durante mi paso por la carrera llegué el 2009 al Laboratorio de Microbiología, evento que cambió totalmente mi destino en la ciencia, me enamoré de la microbiología y del estudio de las interacciones patógeno-hospedero. Es en este lugar donde a lo largo de estos casi 10 años me dieron las herramientas para llegar a ser lo que soy. En el año 2014 decidí que el único programa al que quería entrar era el Doctorado en Ciencias mención Microbiología de la Universidad de Chile y no puedo estar mas contenta de lo que he logrado gracias a esto. La principal enseñanza que saco de todos estos años es que de haber trabajo duro y riguroso, todos los demás problemas que se presenten en el camino se resuelven de alguna manera. Gracias a las habilidades adquiridas durante esta etapa es que ahora me puedo enfrentar el futuro que venga.

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5. LIST OF ABREVIATIONS

Amp:	Ampicillin
BCA:	Bicinchoninic acid
bp:	Base pair
BSA:	Bovine serum albumin
Cam:	Chloramphenicol
CFU:	Colony-forming unit
ºC:	Degree Celsius
DMSO:	Dimethyl sulfoxide
DNA:	Deoxyribonucleic acid
DTT:	Dithiothreitol
EBU:	Evans blue-uranine
EDTA:	Ethylenediaminetetraacetic acid
EGTA:	Ethylene glycol-bis (β-aminoethyl ether)-N,N,N′,N′-tetraacetic acid
ELISA:	Enzyme-Linked Immunosorbent Assay
ER:	Endoplasmic Reticulum
FDR:	False Discovery Rate
F-change:	Fold-change
FRT:	Flp recombinase target sequence
GAP:	GTPase-activating protein
GEF:	Guanine nucleotide exchange factor
GFP:	Green Fluorescent Protein
hpi:	Hours post infection
HB:	Homogenization Buffer
HEPES:	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
HOPS:	Homotypic fusion and Protein Sorting
Kan:	Kanamycin
LB:	Luria-Bertani
LBPA:	Lysobisphosphatidic acid
LCV:	*Legionella*-Containing Vacuole
LDS:	Lithium dodecyl sulfate
LPS:	Lipopolysaccharide
LY294002:	2-Morpholin-4-yl-8-phenylchromen-4-one
min:	Minute
MOI:	Multiplicity of Infection
M6PR:	Mannose-6-phosphate receptor
MS:	Mass Spectrometry
mTOR:	Mammalian target of rapamycin
MVB:	Multivesicular body
OD_{600nm}:	Optic density at 600 nm
O/N:	Overnight
OPD:	o-phenylenediamine

PAGE:	Polyacrylamide Gel Electrophoresis
PBS:	Phosphate-buffered saline
PCR:	Polymerase Chain Reaction
PI3K:	Phosphatidylinositol 3 kinase
PNS:	Post-nuclear supernatant
rpm:	Revolutions per minute
s:	Second
SEM:	Standard error of the mean
SEPro:	Search Engine Processor
SCV:	*Salmonella*-Containing Vacuole
SDS:	Sodium dodecyl sulfate
SIF:	*Salmonella*-Induced Filaments
SKIP:	SifA and Kinesin-Interacting Protein
SPI:	*Salmonella* Pathogenicity Island
Str:	Streptomycin
SVATs:	Spacious Vacuole Associated Tubules
TAE:	Tris-acetate EDTA
TEM:	Transmission Electron Microscopy
Tris:	Tris (hydroxymethyl) aminomethane
T3SS:	Type Three Secretion Systems
V:	Volts
WT:	Wild-type

6. ABSTRACT

Salmonella Typhimurium is an enteric pathogen able to infect different animal hosts, including humans. In immunocompetent humans, *S*. Typhimurium mainly causes gastroenteritis, a disease characterized by an inflammatory diarrhoea with massive neutrophil infiltration in the ileum and colon. The infective cycle of *Salmonella* starts with the ingestion of bacteria that reach the small intestine and invade epithelial cells by its apical face. After crossing the epithelial barrier, bacteria are captured by phagocytic cells of the immune system present in the sub-epithelium, such as macrophages, neutrophils and dendritic cells, being contained within a membrane bound compartment. Here, *Salmonella* subverts the endocytic route, avoiding the fusion of this compartment with the lysosomes and generating the *Salmonella*-containing vacuole (SCV). In this compartment, *Salmonella* is able to survive and replicate. The ability to modify this intracellular niche explains the ability of this pathogen to survive intracellularly. To carry out this process, *Salmonella* employs two Type Three Secretion Systems (T3SS) and an arsenal of secreted effector proteins in order to take control over the eukaryotic cell. An important aspect of *Salmonella*'s life cycle that has not been studied in detail is its survival in the environment, where bacteria are exposed to predation by protozoa, and specially by amoebae. These organisms are specialized phagocytes that feed on bacteria and fungi. To address this interaction, we and other groups use amoeba models to characterise the molecular processes involved in the survival of intracellular pathogens within environmental protozoa. Among these model organisms, the social amoeba *Dictyostelium discoideum* is amenable for molecular analyses in laboratory settings and several tools have been developed in this organism for the study of different aspects of its interaction with bacterial pathogens. Recently, our group described that *S*. Typhimurium is able to survive intracellularly in the social amoeba *Dictyostelium discoideum*, and that mutants in genes required for virulence in other infection models present survival defects in this host. Despite of this, the mechanisms that allow the intracellular survival of this pathogen in this kind of organism have not been studied in detail. This Thesis proposed the characterization at the cellular level of this interaction, with a focus on two secreted effector proteins of *S.* Typhimurium that are directly related to SCV generation and modification in other cell models: SopB and SifA. Our results show that these effectors are needed for intracellular survival of *S.* Typhimurium in *D. discoideum*. Furthermore, by means of a combination of microscopy and proteomic analyses we were able to characterise the protein composition of the vacuolar compartment containing *Salmonella* in this host. Our results show that known markers linked to this compartment in other cell types and the autophagy machinery play a role in the biogenesis of this intracellular niche in *D. discoideum*.

7. RESUMEN

Salmonella Typhimurium es un patógeno enterico que tiene la capacidad de infectar diversos hospederos animals, incluyendo el ser humano. En individuos inmunocompetentes, *S*. Typhimurium provoca gastroenteriris, una enfermedad diarreica inflamatoria caracterizada por la masiva infiltración de neutrófilos en el íleon y el colon. El ciclo infectivo de *Salmonella* comienza con la ingestión de las bacterias que al llegar al intestino delgado invaden las células epiteliales por la cara apical. Luego de cruzar la barrera epitelial, las bacterias son capturadas por las células fagocíticas del sistema inmune que residen en el sub-epitelio, como macrófagos, neutrófilos y células dendríticas, quedando contenida en un compartimento membranoso. En esta etapa, *Salmonella* interviene la ruta endocítica, evitando la fusión de este compartimento con el lisosoma y generando la vacuola contenedora de *Salmonella* (*Salmonella*-containing vacuole: SCV). En este compartimento, *Salmonella* es capaz de sobrevivir y replicarse. La habilidad de modificar este nicho intracelular explica la habilidad de este patógeno de sobrevivir intracelularmente. Para esto, *Salmonella* utiliza dos Sistemas de Secreción Tipo Tres (Type Three Secretion Systems: T3SS) y un arsenal de proteínas efectoras secretadas para tomar control sobre la célula eucarionte. Por otra parte, un importante aspecto del ciclo de vida de *Salmonella* que no ha sido estudiado en detalle es su supervivencia en el ambiente, donde las bacterias se encuentran expuestas a la depredación por protozoos y en particular, amebas.

Estos organismos son fagocitos profesionales que se alimentan de bacteria y hongos. Recientemente, nuestro grupo describió que *S*. Typhimurium es capaz de sobrevivir intracelularmente en la ameba social *Dictyostelium discoideum* y que mutantes en genes requeridos para la virulencia en numerosos modelos de infección también presentan defectos de supervivencia en este hospedero. A pesar de esto, los mecanismos que le permiten a este patógeno en este tipo de organismo no han sido estudiado en detalle. Para entender esta interacción, nosotros y otros grupos usamos modelos de ameba a fin de caracterizar los procesos moleculares involucrados en la supervivencia de patógenos intracelulares en el interior de protozoos ambientales. Dentro de estos organismos modelo, la ameba social *Dictyostelium discoideum* es sencilla para el análisis molecular en condiciones de laboratorio. Por otra parte, numerosas herramientas se han desarrollado en este organismo para el estudio de diversos aspectos de su interacción con patógenos bacterianos. Esta Tesis propuso caracterizar a nivel cellular esta interacción, enfocándonos en dos proteínas efectoras secretadas de *S*. Typhimurium que están directamente relacionadas a la formación y modificación de la SCV en otros modelos celulares: SopB y SifA. Nuestros resultados muestran que estos efectores son necesarios para que *S*. Typhimurium sobreviva intracelularmente en *D. discoideum*. Adicionalmente, mediante una combinación de técnicas de microscopía y análisis proteómicos pudimos caracterizar la composición proteíca de este compartimento vacuolar que contiene a *Salmonella* en este hospedero. Nuestros resultados muestran que marcadores asociados a la SCV en otras líneas celulares se encuentran en el compartimento que se genera en *D. discoideum* y que la maquinaria de autofagia juega un rol importante en la biogénesis de este nicho intracelular en *D. discoideum*.

8. INTRODUCTION

8.1 *Salmonella*

The *Salmonella* genus corresponds to a group of Gram-negative rod-shaped bacteria that includes over 2,500 serotypes or serovars that have been defined according to lipopolysaccharide (O-antigen) and flagella (H-antigen) variations (Popoff, 2001; Popoff et al., 2004). This genus consists of two species: *Salmonella enterica* and *Salmonella bongori*. *S. enterica* is further divided into six subspecies: *enterica*, *salamae*, *arizonae*, *diarizonae*, *houtenae* and *indica*. Serotypes in the *enterica* subspecies are responsible of 99% of the salmonellosis cases in warm-blooded animals. The clinical outcome of infections caused by different *Salmonella* serovars are highly variable and can range from a mild diarrhoea to a systemic disease that can be fatal (Canals et al., 2011).

Worldwide, the different *Salmonella* serotypes cause over 90 million cases of salmonellosis and thousands of deaths every year (CDC, 2005; World Health Organization, 2015), being most prevalent in underdeveloped countries. Nontyphoidal *Salmonella* serovars (such as *S*. Typhimurium) account for over 150,000 deaths annually in the world, most of them associated to foodborne infections (World Health Organization, 2015). It is important to mention that the clinical outcome of the infection depends on several factors, such as the infecting serotype, the strain virulence, the infective dose, the host species, and its age and immune state, among others (Mastroeni & Maskell, 2006). Additionally, different *S. enterica* serotypes have differences in host specificity. Those serotypes named "generalists" are capable of infecting a broad range of animal hosts, including humans. In this group, we can find *S*. Typhimurium and *S*. Enteritidis. In the opposite side of the spectrum we can find the serotypes named "specialists", such as *S*. Typhi and *S*. Gallinarum, which cause systemic disease only in humans and poultry, respectively (Feasey et al., 2012).

S. Typhimurium is a generalist serotype that mainly infects warm-blooded animals. In humans, this pathogen causes a condition characterized by diarrhea, vomit and nausea that is generally self-limited in immunocompetent individuals. This disease, known as gastroenteritis, corresponds to a typical inflammatory diarrhea characterized by a massive neutrophil infiltration in the ileum and colon (Raffatellu et al., 2006). As a result of this infection, immunocompromised patients and children under 5 years can develop a severe disease, with systemic colonization, hepatomegaly, splenomegaly and elevated hepatic enzymes (Bar-Meir et al., 2005; Brent et al., 2006; Graham et al., 2000; Shimoni et al., 1999). On the other hand, in susceptible mice *S*. Typhimurium causes a disease similar to typhoid fever caused by *S*. Typhi in humans (Andrews-Polymenis et al., 2004; Bogomolnaya et al., 2008).

The infective cycle of *Salmonella* starts with the ingestion of the bacteria from contaminated water or food. After ingestion, bacteria surviving the acid pH in the stomach reach the small intestine, where they are able to invade epithelial cells by the apical side. After crossing the epithelial barrier, bacteria are captured by phagocytic cells in the sub-epithelium, such as macrophages, neutrophils and dendritic cells, being contained in a vesicle. Here, *Salmonella* avoids the fusion of this vacuole with the lysosome generating a compartment where the bacterium can survive and replicate (Cirillo et al., 1998; Hensel et al., 1997; Mastroeni & Maskell, 2006; Rappl et al., 2003; Waterman & Holden, 2003).

8.2 Mechanisms of pathogenicity and virulence factors

To date, numerous molecular mechanisms of pathogenicity have been described during the interaction between *Salmonella* and its animal hosts, and most of them have been characterized *in vitro* and *in vivo* using *S*. Typhimurium (Galán & Curtiss, 1989; Galán et al., 1992; Gulig & Doyle, 1993; Hensel et al., 1995). These studies allowed the identification of many virulence factors for these bacteria, most of them encoded in the *Salmonella* pathogenicity islands SPI-1 to SPI-5. These pathogenicity islands are DNA fragments acquired by horizontal gene transfer and contribute directly to bacterial virulence (Juhas et al., 2008; Juhas, 2015; Mel & Mekalanos, 1996). Other studies have also demonstrated the importance of the *Salmonella* virulence plasmid for intracellular growth during the infection of mice hosts (Gulig & Doyle, 1993).

Pathogenicity islands SPI-1 and SPI-2 encode two independent type three secretion systems (T3SS). These systems are macromolecular structures used to inject effector proteins into host cells, and it has been demonstrated its requirement in different steps of the infection cycle. The T3SS encoded in SPI-1 ($T3SS_{SPI-1}$) is required during the intestinal phase of the infection, where it allows the invasion of epithelial cells by injecting effectors inducing a reorganization of the actin cytoskeleton, which ends on the bacterial endocytosis by these non-phagocytic cells (Hardt et al., 1998; Patel & Galan, 2006). After crossing the epithelial barrier, *Salmonella* uses the $T3SS_{SPI-1}$ to enter into phagocytic cells residing in the sub-epithelium, such as macrophages, neutrophils and dendritic cells, ending up being contained into a phagocytic vesicle. Inside this compartment, the T3SS encoded in SPI-2 ($T3SS_{SPI-2}$) is expressed, allowing *Salmonella* to intervene the phagocytic pathway in order to avoid the fusion of the phagosome with the lysosome and generating the *Salmonella*-containign vacuole (SCV), compartment where the bacteria can survive and replicate (Cirillo et al., 1998; Hensel et al., 1997; Mastroeni & Maskell, 2006; Rappl et al., 2003; Waterman & Holden, 2003).

Other relevant *Salmonella* virulence factors are magnesium transporters and proteins of unknown function encoded in SPI-3. These factors are essential for bacterial survival within macrophages (Blanc-Potard & Groisman, 1997; Blanc-Potard et al., 1999). SPI-4 encodes a type one secretion system (Wong et al., 1998; Kiss et al., 2007), and its secreted protein (SiiE) acts as a non-fimbrial adhesin mediating contact with epithelial cells being important for the intestinal phase of the infection (Gerlach et al., 2007). SPI-5 includes genes encoding efector proteins differentially translocated by T3SS$_{SPI-1}$ and T3SS$_{SPI-2}$ (Knodler et al., 2002; Wood et al., 1998). Other important virulence factors not encoded in pathogenicity islands include the two-component system PhoP/PhoQ that controls the expression of genes encoding virulence factors such as the regulon associated to SPI-2, Mg^{2+} transporters and genes involved in resistance to acidic pH and antimicrobial peptides (Thompson et al., 2011; Garvis et al., 2001; Shprung et al., 2012). Additionally, genes encoding proteins associated with lipopolysaccharide (LPS) biosynthesis and modification, and the biosynthesis of aromatic compounds and purines, are critical for the virulence of this pathogen (Hensel et al., 1995).

8.3 Generation and maturation of the *Salmonella*-Containing Vacuole

The maturation of the SCV is one of the main processes allowing the survival of *Salmonella* within eukaryotic cells. Using cell models *in vitro*, such as epithelial and phagocytic cells (i.e., macrophages) it has been determined that there are three stages in the SCV maturation: early (<30 min post infection), intermediate (1-5 h post infection) and late (>5 h post infection) (Santos & Enninga, 2016), which are depicted in **Figure 1**. The early stage is commanded mainly by T3SS$_{SPI-1}$ effectors, being SopB the most important for this stage. This protein activates the RhoG GTPase promoting invasion (Patel & Galán, 2006), and also has a phosphatidylinositol phosphatase activity that hydrolyses PI(4,5)P_2 species during the internalization, facilitating membrane fission (Terebiznik et al., 2002).

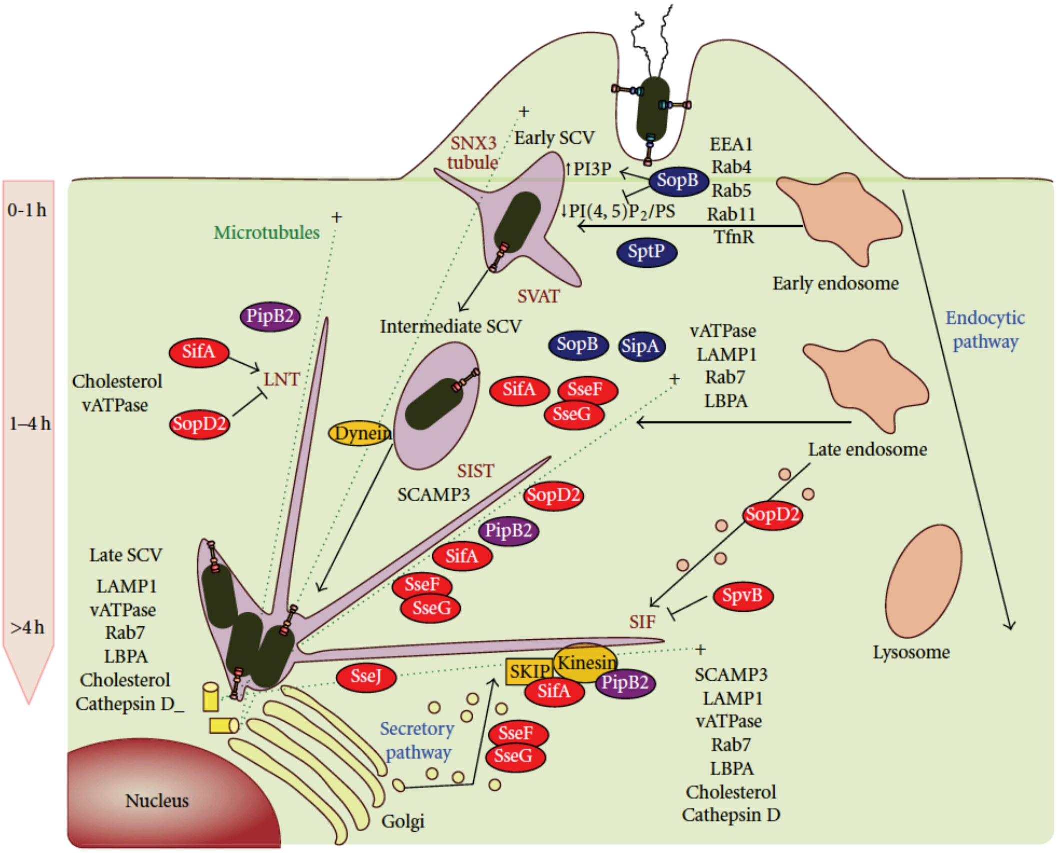


Figure 1 - Biogenesis of the *Salmonella*-containing vacuole. The diagram shows the maturation process of the modified phagosome known as the *Salmonella*-containing vacuole (SCV) by the interaction of T3SS effector proteins with the host endocytic and secretory pathways. The early stage in SCV biogenesis (0-1 h) is driven by T3SS$_{SPI-1}$ effectors (in blue) SopB and SptP. The intermediate stage of development (1-4 h) requires the participation of T3SS$_{SPI-1}$ effectors SipA and SopB, and T3SS$_{SPI-2}$ effectors (in red) SifA, SseF and SseG to allow the movement of the SCV to a juxtanuclear position. Many effectors are involved in the late stage of maturation and in the maintenance of the SCV. Bacterial replication is initiated 4-6 h post invasion and is accompanied by the formation of different kinds of tubules known as SIFs, SISTs and LNTs. Effectors involved in the formation of these tubules are depicted in red (T3SS$_{SPI-2}$ effectors) and in purple (effectors that can be secreted via both T3SS). Obtained from Ramos-Morales, 2012.

After that, SopB modulates the SCV fate by recruiting the Rab5 GTPase and its cognate phosphatidylinositol 3 kinase (PI3K) Vps34 in order to increase the levels of PI3P at the SCV membrane (Hernandez et al., 2004, Mallo et al., 2008). This controls the surface charge of the SCV membrane, allowing the exclusion of several host proteins and thus avoiding the fusion of this compartment with the lysosomes (Bakowski et al., 2010). On the other hand, the increase in PI3P at the SCV membrane recruits sorting nexins SNX1 and SNX3. These are part of a family of proteins involved in intracellular trafficking by binding to phospholipids, either by their phospholipid binding domain or by interacting with other membrane-associated proteins. SNX1 changes its locations, migrating from endosomes to the bacterial entry site. Then, dynamic structures named Spacious Vacuole Associated Tubules (SVATs) are formed, the SCV shrinks in size and a lysosome marker, the manose-6-phosphate receptor, is removed. SNX3 is associated to tubular structures known as SNX3 tubules, allowing the recruiting of Rab7 and LAMP1 to the maturing SCV. This process allows the movement of the SCV by the SNX3 tubules (Bujny et al., 2008; Drecktrah et al., 2007; García-del Portillo & Finlay, 1995; Oh et al., 1996).

The intermediate stage of the SCV maturation is controlled by $T3SS_{SPI-1}$ effectors SopB and SipA, along with $T3SS_{SPI-2}$ effectors SifA, SseF and SseG. This stage is characterized by the movement of the SCV to a perinuclear position, mediated by the interaction between a complex formed by SifA, SseF and SseG with dynein (Ramsden et al., 2007). This complex is also involved in the recruitment of Rab7, LAMP1 and the vacuolar ATPase to the SCV membrane.

The late stage of the SCV maturation is commanded by a variety of effectors exerting both cooperative and antagonistic activities. The balance between their functions allows the vacuole to maintain its perinuclear position and the formation of different tubule networks. Among these, the so-called *Salmonella*-induced filaments (SIFs) are the most important. SIFs are a network of tubular cisternae extending from the SCV over a scaffold of microtubules. These structures have the same membrane composition as the mature SCV, being enriched in late endosome markers LAMPs, Rab7, cholesterol and the vATPase, while lacking the characteristic late endosomal/lysosomal markers cathepsin D, lysobisphosphatidic acid (LBPA) and mannose-6-phosphate receptor (M6PR) (Drecktrah et al., 2007; Rajashekar et al., 2008; Steele-Mortimer, 2008 Méresse et al., 1999; Brumell et al., 2001; Knodler & Steele-Mortimer, 2005). SIF formation is dependent on the action of $T3SS_{SPI-2}$ effectors PipB2, SifA, SopD2, SseF, SseG and SseJ. The current model of SIF formation suggests that SifA's GTP exchanging activity activates RhoA GTPase, allowing its interaction with SseJ activating it. SseJ is a lipase that modifies the lipid composition of the SCV membrane, promoting SIF formation. After that, PipB2 and the SifA-SKIP complex bind kinesin-1, allowing its interaction with the SCV membrane and connecting the forming SIFs to microtubules. This process allows the elongation of these tubular structures outwards (Krieger et al., 2014; Schroeder et al., 2011). Additionally, SopD2 associates to late endosomes redirecting the trafficking of vesicles to the SCV and elongating SIFs, thus allowing their growth by increasing the available membranes (Schroeder et al., 2010). Effectors SseF and SseG are also involved in this process, allowing the aggrupation of microtubules in the vicinity of the SCV, which promotes the fusion of vesicles to the nascent tubules (Deiwick et al., 2006). While the role of the SIF network is not completely dilucidated, a couple of hypothesis have been proposed: (1) the SIF network allows *Salmonella* to gain access to endocytosed nutrients to promote intravacuolar proliferation, as labeled endosomal cargo can be detected within the SIF network of infected cells, demonstrating the access of these structures to endocytosed material; and (2) the connections between the SCV and the SIF network reduces exposure of intravacuolar *Salmonella* to host defenses, for example by diluting lysosomal enzymes that can be acquired by the SCV (Drecktrah et al., 2008; Knuff & Finlay, 2017; Krieger et al., 2014; Liss et al., 2017; Mota el at, 2009; Rajashekar et al., 2008; Zhang & Hensel, 2013).

As described in this section, *Salmonella* modifies the SCV to generate a replicative niche by means of a complex maturation process. This phenomenon has been reported in several cell lines *in vitro*, but it is worth noticing that none of these mechanisms have been studied in the context of the interaction of *Salmonella* and protozoa. On the other hand, other pathogens that survive intracellularly by modifying a vacuolar compartment have been extensively studied in the context of their interaction with protozoa. For example, it has been shown that several mechanisms involved in the interaction with amoeba, including *Dictyostelium discoideum* are common with those involved in the interaction with other cell types such as macrophages *in vitro* (Dolinsky et al., 2014; Hilbi et al., 2014; Prashar & Terebiznik, 2015).

8.4 Interaction between *Salmonella* and protozoa

One aspect of *Salmonella* that has not been studied in detail is its survival in the environment, were bacterial enteropathogens spend an important part of their life cycle. In this niche, *Salmonella* is exposed to predation by protozoa such as amoebas. These organisms are phagocytic cells that feed on bacteria. Studies published to date demonstrate that different *Salmonella* serotypes are able to survive within several protozoa species such as *Acanthamoeba*, *Tetramitus*, *Naegleria*, *Hartmannella* and *Tetrahymena* (Bleasdale et al., 2009; Brandl et al., 2005; Feng et al., 2009; Gaze et al., 2003; Rehfuss et al., 2011; Tezcan-Merdol et al., 2004; Wildschutte et al., 2004; Wildschutte & Lawrence, 2007;). In the case of other intracellular pathogens, such as *Legionella pneumophila*, several mechanisms employed by the bacteria to survive and replicate in amoebae have been determined (Rowbotham et al., 1980). Moreover, it has been reported that this pathogen exploits a common set of genes to survive within amoebae and human macrophages (Gao et al., 1997; Segal & Shuman, 1999). This suggest that at least some intracellular pathogens evolved by adapting to survive inside phagocytic organisms present in the environment. This gain of function contributed to their survival when they reached a new niche: within phagocytic cells of the immune system of a complex host. Understanding the mechanisms used by *Salmonella* to survive intracellularly in amoebae, and the comparison of these mechanisms with those used to survive in other phagocytic cells, will allow us to understand how these bacteria acquired the ability to colonize an environment so hostile as the macrophages of an animal host during evolution.

Very few studies have addressed the molecular mechanisms allowing the intracellular survival of *Salmonella* within amoebae. A 2004 study showed that genes in the virulence plasmid and SPI-1 of *S*. Dublin contribute to the interaction between this bacterium and the amoeba *A. rhysodes* (Tezcan-Merdol et al., 2004). Other study on *A. polifaga* determined than both PhoP/PhoQ and SPI-2 are essential for the survival of *S*. Typhimurium inside this amoeba, while SPI-1 is dispensable for this process (Bleasdale et al., 2009). These observations indicate that some genes involved in the interaction between *Salmonella* and the phagocytic cells of animal hosts also play a role in its interaction with free living amoebea. On the other hand, there are a couple of reports that show the gene expression of different *Salmonella* serotypes within protozoa. A first study on the transcriptional profile of *S*. Choleraesuis within *A. rhysodes* showed that genes on SPI-1, SPI-4 and SPI-5 are highly expressed at 12 h post infection, while genes in SPI-2, SPI-3, SPI-9 and SPI-11 are expressed preferentially at 2 h post infection. These expression patters suggest a temporal regulation of these genes, allowing the interaction of *Salmonella* with this amoeba (Feng et al., 2009). Other study evaluated the transcriptional profile of *S*. Typhimurium within *Tetrahymena* (Rehfuss et al., 2011), and determined that several genes required to survive and replicate within macrophages and epithelial cells are overexpressed intracellularly in *Tetrahymena.* These genes include those regulated by the two-component system PhoP/PhoQ, such as *pagC*, *pagK*, *envE*, *virK*, *mgtB* and *mgtC*; genes encoding structural components of the $T3SS_{SPI-2}$, like *ssaV*; and genes encoding effectors secreted by this system, like *sifB* and *sopB*. The overexpression of *adiA* was also observed. This gene encodes an arginine decarboxylase involved in the resistance to acid pH. The resistance to acid pH in the phagosomes of this protozoan would be a common mechanism allowing the survival of this bacterium inside the phagosomes of macrophages, neutrophils and dendritic cells. Once again, these observations support the idea that *Salmonella* uses similar molecular mechanisms to survive within macrophages and free living amoebae.

8.5 *Dictyostelium discoideum* as a model organism to study host-microbe interactions

To understand the processes involved in the intracellular survival of *S*. Typhimurium in amoeba, a valid model is needed. Among the variety of amoeba especies, we decided to use the social amoeba *D. discoideum* as this organism has proven to be a useful model to study relevant aspects of the host-pathogen interaction. In addition, many intracellular pathogens can survive within *D. discoideum* cells using similar mechanisms to those used in other host cells.

This eukaryotic organism has three life cycles in nature: (1) as a free-living amoeba, feeding on bacteria and fungi by phagocytosis; (2) forming multicellular aggregates with cell differentiation to develop spores in conditions of nutrient starvation, in what is called the social cycle; and (3) forming macrocysts due to sexual reproduction to allow genetic recombination when cells are starving in dark and humid conditions (Flowers et al., 2010; Bloomfield et al., 2010). Currently, several established axenic lines of this amoeba are available, facilitating the work in this organism. Furthermore, this is a genetically plastic organism and several genetic tools are available to mutate genes of interest or to express fluorescent reporters. These tools allow the modification of host factors and the performing of live imaging microscopy (Müller-Taubenberger et al., 2013). Even more, several of these tools are available at the Dicty Stock Center, a central repository for *D. discoideum* genomes, strains and plasmids (Fey et al., 2013). On the other hand, the 34 Mpb genome of this organism was sequenced and published in 2005, and it is predicted to contain over 12,500 encoded proteins (Eichinger et al., 2005).

Regarding the literature about the interaction between *Salmonella* and *D. discoideum*, initially it was described that *S*. Typhimurium resides transiently in a vacuole and is degraded by this amoeba (Skriwan et al., 2002), as shown in **Figure 2**. In this study, gentamicin protection assays were used. Several years after that initial study, it was described that these kind of assays were not suitable to study the interaction between *Salmonella* and *D. discoideum*, as the antibiotic enters in the amoeba killing intracellular bacteria (Sillo et al., 2011). Additionally, it was described that *S*. Typhimurium avoids been degraded by *D. discoideum* by specifically inhibiting the expression of genes related to the social development cycle of the amoeba (Sillo et al., 2011).

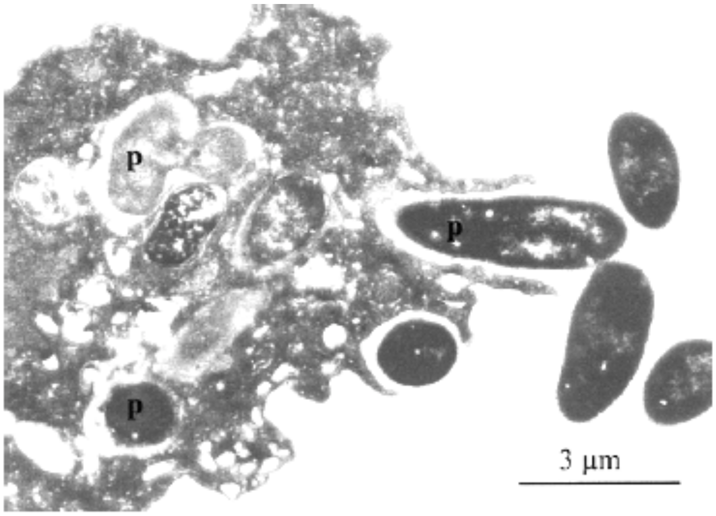


Figure 2 - Transmission electron microscopy image of *S.* Typhimurium within *D. discoideum*. The image shows the presence of *S*. Typhimurium within a vacuole at 3 h post infection*.* P indicates pathogen. Adapted from Skriwan et al., 2002.

Besides these two reports, the molecular mechanisms involved in the intracellular survival of *Salmonella* within this amoeba have not been further studied. Recently, our group described that *S*. Typhimurium 14028s is able to survive intracellularly, and proliferate at later times of infection, in *D. discoideum* strain AX4 and that mutants in genes related to virulence in other models, including $T3SS_{SPI\text{-}1}$ and $T3SS_{SPI\text{-}2}$, show defects in intracellular survival (Riquelme et al., 2016, Urrutia et al., 2018). These observations support the use of *D. discoideum* as a suitable model to study host-pathogen interactions for *Salmonella*.

On the other hand, because effectors secreted by T3SS$_{\text{SPI-1}}$ and T3SS$_{\text{SPI-2}}$, have a well-documented role in the modification of the SCV, we decided to focus on two of them: SopB (secreted by T3SS$_{\text{SPI-1}}$) and SifA (secreted via T3SS$_{\text{SPI-2}}$). These proteins are the main effectors involved in the biogenesis and maturation of the SCV in eukaryotic cells (Ramos-Morales, 2012). SopB is a phosphatidylinositol phosphatase, involved in reducing the levels of PI(4,5)P$_2$ in the nascent SCV and in modifying the proteins that interact with this compartment, in particular Rab5 (and its cognate PI3K, Vps34), Rab7 (that is involved in recruiting LAMP1, vATPase and other late endosome markers). SifA on the other hand, is involved in the manteinance of the integrity of SCV membranes, by its interaction with other *Salmonella* effectors (mainly SseJ, a lipase that change the lipid composition of the SCV; SseF and SseG, proteins that anchor the SCV to the Golgi). SifA also interacts with the molecular motor kinesin using SKIP as adaptor protein, this interaction is crucial to allow formation of SIFs. Therefore, this Thesis aimed to characterize for the first time the role played by *S*. Typhimurium effectors SopB and SifA in the modification of the intracellular vacuole that *Salmonella* uses to reside in *D. discoideum*, explaining diverse aspects of the survival of this pathogen in the environment and its potential to exploit phagocytic amoebae as a reservoir and their role in the evolution of *Salmonella* as intracellular pathogen.

9. HYPOTHESIS AND AIMS

9.1 Hypothesis

"Effector proteins SopB and SifA modify the proteome of the vacuolar compartment containing *S*. Typhimurium in *D*. *discoideum*, contributing to the intracellular survival of the pathogen in this host"

9.2 General Aim

To define the contribution of effectors SopB and SifA in the modification of the protein content of the vacuolar compartment containing *S*. Typhimurium in *D. discoideum* and in the intracellular survival of the pathogen in this host.

9.3 Specific Aims

1) To determine the contribution of effectors SopB and SifA to the intracellular survival of *S*. Typhimurium in *D. discoideum*.
    a. Construction of *S*. Typhimurium mutants ∆*sopB* and ∆*sifA*.
    b. Cloning of *sopB* and *sifA* genes in the pBAD-TOPO plasmid for complementation assays.
    c. Intracellular survival assays, to evaluate the internalization and intracellular survival of the wild-type strain, each mutant and the corresponding mutants complemented in *trans*.

2) To confirm the presence of a vacuolar compartment containing *S*. Typhimurium in *D. discoideum*.
    a. Confirm the presence of a membranous compartment containing *S*. Typhimurium within *D. discoideum* by transmission electron microscopy.
    b. Confirm the presence of the vATPase (VatM) in the SCV-like compartment by confocal microscopy, using a *D. discoideum* strain expressing a VatM-GFP fusion.

3) To determine the role of SopB and SifA in defining the repertoire of host proteins associated to the vacuolar compartment containing *S*. Typhimurium in *D. discoideum*.
    a. Infection assays using the wild-type strain, Δ*sopB* and Δ*sifA* mutants.
    b. Subcellular fractionation of infected cells to obtain a fraction enriched in intact vacuoles containing *S*. Typhimurium.
    c. Analysis of the vacuoles by quantitative proteomics, identification of host proteins recruited to these vacuoles by the wild-type strain, Δ*sopB* and Δ*sifA* mutants, and comparative analysis.

10. MATERIALS AND METHODS

10.1 Bacterial growth

The bacterial strains used in the present study are listed in **Table 1**. Bacteria were routinely grown in Luria-Bertani (LB) medium (10 g/L tryptone, 5 g/L yeast extract, 5 g/L NaCl) at 37ºC with aeration. LB medium was supplemented with ampicillin (Amp; 100 mg/L), chloramphenicol (Cam; 20 mg/L) or kanamycin (Kan; 75 mg/L) as appropriate. Media were solidified by the addition of agar (15 g/L).

Table 1 – Bacterial strains used in this study.

Strain	Characteristics / Genotype	Origin / Reference
***S*. Typhimurium**		
WT	*S*. Typhimurium wild-type strain14028s	Laboratory Collection
Δ*invA*	14028s Δ*invA*::Kan	This study
Δ*ssaV*	14028s Δ*ssaV*::Kan	This study
Δ*sopB*	14028s Δ*sopB*::Kan	This study
Δ*sifA*	14028s Δ*sifA*::Kan	This study
WT / pBAD	14028s / pBAD-TOPO	This study
Δ*sopB* / pBAD	14028s Δ*sopB*::Kan / pBAD-TOPO	This study
Δ*sifA* / pBAD	14028s Δ*sifA*::Kan / pBAD-TOPO	This study
Δ*sopB* / p*sopB*	14028s Δ*sopB*::Kan /p*sopB*	This study
Δ*sifA* / p*sifA*	14028s Δ*sifA*::Kan / p*sifA*	This study
WT / pFCcGi	14028s / pFCcGi	Figueira et al., 2013
E. coli		
TOP10	F$^-$ *mcrA* Δ(*mrr-hsd* RMS-*mcrBC*) Φ80*lacZ*ΔM15 Δ*lacX74 recA1 araD139* Δ(*ara-leu*)7697 *galUK galK rpsL* (Str^R) *endA1 nupG*	Invitrogen
K. aerogenes		
Wild-type strain	DBS0305928	Dicty Stock Center (DictyBase)

10.2 Construction of mutant strains

S. Typhimurium mutants with specific deletions of *sopB*, *sifA*, *invA* and *ssaV* genes and the concomitant insertion of a Kan-resistance cassette were constructed using the Lambda-Red recombination method, also referred to as the "Red-swap" method (Datsenko & Wanner, 2000; Santiviago et al., 2009). PCR primers 60 bases long were synthesized with 40 nt on the 5' ends corresponding to the ends of the desired deletion (**Table 2**). The and the 20 nt at the 3' of each primer were complementary to the 5' or 3' end of a Kan-resistance cassette flanked by FRT sites (Flp recombinase target sequence) present in plasmid pCLF4 (GenBank accession number HM047089). PCR amplifications using pCLF4 as template DNA were carried out as described below.

Taq Buffer 10x	5	µL
$MgCl_2$ (50 mM)	1.5	µL
Primer 1 (10 µM)	1	µL
Primer 2 (10 µM)	1	µL
dNTPs (10 mM each)	1	µL
pCLF4 (100 nM)	0.5	µL
Taq DNA polymerase 5 U/µL (Invitrogen)	0.3	µL
H_2O	39.7	µL
	50	µL

95ºC	2 m	
95ºC	30 s	30 cycles
55ºC	30 s	
72ºC	2 m	
72ºC	5 m	

S. Typhimurium strain 14028s carrying the temperature-sensitive plasmid pKD46, which expresses the Lambda-Red recombinase system, was grown to an OD_{600nm} of 0.5-0.6 at 30ºC in LB medium containing Amp and L-arabinose (10 mM). Bacteria were made electrocompetent by sequential washes with ice-cold sterile

10% glycerol, and transformed with ~500 ng of each purified PCR product. Transformants were selected on LB agar plates containing Kan at 37ºC. The presence of each mutation was confirmed by PCR amplification using primers flanking the sites of substitution (**Table 2**).

Table 2 - Oligonucleotides used in this study. Underlined sequences anneal to the 5’ or 3’ end of the antibiotic-resistance cassette in template vector pCLF4.

Primer	Sequence
*invA*_H1+P1	GATACCTATAGTGCTGCTTTCTCTACTTAACAGTGCTCGTGTGCAGGCTGGAGCTGCTTC
*invA*_H2+P2	AATTAAGCCCTTATATTGTTTTTATAACATTCACTGACTTCATATGAATATCCTCCTTAG
*invA*_Out5	TGAGGGTTCGCTATTAACCG
*invA*_Out3	TGGCAATGCAAATAAATCCA
*ssaV*_H1+P1	TGGAGTCGCAATGCGTTCATGGTTAGGTGAGGGAGTCAGGGTGCAGGCTGGAGCTGCTTC
*ssaV*_H2+P2	TTGCATCAATTCATTCTTCATTGTCCGCCAACTCCTCTTCCATATGAATATCCTCCTTAG
*ssaV*_Out5	TGCTTTTTAAAGCGTTGGCT
*ssaV*_Out3	AACTCGCCCATAAATACCCC
*sopB*_H1+P1	TAAAAACGCTATGCAAATACAGAGCTTCTATCACTCAGCTGTGCAGGCTGGAGCTGCTTC
*sopB*_H2+P2	ACCTCAAGACTCAAGATGTGATTAATGAAGAAATGCCTTTCATATGAATATCCTCCTTAG
*sopB*_Out5	AGAGACAAAAGCGGCAAAAA
*sopB*_Out3	GGCATAAAGGGACAGCACAT
*sifA*_H1+P1	TGAGATTAATATGCCGATTACTATAGGGAATGGTTTTTAGTGCAGGCTGGAGCTGCTTC
*sifA*_H2+P2	TCGTCTGATTTTATAAAAAACAACATAAACAGCCGCTTTGCATATGAATATCCTCCTTAG
*sifA*_Out5	ATCCGCGGTAGTCCTTCTTT
*sifA*_Out3	TATTGTGCCTGGCAAGAGGT
pBAD_Fw	ATGCCATAGCATTTTTATCC
pBAD_Rv	GATTTAATCTGTATCAGG

Each mutant was assayed for Amp sensitivity (to confirm the loss of pKD46) and transferred to the wild-type background by generalized transduction using phage P22 HT105/1 *int*-201. First, phage lysates were obtained by mixing 1 mL of P22 broth with 0.2 mL of an overnight (O/N) culture of the corresponding donor strain. Following an O/N incubation at 37ºC in an orbital shaker, the culture was centrifuged during 2 min at 13,000 rpm to pellet the cell debris. Next, several drops of $CHCl_3$ were added and the mix was vortexed. Each lysate was stored at 4ºC. For transductions, 200 µL of an O/N culture of the wild-type strain was mixed with 5-10 µL of a P22 phage lysate prepared from the donor strain and incubated at room temperature during 15 min to allow phage adsorption, and then 30 min at 37ºC to allow phenotypic expression of the antibiotic resistance gene. Each transduction mix was plated on LB agar containing the appropriate antibiotics and incubated at 37ºC O/N. The transductants were cleared from remaining P22 phage particles by several rounds of isolation for single colonies on EBU plates and were checked for sensitivity to lytic phage P22 H5 by cross-streaking (Maloy, 1990).

10.3 Cloning and complementation

For complementation assays, genes *sopB* and *sifA* were PCR amplified from gDNA obtained from the wild-type strain using primers flanking the gene and including the promoter region (**Table 2**). PCR products were ligated to pBAD-TOPO vector (Invitrogen) according to the manufacturer instructions. Ligation products were transformed into chemocompetent *E. coli* TOP10 cells

(Invitrogen) and transformant clones were selected on LB agar plates containing Amp. Orientation of the insert in each recombinant plasmid generated was determined by PCR using different mixes of primers flanking the site of insertion (pBAD_Fw and pBAD_Rv) and those used to amplify each gene (**Table 2**). One clone harbouring a recombinant plasmid with the cloned gene in the same orientation of the P_{araBAD} promoter in the plasmid was selected. Each plasmid was purified using the QIAPrep Spin Miniprep Kit (Qiagen) and transformed in the corresponding mutant strain for complementation assays. In addition, mutant strains containing the empty pBAD-TOPO vector were also generated as controls.

10.4 Amoeba growing conditions

Dictyostelium discoideum strains used in this study are listed in **Table 3** and were cultured according to standard protocols (Fey et al., 2007). Amoeba were first grown in SM agar (10 g/L tryptone, 1 g/L yeast extract, 1.08 g/L $MgSO_4 \times 7H_2O$, 1.9 g/L KH_2PO_4, 0.78 g/L $K_2HPO_4 \times 3H_2O$, 10 g/L glucose, 20 g/L agar agar) on top of a confluent lawn of *Klebsiella aerogenes* DBS0305928 at 23ºC, until phagocytosis plaques were visible. Growing cells were transferred to liquid HL5 media (14 g/L tryptone, 7 g/L yeast extract, 0.35 g/L Na_2HPO_4, 1.2 g/L KH_2PO_4, 15.2 g/L glucose) containing Amp (100 µg/mL) and streptomycin (Str; 300 µg/mL), and incubated at 23ºC in tissue culture flasks when adherent cells were needed or in glass flasks when cells in suspension were needed. Cells were subcultured and used in the different assays when they reached 70-80% confluence in tissue culture flasks or when they reached exponential phase (1-2 x 10^6 cells/mL) when cultured in suspension. G418 (20 µg/mL) was added to HL5 media when required. To ensure the use of healthy cells, only subcultures 1 to 6 obtained in the course of two weeks at most were used.

Table 3 - Amoeba strains used in this study.

Strain	Characteristics	Reference
D. discoideum AX2	Wild-type axenic strain (DictyBase ID DBS0235519)	Watts & Ashworth, 1970.
D. discoideum AX2 VatM-GFP	Strains constitutively expressing the vacuolar ATPase VatM fused to GFP from plasmid pDXA (DictyBase ID DBS0235537)	Clarke et al., 2002

10.5 Infection assays for confocal microscopy

D. discoideum AX2 VatM-GFP grown in suspension in HL5 medium supplemented with G418 (10 mg/L) were centrifuged at 210 x *g* (1,500 rpm) during 5 m at 4ºC and the pellet was suspended in Soerensen buffer (2 g/L KH_2PO_4, 0.36 g/L $Na_2HPO_4 \times 2H_2O$, pH 6.0). This procedure was repeated 3 times. Bacteria were prepared from overnight cultures by centrifuging at 3,420 x *g* (6,000 rpm) during 5 m at 4ºC and suspended in Soerensen buffer. Amoeba were infected using a MOI of 100 bacteria/cell and co-incubated at 23ºC during 1 h without shaking to allow internalization. After 1 h, extracellular bacteria were removed by centrifugation at 210 x *g* (1,500 rpm) during 5 m at 4ºC, and the pellet was washed in Soerensen buffer. This procedure was repeated 3 times. Finally, infected cells were suspended in Soerensen buffer and incubated for up to 4.5 h. Each sample was concentrated 5 times and 12 µL were mounted on a glass slide on top of a

100 µL layer of agarose 1% in PBS. A coverslip was placed over the sample and the borders sealed with colorless nail polish. Images were acquired with a Zeiss LSM 710 confocal microscope using the ZEN 2012 Back software (Zeiss). To detect the GFP label (amoebae), the sample was excited at 488 nm with an Argon laser and the emitted fluorescence was detected with a 493-549 nm filter. To detect mCherry label (bacteria), the sample was excited at 543 nm with a HeNe laser and fluorescence was detected with a 548-679 nm filter. All images were analysed and edited using FIJI software (Schindelin et al., 2012; Schneider et al., 2012).

10.6 Infection assays for transmission electron microscopy

Infection assays were performed as described for confocal microscopy experiments, even though samples were collected after 3 h after the infection, and cells were fixed in glutaraldehyde using reagents and protocols provided by the processing facility at *Núcleo de Servicios de Histopatología para Investigación*, *Pontificia Universidad Católica de Chile* were samples were sent for processing and mounting. Prepared grids were visualised by Transmission Electron Microscopy (TEM) at *Unidad de Microscopía Avanzada, Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile*.

10.7 Infection assays for intracellular survival

Amoebae grown in suspension in HL5 media were centrifuged at 210 x *g* (1,500 rpm) during 5 m at 4ºC, and the pellet was suspended in Soerensen buffer. This procedure was repeated 3 times. Bacteria were prepared from O/N cultures by centrifuging at 3,420 x *g* (6,000 rpm) during 5 m at 4ºC and suspended in Soerensen buffer. Amoebae were infected using a multiplicity of infection (MOI) of 100 bacteria/cell and co-incubated at 23ºC during 1 h without shaking to allow internalization. After 1 h, the mixture was centrifuged at 210 x *g* (1,500 rpm) during 5 m at 4ºC, and the pellet was washed in Soerensen buffer. This procedure was repeated 3 times to remove extracellular bacteria. Finally, infected cells were suspended in Soerensen buffer and further incubated for up to 6 h. For each time point analysed, an aliquot was taken to determine viable amoeba cells by Trypan staining and counting in a Neubauer chamber. Another aliquot was used to determine intracellular CFUs. To do this, infected cells were washed once with Soerensen buffer supplemented with 10 µg/mL gentamicin, centrifuged at 210 x *g* (1,500 rpm) during 5 min, washed with Soerensen buffer to remove the antibiotic and centrifuged at 210 x *g* (1,500 rpm) during 5 min. Finally, the infected cells were lysed using 0.1% Triton X-100, diluted and plated on LB agar plates. The internalization of each bacterial strain was calculated as intracellular CFUs after the hour of internalization (t=0) divided by the inoculated CFUs. Intracellular survival was calculated as the intracellular CFUs at each time analysed (t=3 and t=6) divided by the intracellular CFUs at t=0. Statistical significance was determined by a two-way ANOVA with Dunnett’s test. All experiments were performed at least as biological triplicates.

For experiments using the PI3K inhibitor LY294002 (2-(4-Morpholinyl)-8-phenyl-1(4H)-benzopyran-4-one), amoebae were incubated in Soerensen buffer containing LY294002 10 µM or the equivalent volume of the vehicle (DMSO) during 1 h prior to the infection. After that, the assay was performed as described above maintaining the LY294002 (or DMSO) in all solutions during the course of the experiment at the same concentration.

10.8 Infection assays for enrichment in SCV-like compartments

Amoebae grown in T225 tissue culture flasks in HL5 medium were washed 3 times in Soerensen buffer. Bacteria from late exponential cultures were collected by centrifugation at 3,420 x *g* (6,000 rpm) during 5 min at 4ºC, and suspended in Soerensen buffer. For the wild-type strain 1.2 x 10^8 amoebae were infected using a MOI of 100 bacteria/cell, and for the ∆*sopB* and ∆*sifA* mutants 2.4 x 10^8 amoebae were infected also using a MOI of 100 bacteria/cell. In both cases, amoebae and bacteria were co-incubated at 23ºC to allow internalization. After 1 h, extracellular bacteria were removed by washing 3 times with Soerensen buffer. Finally, infected cells were suspended in Soerensen buffer and incubated during 3 h at 23ºC.

10.9 SCV-like compartment enrichment using density gradients

Infected *D. discoideum* cells were lysed and treated to obtain a fraction enriched in compartments containing *S*. Typhimurium using the protocol described in

Santos et al., 2015 with modifications. Cells infected for 3 h with the different *S*. Typhimurium strains were washed 3 times using Homogenization Buffer (HB; 150 mM sucrose, 0.5 mM EGTA, 20 mM HEPES pH 7.4). Cells were then scrapped from the tissue culture flask and suspended in 4 mL of HB supplemented with Complete Protease Inhibitor (Roche) and 5 µg/mL Cytochalasin D, to decrease organelle clumping (HB complete). Cell suspension was then transferred to a Dounce homogenizer (Sigma-Aldrich) and lysed by stroking the pestle 35-40 times (1 stroke = 1 up + 1 down) until more than 80% of free nuclei were visible. The homogenate was centrifuged at 100 x *g* (1,000 rpm) during 5 min at 4ºC to remove cell debris, the supernatant was collected, and the pellet suspended in 1 mL of HB complete and centrifuged again. This procedure was repeated 2 times and the supernatants from the 3 centrifugations were combined (~6 mL) and called post-nuclear supernatant (PNS). In the case of the PNS from non-infected control, 1 x 10^8 CFU of the wild-type strain were added. Each PNS was loaded on top of a linear 10% (1.08 g/cm^3) to 25% (1.15 g/cm^3) OptiPrep gradient (Sigma-Aldrich) in HB with a 50% cushion prepared in 13.2 mL tubes (Beckman Coulter). Gradients were centrifuged at 210,000 x *g* (35,000 rpm) during 3 h at 4ºC using a SW-41 swinging bucket rotor (Eppendorf) in an Optima L-100 XP Ultracentrifuge (Beckman Coulter) with low acceleration and no brake settings. After centrifugation, 1 mL fractions were collected from the top of the gradient with a micropipette. Each fraction was analysed by titrating the CFU number by serial dilution and plating, and by measuring the refraction index in a refractometer to determine its density. Fractions containing bacteria were also analysed by ELISA to determine the presence of intact vacuoles.

10.10 ELISA for *Salmonella* quantification

The anti-*Salmonella* ELISA was performed as described in Santos et al., 2015. A 96-well ELISA plate (Nunclon Imobilon) was coated with 70 µL of the polyclonal rabbit anti-*Salmonella* capture antibody ab35156 (Abcam) suspended in PBS (5 µg/mL; 1:1000) and incubated O/N at 4ºC. The coated plate was washed twice with PBS and blocked using 200 µL of blocking buffer (2% BSA from Sigma-Aldrich in PBS) during 1.5 h at room temperature. The plate was then washed four times with PBS and the different samples were loaded. To quantify the bacteria per fraction, a standard curve of dilutions of a known number of bacteria was prepared. For this, serial 2-fold dilutions were prepared containing 3.1 x 10^5 to 3.2 x 10^8 bacteria/mL. For the fraction samples, an aliquot of 50 µL from F6 to F9 were diluted in 500 µL of HB (for pre-osmotic shock treatment) or in H_2O (for osmotic shock treatment). Next, 50 µL of each sample was loaded on different wells of the ELISA plate and incubated during 1 h at room temperature. After that, the plate was washed four times with PBS and incubated O/N at 4ºC with 50 µL of detection antibody diluted in blocking buffer (biotinylated rabbit anti-*Salmonella* 2 µg/mL; 1:2000). Then, the plate was washed four times with PBS and incubated with 70 µL of Streptavidin-Peroxidase diluted in blocking buffer (Sigma-Aldrich, 1 mg/mL, 1:5000) during 1 h at room temperature. After that, the plate was washed 6 times with PBS, the buffer was removed, 100 µL of SigmaFast OPD substrate solution (Sigma-Aldrich) was added, and the plate was incubated during 20-30 min at room temperature protected from light. The reaction was stopped by adding 50 µL of 10% SDS, and absorbance at 450 nm was determined in a FluoSTAR Omega microplate reader (BMG Labtech) at 450 nm.

10.11 Protein precipitation

Protein content in each fraction obtained as described in section 10.9 was determined using the Micro BCA Protein Assay kit (Thermo Fisher Scientific). Then, each sample was precipitated to obtain 20 µg of protein using the chloroform/methanol method (Wessel and Flügge, 1984). To do this, 1 volume of sample containing 20 µg of protein was mixed thoroughly with 4 volumes of methanol 100%, and then 1 volume of chloroform was added and mixed. After that, 3 volumes of MilliQ water were added, the mixture was thoroughly vortexed and then centrifuged at 15,700 x *g* (13,000 rpm) during 10 min at 4ºC. The organic (upper) layer was discarded and 3 volumes of methanol 100% were added, mixed thoroughly and centrifuged as mentioned. Finally, the supernatant was discarded and the protein pellet was air dried and stored frozen at -20ºC.

10.12 SDS-PAGE

The treatment of samples for proteomic studies was performed as described in Santos et al., 2015. The protein pellets corresponding to F6 and F7 obtained as described in section 10.11 from each experiment and condition were combined. To do this, 30 µL of Laemmli sample buffer (Bio-Rad; 62.5 mM Tris-HCl pH 6.8, 10% glycerol, 1% LDS, 0.005% bromophenol blue) were added to the tube containing the F6 sample, and then heated at 95ºC during 10 min. Then, the liquid was transferred to the tube containing the F7 sample, and heated at 95ºC during 10 min. The samples were loaded in a NuPAGE 4-12% Bis-Tris pre-cast Gel (Invitrogen) and run at 200 V constant during 45 min. Kaleidoscope protein standard (Bio-Rad) was used as molecular weight marker. The gel was then fixed during 30 min in a 10% acetic acid, 40% ethanol aqueous solution with shaking (50 rpm). Proteins were stained by O/N incubation in Colloidal Coomassie Blue G-250 working solution (8% ammonium sulfate, 0.8% phosphoric acid, 0.08% Coomassie Blue G-250, 20% ethanol)., and destained in MilliQ water until bands were visible.

10.13 Mass spectrometry sample preparation

The treatment of each sample for mass spectrometry was performed as described in Santos et al., 2015. Each gel lane obtained as described in section 10.12 corresponding to a sample was cut into 10 pieces and destained in 100 µL of a 1:1 mixture of 0.2 M ammonium bicarbonate pH 8 and acetonitrile. Each gel piece was incubated at 30ºC during 30 min with shaking (1,400 rpm). The liquid was discarded and the process repeated one more time. For any gel pieces still retaining the Coomassie staining, the procedure was repeated using a mixture of 60% 0.2 M ammonium bicarbonate pH 8 and 40% acetonitrile. Then, the cysteines present in the proteins were reduced and alkylated to prevent the formation of chimeras. To do this, the gel pieces were incubated in 100 µL of 10 mM DTT in

67 mM ammonium bicarbonate pH 8 at 56ºC during 1 h with shaking (1,400 rpm). Samples were cooled down at room temperature, the liquid was discarded and the gel pieces were washed twice with MilliQ water. The reduced cysteines were then alkylated using 55 mM iodoacetamide in 67 mM ammonium bicarbonate pH 8 and incubating at 25ºC during 45 min with shaking (1,400 rpm). Then, the liquid was discarded and the samples washed twice with MilliQ water. The gel pieces were then desiccated by adding 100 µL of 100% acetonitrile and incubating at 30ºC during 30 min with shaking (1,400 rpm). The liquid was then removed and the gel pieces let to air dry. In-gel protein digestion was performed by O/N incubation of the gel pieces with 1 µg of Sequencing Grade Modified Trypsin (Promega) in 67 mM ammonium bicarbonate pH 8 at 37ºC. The next day, peptides were extracted by eluting them using 100 µL of a mixture containing 42.5% 50 mM ammonium bicarbonate, 42.5% acetonitrile and 5% formic acid, and incubating at 30ºC during 1 h with shaking (1,400 rpm). The liquid was recovered and transferred to a new tube, the procedure was repeated one more time, and the samples were stored frozen at -20ºC until further use.

On the day prior to mass spectrometry analysis, the samples were dried using a lyophilizer and suspended in 100 µL of solvent A (2% acetonitrile, 0.1% formic acid), and sonicated during 10 min in a water bath. The samples were then desalted using Bond Elute OMIX C18 tip filters (Agilent) according to the manufacturer instructions, and the peptides were finally eluted in 100 µL of elution solvent (50% acetonitrile, 1% formic acid in H_2O). These samples were lyophilized again and suspended in 10% of solvent A, sonicated during 10 min in a water bath, the protein concentration was measured in a NanoDrop and finally transferred to the injection vials.

10.14 LC MS/MS data acquisition

Tryptic digests were analyzed by nanoLC-MS/MS. Each sample was injected into a nano-HPLC system (EASY-nLC 1000, Thermo Scientific) fitted with a reverse-phase column (Acclaim column, 15 cm x 50 μm ID, PepMap RSLC C18, 2 μm, 100 Å pore size, Thermo Scientific) equilibrated in solvent A (2% acetonitrile, 0.1% formic acid). Peptides were separated at a flow rate of 300 nL/min on a linear gradient of 3% to 55% solvent B (80% acetonitrile, 0.08% formic acid) during 30 min. Peptide analysis was conducted in a Q-Exactive Plus mass spectrometer (Thermo-Scientific) set in data-dependent acquisition mode using a 30 s dynamic exclusion list. A resolution of 70,000 (at m/z 400) was used for MS scans. The 10 most intense ions were selected for HCD fragmentation and fragments were analyzed in the Orbitrap.

10.15 Proteomic data analysis

A target-decoy database including sequences from *Dictyostelium discoideum* (taxon identifier: 44689), *Salmonella enterica* subspecies *enterica* serovar Typhimurium strain 14028s (taxon identifier: 588858) downloaded from Uniprot consortium in March 2018, and 127 most common mass spectrometry contaminants was generated using PatternLab for Proteomics (version 4.0)

(Carvalho et al., 2016). For protein identification, the Comet search engine was set as follows: tryptic peptides; oxidation of methionine and carbamidomethylation as variable modifications; and 40 ppm of tolerance from the measured precursor m/z. XCorr and Z-Score were used as the primary and secondary search engine scores, respectively. Peptide spectrum matches were filtered using the Search Engine Processor (SEPro) and acceptable false discovery rate (FDR) criteria was set on 1% at the protein level. PatternLab's Approximately Area Proportional Venn Diagram module was used to perform comparisons between conditions and to determine proteins uniquely identified in each situation. Proteins found in at least three biological replicates of one condition were considered as "uniquely identified" when absent in all replicates of the other condition. For enrichment analysis, the PatternLab TFold module was used to generate a volcano plot of the samples. This tool maximizes the identifications of proteins differentially expressed between two conditions that satisfies both a Fold-change cutoff (that varies with the *t*-test P-value) and a stringency criterion that aims to detect proteins of low abundance under a Benjamini and Hochberg False Discovery Rate (FDR) estimator. For all comparisons, the FDR was fixed at 0.05, meaning that a maximum of 5% of the proteins identified could represent a false positive. The TFold module then explored several values of the F-Stringency parameter and selected the one that maximizes the number of differentially expressed proteins between the two datasets, for the specified Q-value of 0.05, which is the adjusted P-value found using the FDR approach optimised by analysing the distribution of the P-values obtained during the multiple tests in the comparison (Carvalho et al., 2012; Carvalho et al., 2012b).

11. RESULTS

11.1 Specific Aim 1: To determine the contribution of effectors SopB and SifA to the intracellular survival of *S*. Typhimurium in *D. discoideum*

Using the Red-swap allelic exchange method (Datsenko & Wanner, 2000; Santiviago et al., 2009) we generated deletion mutants of *S*. Typhimurium for genes *invA* (encoding a structural component of $T3SS_{SPI-1}$), *ssaV* (encoding a structural component of $T3SS_{SPI-2}$), *sopB* (encoding an effector protein secreted by $T3SS_{SPI-1}$) and *sifA* (encoding an effector protein secreted by $T3SS_{SPI-2}$).

Infection assays using the different strains were performed to determine their intracellular survival in *D. discoideum* over time. Amoebae were infected at a MOI of 100 bacteria/cell and incubated for 1 h at 23ºC to allow the internalization of bacteria. These infection conditions were defined by our group in a previously published work (Riquelme et al., 2016), as they maximize the number of infected cells and intracellular titers while maintaining the number of viable *D. discoideum* cells during the assay. Infected cells were washed to remove extracellular bacteria and incubated up to 6 h. Samples were taken at t=0 (1 hour post infection, hpi), t=3 and t=6 (3 or 6 h after t=0). The internalization percentage was calculated as the intracellular bacteria at t=0 divided by the inoculum. Intracellular survival was calculated as the number of intracellular bacteria per cell at the different times divided by the number of intracellular bacteria per cell at t=0. Results from these experiments are shown in **Figures 3** and **4**. It is worth mentioning that the internalization percentages are similar between the different strains (**Figures 3A** and **4A**), so we can conclude that the deletion of any of these genes does not affect the ability of *D. discoideum* AX2 to internalize *S*. Typhimurium. In addition, none of the strains tested significatively changed the number of viable amoebae during the course of the experiment, suggesting that there are no differential toxic effects exerted by any of these strains (**Figures 3B** and **4B**). On the other hand, we observed that the deletion of *ssaV* causes an important reduction in the intracellular population of bacteria from 3 h and onwards, indicating that $\text{T3SS}_{\text{SPI-2}}$ is required for intracellular survival in *D. discoideum* even in early stages of infection. Furthermore, at 6 h post infection we observed that all mutants tested are in a lower proportion as compared to the wild-type strain, indicating that mutants in components of the two T3SS and effectors *sopB* and *sifA* are defective for intracellular survival in *D. discoideum* at later times during infection.

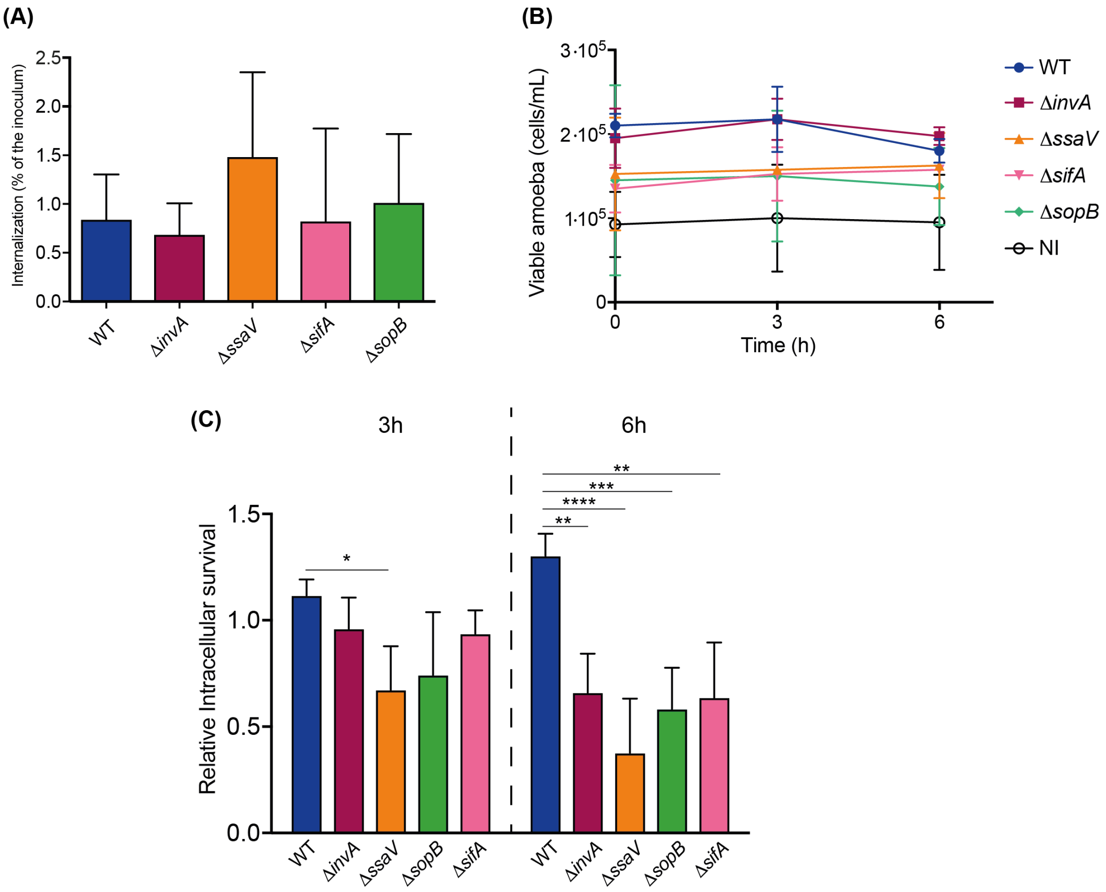


Figure 3 - Intracellular survival of *Salmonella* Typhimurium 14028s and derived mutants within *Dictyostelium discoideum* AX2 using infection assays. (A) Population of viable amoeba at each time post infection. Statistical significance was determined using one-way ANOVA **(B)** Bacterial internalization expressed as the percentage of intracellular bacteria at t=0 divided by the inoculum. Statistical significance was determined using one-way ANOVA. **(C)** Relative intracellular survival was calculated as CFU/cell at t=3 or t=6 divided by the CFU/cell at t=0. Statistical significance was determined using two-way ANOVA with Dunnet's test (* = $p<0.05$, ** = $p<0.01$, *** = $p<0.001$, **** = $p<0.0001$). All graphs show the mean values +/- SEM of at least three independent assays.

In the case of the complementation assays, no change was observed for internalization levels between the different strains (**Figure 4A**). Again, no change was detected in amoeba viability between the wild-type and the isogenic mutant strains tested (**Figure 4B**). In terms of intracellular survival, we observed that the Δ*sifA/*pBAD mutant present defects in intracellular survival at 3 h post infection, in contrast to our results using the ∆*sifA* mutant (without the pBAD plasmid). This difference is probably due to a slight effect of this plasmid on the bacterial fitness, as we also observed a slight level of replication in the case of the WT strain that we did not observed in the case of the WT/pBAD strain (compare **Figure 3C** and **Figure 4C**). At 6 h post infection it can be seen that ∆*sopB* y ∆*sifA* mutants are significatively different than the wild-type strain. This phenotype is reverted by the addition of the wild-type gene in a plasmid vector (**Figure 4C**).

Of note, none of the strains tested in this work showed a reduced in vitro growth rate (data not shown), therefore all phenotypes observed are due to their inability to survive intracellularly. Altogether, our results indicate that $T3SS_{SPI-1}$ and $T3SS_{SPI-2}$ play a role in the intracellular survival of *S*. Typhimurium in *D. discoideum* (**Figure 3**). Because ∆*sopB* and ∆*sifA* mutants also showed a decreased intracellular survival at 6 h post infection when compared to the wild-type strain (**Figures 3C** and **4C)**, our results suggest that SopB and SifA effectors play an important role in the intracellular survival of *S*. Typhimurium in *D. discoideum*. These two proteins are some of the main modulators of the SCV fate in other cellular models.

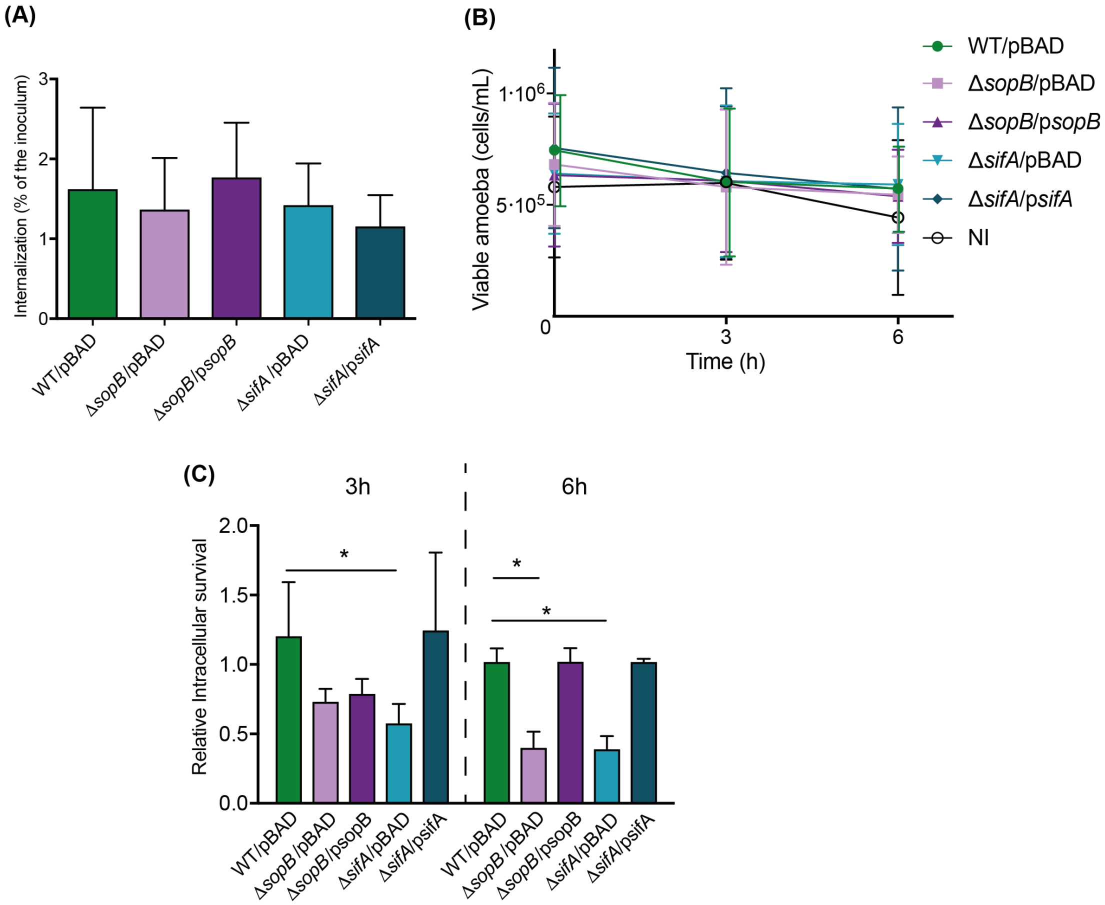


Figure 4 - Intracellular survival of *Salmonella* Typhimurium 14028s and derived mutants within *Dictyostelium discoideum* AX2 using infection assays*.* (A) Population of viable amoeba at each time post infection, statistical significance was determined using one-wat ANOVA. **(B)** Bacterial internalization expressed as the percentage of intracellular bacteria at t=0 divided by the initial inoculum. Statistical significance was determined using one-way ANOVA. **(C)** Intracellular survival expressed as CFU/cell at t=3 or t=6 divided by the CFU/cell at t=0. Statistical significance was determined using two-way ANOVA with Dunnet's test (* = *p*<0.05). All graphs show the mean values +/- SEM of at least three independent assays.

11.2 Specific Aim 2: To confirm the presence of a vacuolar compartment containing *S*. Typhimurium in *D. discoideum*

In order to evaluate the presence of a membranous compartment containing *S*. Typhimurium in *D. discoideum* cells, transmission electron microscopy (TEM) experiments were performed. **Figure 5** shows an infected amoeba, with the bacterium being surrounded by membranes, although given the resolution obtained it is not possible to evaluate the nature of such membranes.

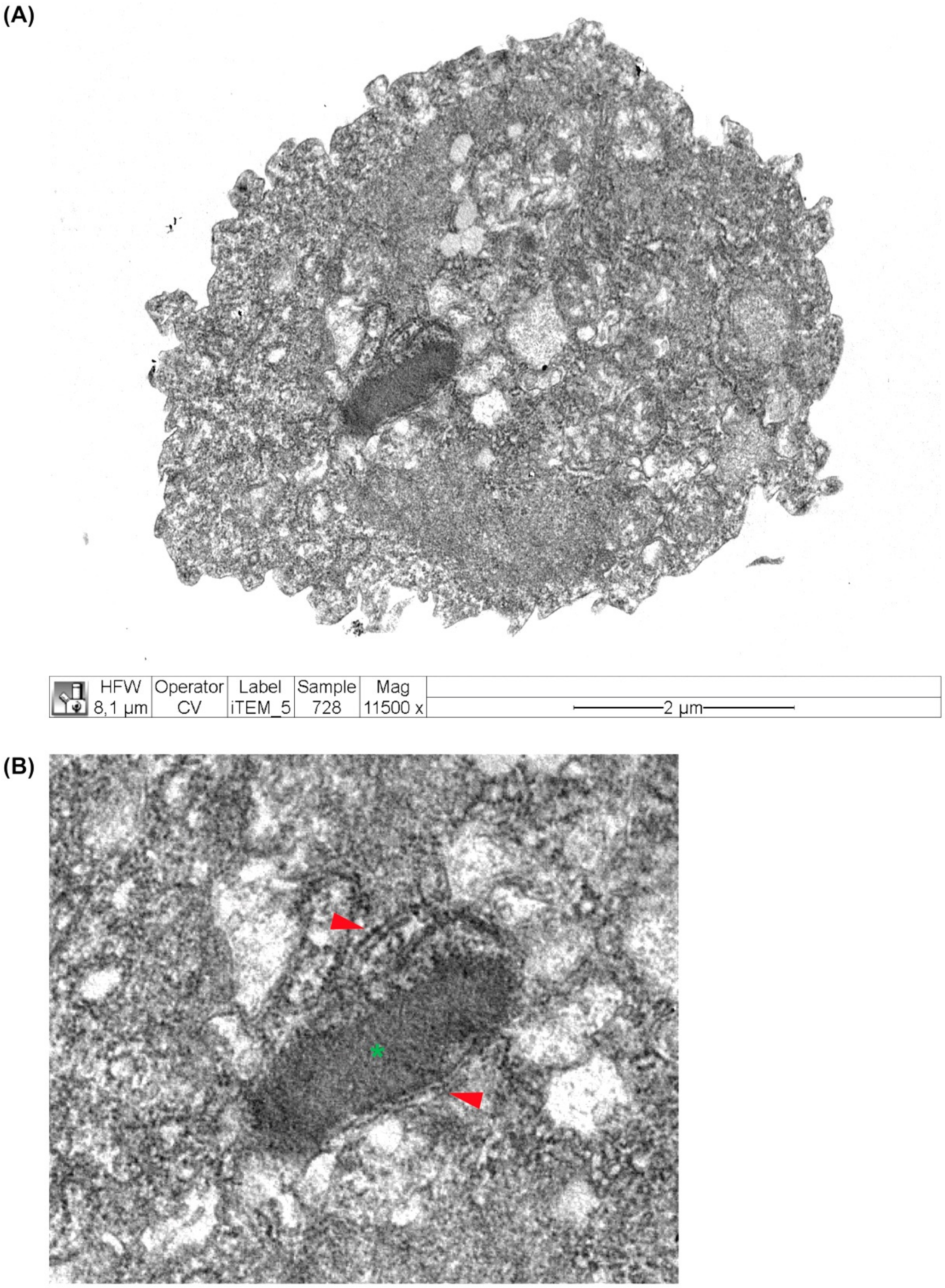
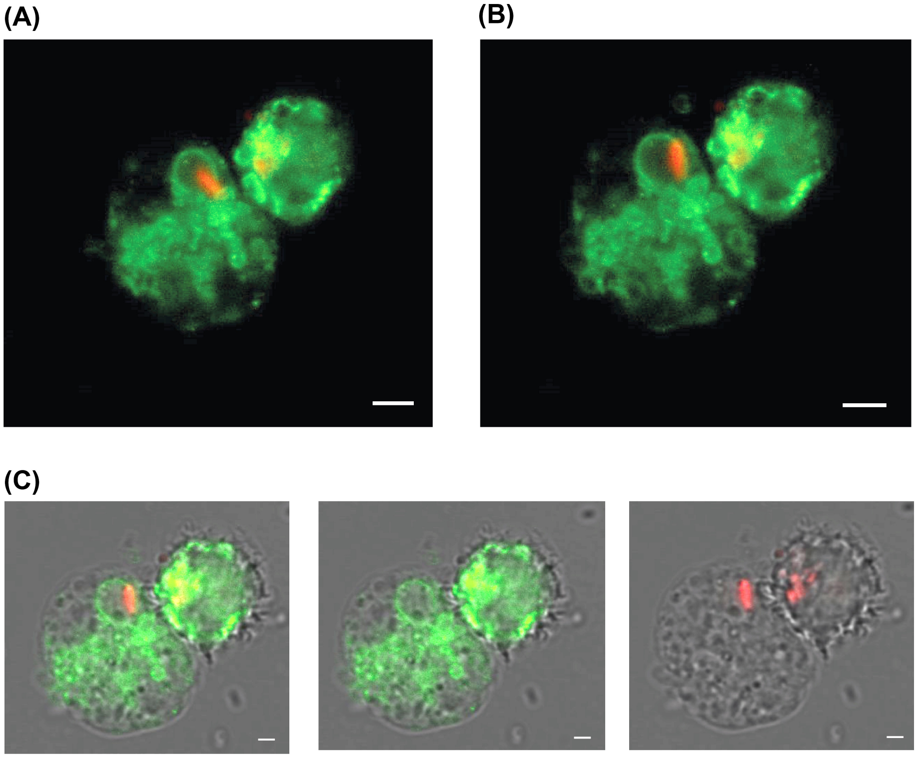


Figure 5 - *S.* Typhimurium resides in a membranous compartment in *D. discoideum.* **(A)** The image shows a *D. discoideum* cell containing one *S*. Typhimurium bacterium. **(B)** Zoom of the same cell in the image above to indicate the presence of the bacterium surrounded by a membranous compartment. Green asterisk indicates the bacterium and red arrowheads indicate double membrane segments.

As an alternative method to evaluate the presence of a vacuolar compartment containing *S*. Typhimurium in *D. discoideum*, infection assays were performed using a reporter *D. discoideum* strain that expresses the vacuolar ATPase VatM fused to GFP (VatM-GFP), allowing the visualization of vacuolar compartments by confocal microscopy. VatM is present in the membrane of different vacuolar compartments including phagosomes, endosomes, lysosomes and the contractile vacuole (Clarke et al., 2002), and is one of the proteins recruited to the SCV in other cellular models (Ramos-Morales, 2012). For these experiments, a *S*. Typhimurium wild-type strain carrying a plasmid that allows the constitutive expression of the fluorescent protein mCherry was used (14028s/pFCcGi) (Figueira et al., 2013).

Representative images of several fields where the VatM-GFP label is observed surrounding the red fluorescent bacteria at 4,5 (**Figure 6**) and 3 h (**Figure 7A**) post infection. **Figures 6A** and **6B** are two images of the same field taken with two minutes of difference that show the change of position of *Salmonella*. In addition, these are the unique images obtained where a spacious vacuolar compartment containing *S*. Typhimurium was observed. **Figure 7A** shows the presence of several bacteria per cell. Additionally, a quantitative analysis of the microscopy data indicated that 93% of the intracellular bacteria present in infected *D. discoideum* are surrounded by the VatM-GFP signal (**Figure 7B**).



Merge + BF VatM-GFP + BF WT mCherry + BF

Figure 6 – *S.* Typhimurium resides in a spacious vacuolar compartment surrounded by the vacuolar ATPase VatM at 4.5 hpi*.* *S.* Typhimurium 14028s expressing mCherry constitutively was used to infect the axenic strain *D. discoideum* AX2 VatM-GFP. **(A)** and **(B)** show two images of the same field taken with 2 minutes of difference. **(C)** Show the different channels form the image showed in **(B)**. Images were acquired at 4.5 h post infection with a Zeiss LSM 710 confocal microscope using ZEN 2012 Black software (Zeiss), and edited using FIJI software. The green fluorescence corresponds to the fusion protein VatM-GFP and the red fluorescence corresponds to bacteria. BF: brightfield. Bar is 2 μm.

Overall, these experiments strongly suggest the presence of a vacuolar compartment containing *S*. Typhimurium within infected *D. discoideum*. The membrane of this compartment is decorated with the vATPase, a marker present in the SCV in other cellular models (Ramos-Morales, 2012).

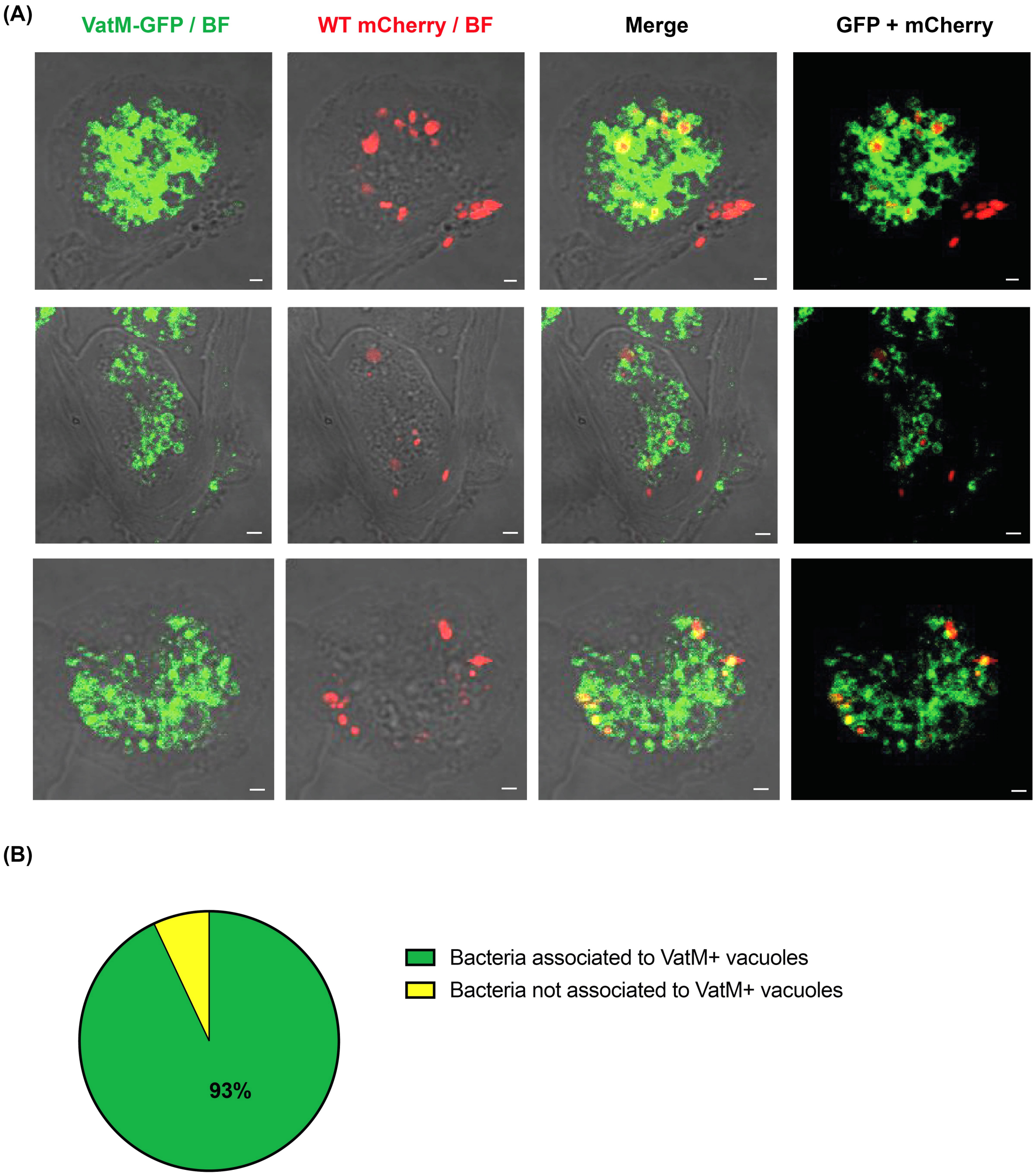


Figure 7 - *S.* Typhimurium resides in vacuolar compartments surrounded by the vacuolar ATPase VatM at 3 hpi. (A) *S.* Typhimurium 14028s expressing mCherry constitutively was used to infect the axenic strain *D. discoideum* AX2 VatM-GFP. Images were acquired at 3 h post-infection with a Zeiss LSM 710 confocal microscope using ZEN 2012 Black software (Zeiss) and edited using FIJI software. Representative fields of several biological replicates are shown, were the green fluorescence corresponds to the fusion protein VatM-GFP and the red fluorescence corresponds to bacteria. **(B)** Quantification of intracellular bacteria associated to vacuoles with the VatM-GFP label (green) and intracellular bacteria not associated to this type of vacuoles (yellow), calculated from 50 infected cells. BF: brightfield. Bar is 2 μm.

11.3 Specific Aim 3: To determine the role of SopB and SifA in defining the repertoire of host proteins associated to the vacuolar compartment containing *S*. Typhimurium in *D. discoideum*

11.3.1 Preparation of a fraction enriched in intact vacuoles containing *S*. Typhimurium wild-type and derived mutants

We adapted a protocol developed to obtain a subcellular fraction highly enriched in intact SCVs from infected HeLa cells (Santos et al., 2015) to analyse *D. discoideum* cells infected with different *S*. Typhimurium strains (**Figure 8** and **9**). As described in the Materials and Methods section, infected and control cells were lysed, and the different PNS obtained were loaded on top of linear 10-25% Optiprep gradients. After centrifugation, 12 fractions obtained from each sample were analysed. **Figure 10** shows representative results from these experiments using the wild-type strain. As shown in **Figure 10A**, in the case of fractions obtained from control samples, bacteria accumulate in F8 and F9 (1.12-1.13 g/cm^3), while in samples from infected cells (**Figure 10B**) there is a shift in bacterial distribution and bacteria also accumulate at lower-density fractions F6 and F7 (1.09-1.10 g/cm^3). It is important to mention that densities did not varied between gradients (**Figure 10C**).

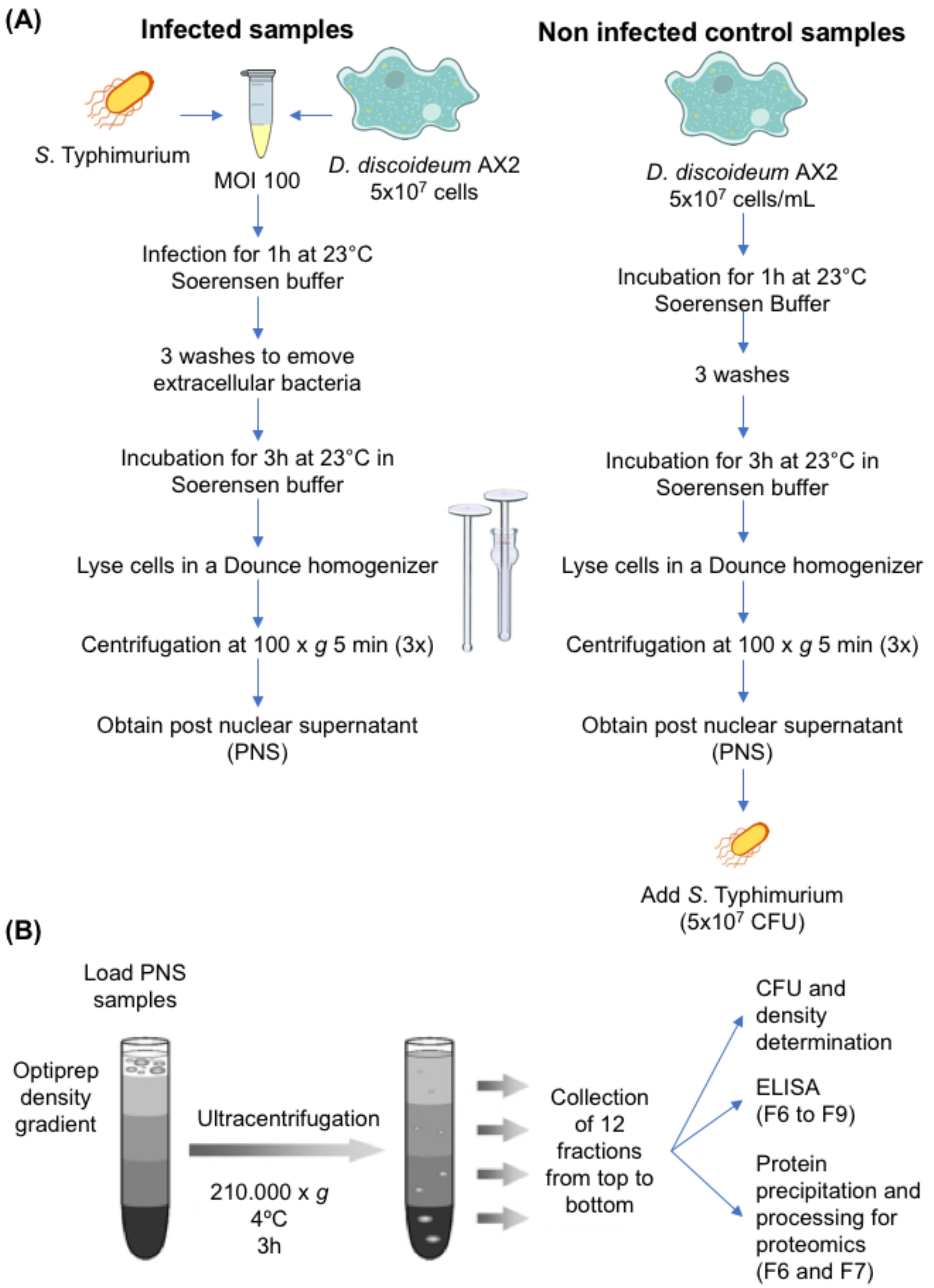


Figure 8 – Protocol used for the subcellular fractionation of *D. discoideum* cells infected with different *S.* Typhimurium strains and uninfected control cells. **(A)** Diagram of the procedure to obtain the PNS sample from infected and control cells. **(B)** Diagram of the procedure to obtain fractions of the PNS from infected and control cells and the analyses performed to each fraction.

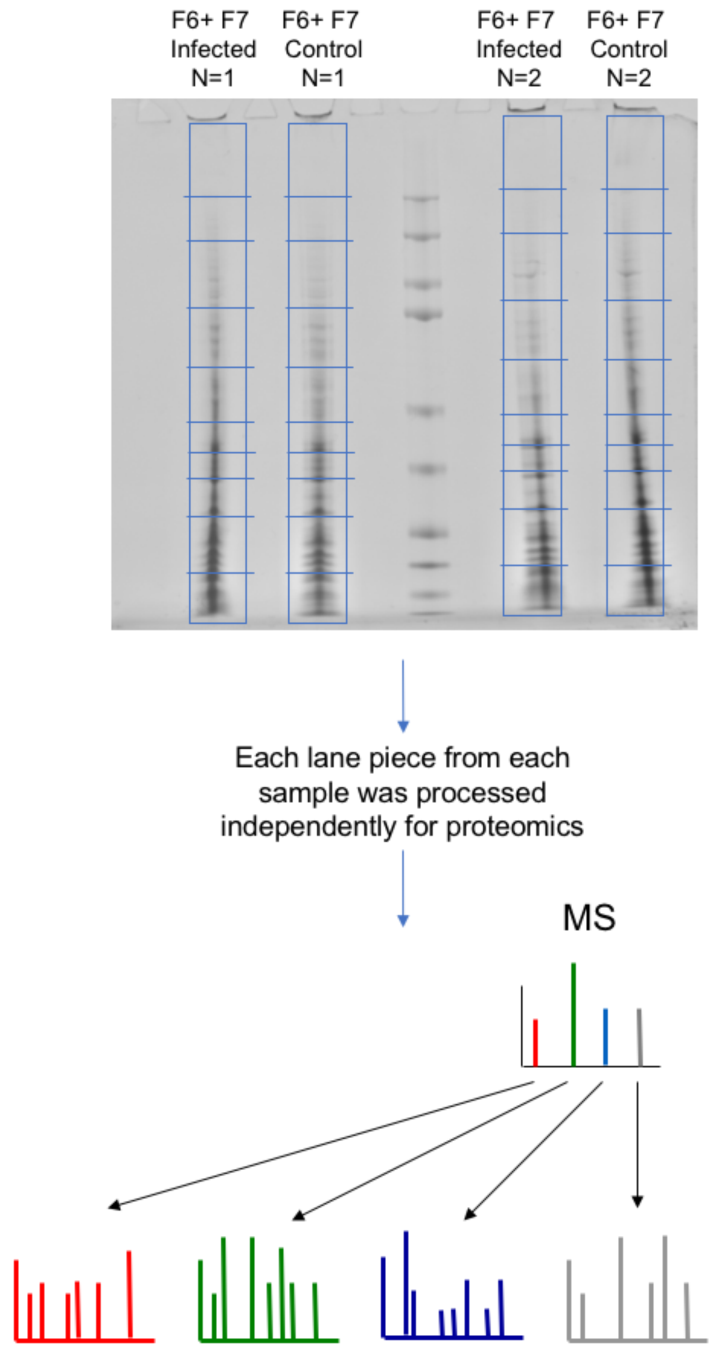


Figure 9 – Diagram of the procedure used to obtain the proteome of fractions enriched in vacuolar compartments from *D. discoideum* cells infected with different *S*. Typhimurium strains or uninfected control cells. Fractions 6 and 7 from each sample were combined and used to prepare the samples for proteomics. Proteins were precipitated, separated by molecular mass by SDS-PAGE and each lane was cut into 10 pieces that were independently processed before injection into the Q-Exactive Plus mass spectrometer.

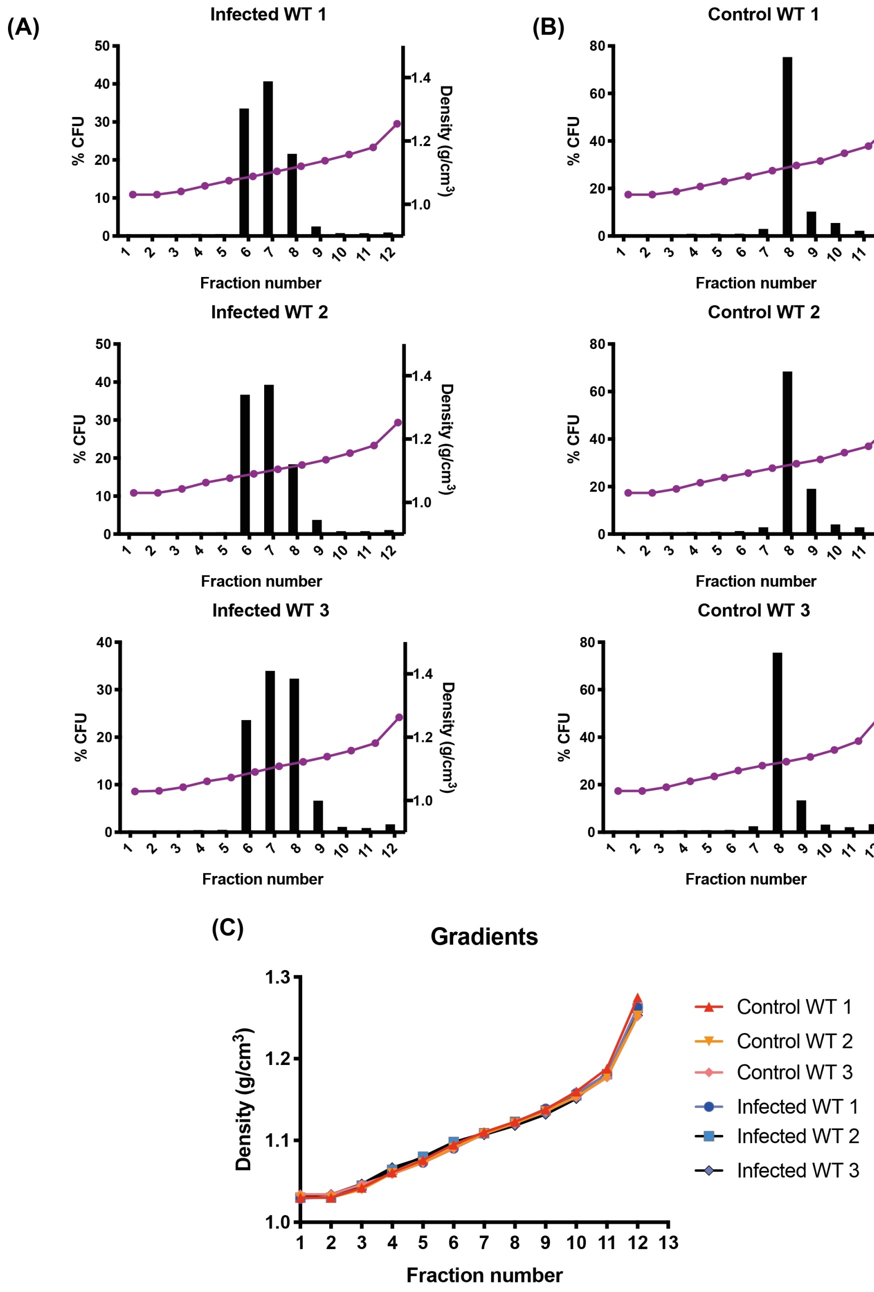


Figure 10 - Subcellular fractionation of *D. discoideum* cells infected with *S*. Typhimurium WT strain and uninfected control cells. Graphs show the CFU distribution and density per fraction of PNS samples obtained from **(A)** cells infected with *S*. Typhimurium 14028s (Infected with WT) or **(B)** uninfected control cells spiked with a known amount of *S*. Typhimurium 14028s (Control WT). **(C)** Comparison of density between gradients from the different samples, calculated from the refractive index. Each graph show data from one of three independent experiments (denoted with numbers 1, 2 and 3).

The presence of this differential bacterial distribution between infected and control samples suggest the presence of bacteria inside vacuoles, as described in the original protocol (Santos et al., 2015). To validate the presence of vacuoles containing bacteria, we performed an anti-*Salmonella* ELISA-based assay (Santos et al., 2015). In this assay, an immobilized anti-*Salmonella* antibody was used to capture free bacteria in each sample that were subsequently detected using a biotin-conjugated anti-*Salmonella* antibody. To determine the presence of bacteria inside intact vacuoles, the sample was analysed before and after an osmotic shock treatment. As shown in **Figure 11**, in the case of samples from infected cells there is an increase in *Salmonella* detection after the osmotic shock in F6 to F8, while in the case of control samples, there is no increase in the number of *Salmonella* detected before and after the treatment. Together, these results indicate that fractions 6 and 7 were enriched in intact vacuoles containing *Salmonella*. Three biological replicates in these conditions were obtained and analysed.

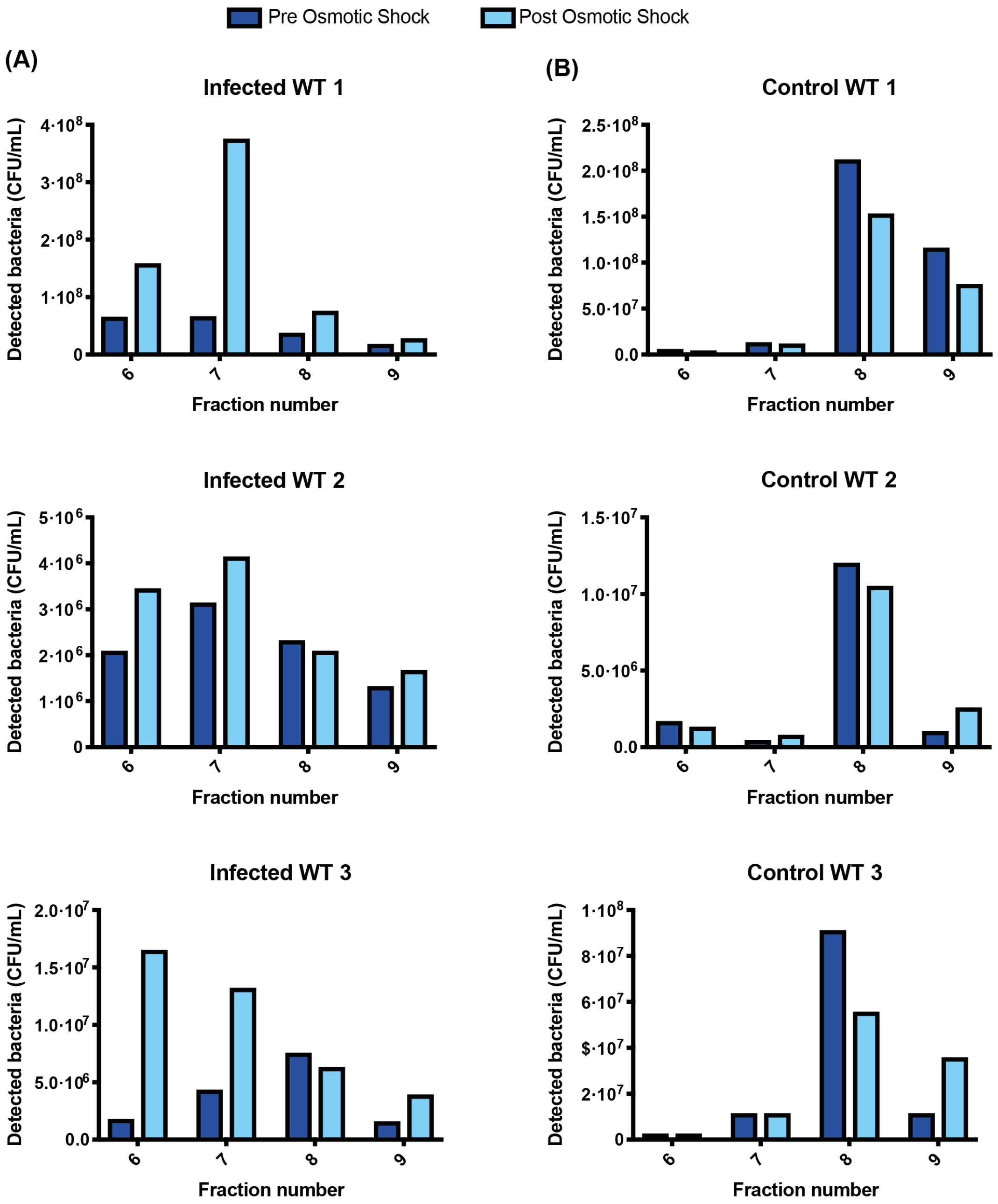
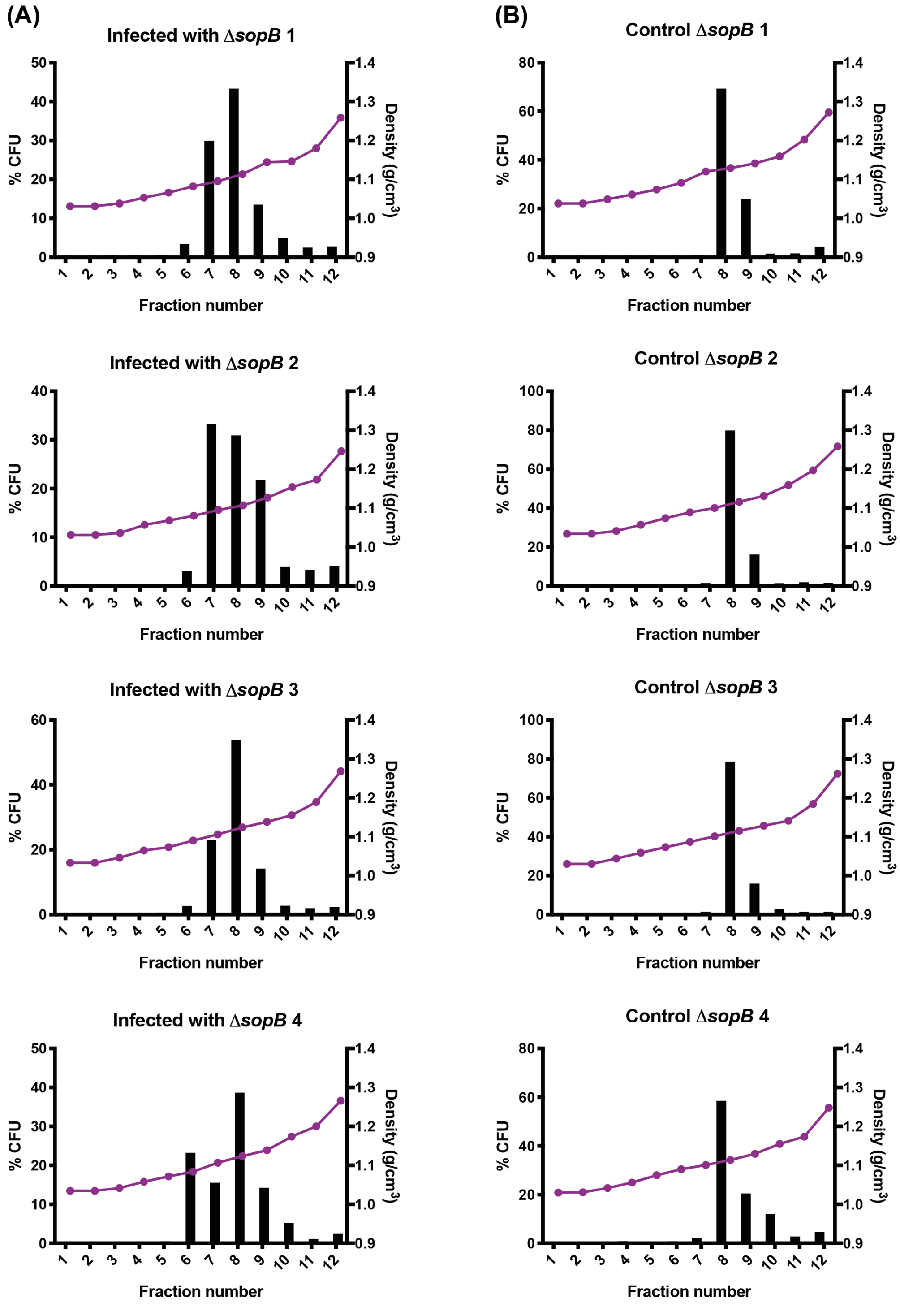
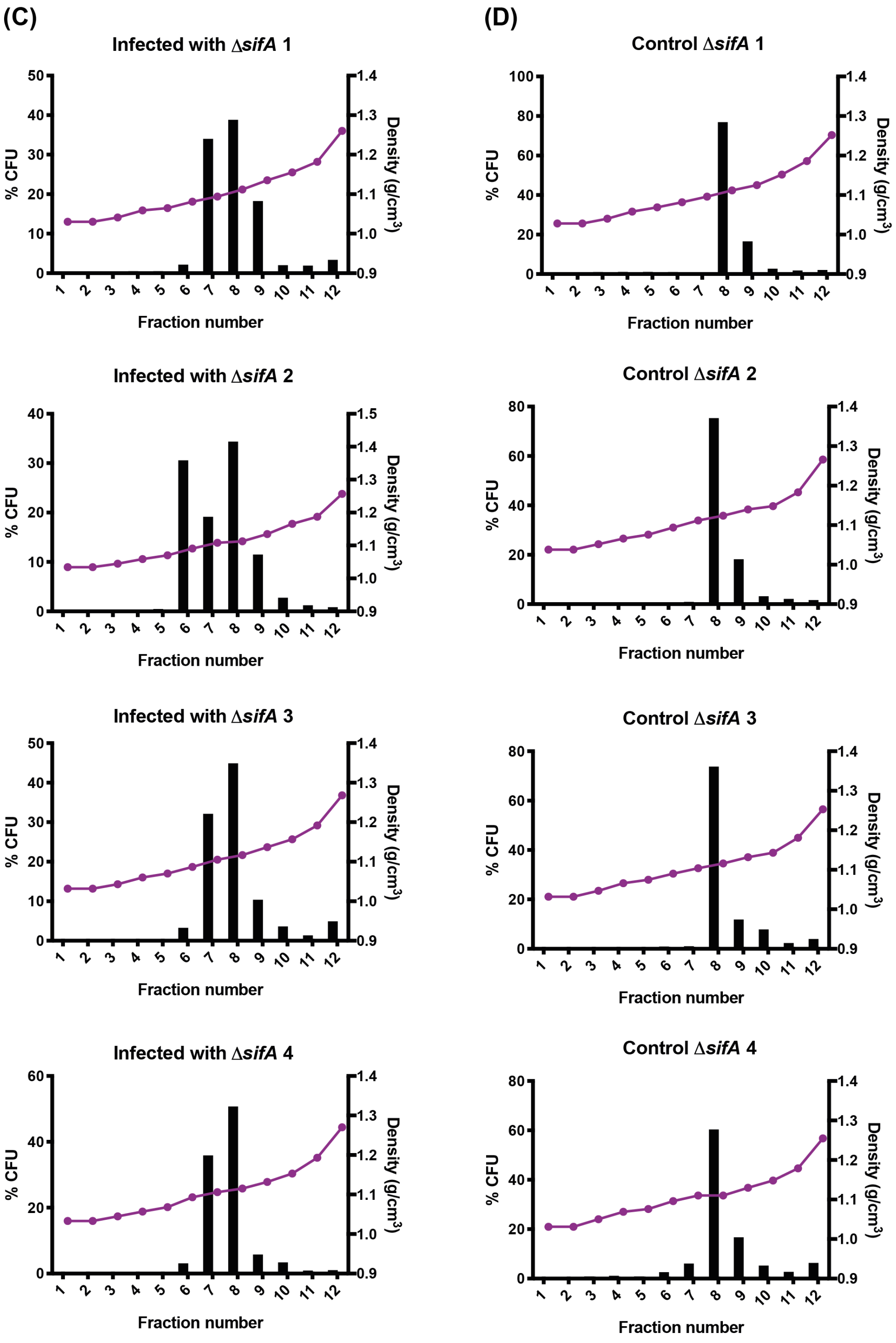


Figure 11 - ELISA analysis of fractions obtained form *D. discoideum* cells infected with *S.* Typhimurium WT and uninfected control cells. (A) Graphs show the CFU detected per fraction of samples from infected cells for fractions F6 to F9, before and after the osmotic rupture of vacuolar compartments. **(B)** Graphs show the CFU detected per fraction of uninfected control samples for fractions F6 to F9, before and after the osmotic shock. Each graph show data from one of three independent experiments (denoted with numbers 1, 2 and 3).

In the case of samples from cells infected with mutants ∆*sopB* and ∆*sifA*, we also observed the shift in bacterial distribution between control and infected samples (**Figure 12**, panels **A - D**), although the increase of bacteria in F6 was not as evident as in samples from cells infected with the wild-type strain (**Figure 12**). The densities did not vary between gradients (**Figure 12E**). When these samples were analysed by ELISA, we observed an increase in *Salmonella* detected after the osmotic rupture of the vacuoles (**Figure 13**), indicating the presence of intact vacuoles containing *Salmonella* in the samples obtained from infected cells. In each case, four biological replicates were obtained and analysed.

Fractions F6 and F7 from each experiment were selected as they were clearly enriched in intact vacuoles containing *Salmonella*. These fractions were subjected to protein precipitation and analysis by Q-Exactive proteomics in the Proteomics Platform at Institut Pasteur, Paris, France.


(A)
Infected with Δ*sopB* 1
Infected with Δ*sopB* 2
Infected with Δ*sopB* 3
Infected with Δ*sopB* 4
(B)
Control Δ*sopB* 1
Control Δ*sopB* 2
Control Δ*sopB* 3
Control Δ*sopB* 4
% CFU
Density (g/cm^3)
Fraction number
1
2
3
4
5
6
7
8
9
10
11
12
0
10
20
30
40
50
60
80
100
0.9
1.0
1.1
1.2
1.3
1.4


(C)
(D)
Infected with ΔsifA 1
Infected with ΔsifA 2
Infected with ΔsifA 3
Infected with ΔsifA 4
Control ΔsifA 1
Control ΔsifA 2
Control ΔsifA 3
Control ΔsifA 4
% CFU
Density (g/cm³)
Fraction number
1
2
3
4
5
6
7
8
9
10
11
12
0
10
20
30
40
50
60
80
100
0.9
1.0
1.1
1.2
1.3
1.4
1.5

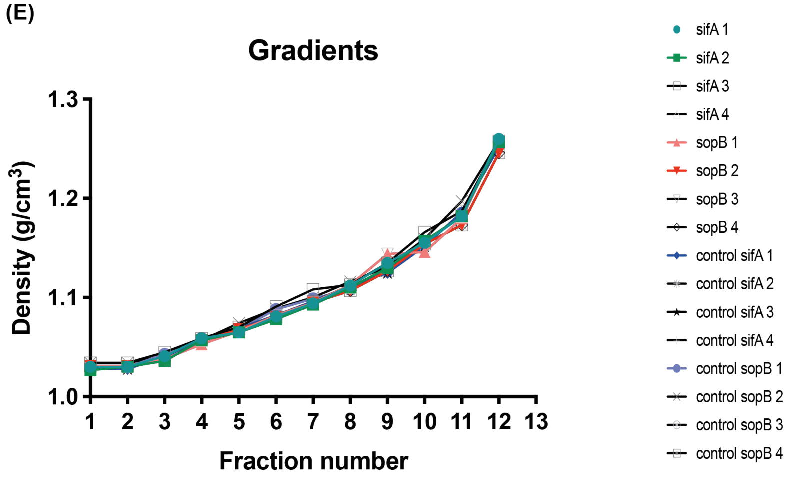
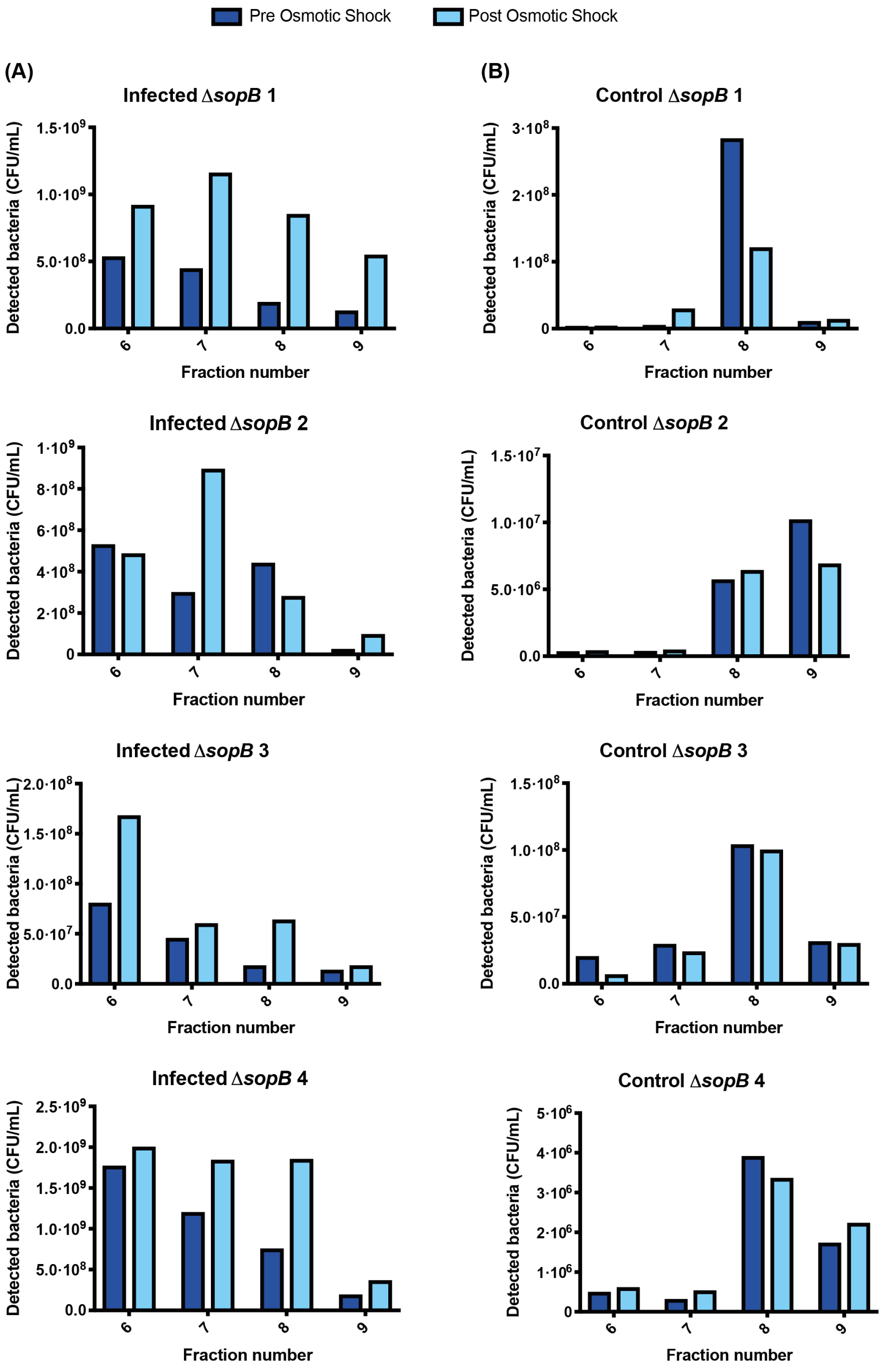


Figure 12 – Subcellular fractionation of *D. discoideum* cells infected with *S*. Typhimurium Δ*sopB* and Δ*sifA* mutants and uninfected control cells. Graphs show the CFU distribution and density per fraction for PNS samples obtained from cells infected with *S*. Typhimurium Δ*sopB* **(A)** or Δ*sifA* **(C)**, or uninfected control cells spiked with a known amount of *S*. Typhimurium Δ*sopB* **(B)** or Δ*sifA* **(D)** (Control Δ*sopB* and Control Δ*sifA*, respectively). **(E)** Comparison of density between gradients from the different samples, calculated from the refractive index. Each graph show data from one of four independent experiments (denoted with numbers 1, 2, 3 and 4).


■ Pre Osmotic Shock
■ Post Osmotic Shock
(A)
Infected ΔsopB 1
Detected bacteria (CFU/mL)
1.5·10⁹
1.0·10⁹
5.0·10⁸
0.0
6
7
8
9
Fraction number
(B)
Control ΔsopB 1
Detected bacteria (CFU/mL)
3·10⁸
2·10⁸
1·10⁸
0
6
7
8
9
Fraction number
Infected ΔsopB 2
Detected bacteria (CFU/mL)
1·10⁹
8·10⁸
6·10⁸
4·10⁸
2·10⁸
0
6
7
8
9
Fraction number
Control ΔsopB 2
Detected bacteria (CFU/mL)
1.5·10⁷
1.0·10⁷
5.0·10⁶
0.0
6
7
8
9
Fraction number
Infected ΔsopB 3
Detected bacteria (CFU/mL)
2.0·10⁸
1.5·10⁸
1.0·10⁸
5.0·10⁷
0.0
6
7
8
9
Fraction number
Control ΔsopB 3
Detected bacteria (CFU/mL)
1.5·10⁸
1.0·10⁸
5.0·10⁷
0.0
6
7
8
9
Fraction number
Infected ΔsopB 4
Detected bacteria (CFU/mL)
2.5·10⁹
2.0·10⁹
1.5·10⁹
1.0·10⁹
5.0·10⁸
0.0
6
7
8
9
Fraction number
Control ΔsopB 4
Detected bacteria (CFU/mL)
5·10⁶
4·10⁶
3·10⁶
2·10⁶
1·10⁶
0
6
7
8
9
Fraction number

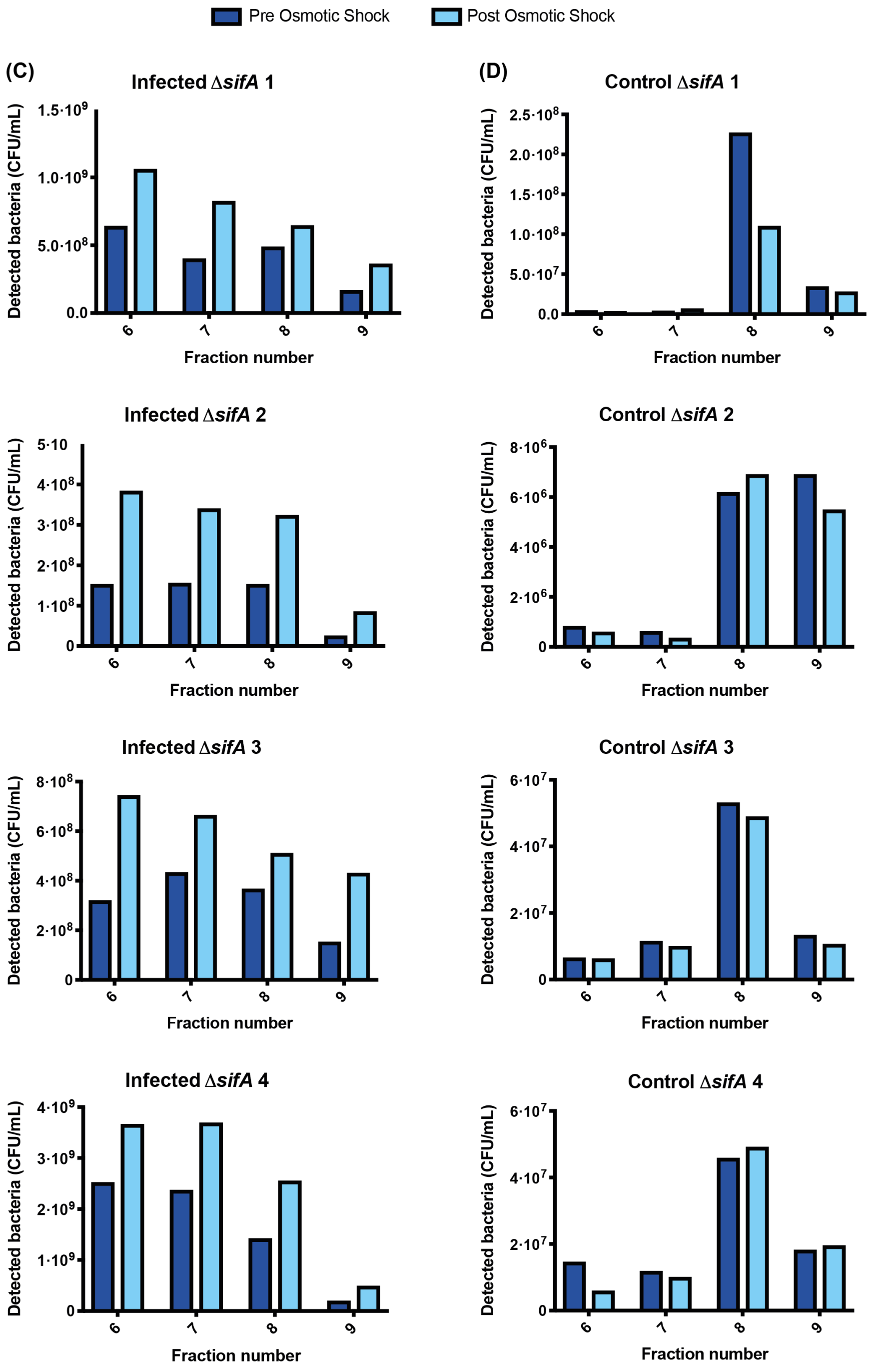


Figure 13 - ELISA analysis of fractions obtained form *D. discoideum* cells infected with *S*. Typhimurium Δ*sopB* and Δ*sifA* and uninfected control cells. Graphs show the CFU detected by ELISA in fractions F6 to F9 before and after the osmotic rupture of vacuolar compartments obtained from **(A)** Δ*sopB* infected samples, **(B)** Δ*sopB* control samples, **(C)** Δ*sifA* infected samples and **(D)** Δ*sifA* control samples. Each graph show data from one of four independent experiments (denoted with numbers 1, 2, 3 and 4).

11.3.2 Proteomic analysis

Proteomic data analysis was performed using the PatternLab for proteomics 4.0 software (http://www.patternlabforproteomics.org) (Carvalho et al., 2016). We first analysed the data obtained from WT-infected cells and the corresponding control samples. For infected samples 1,319 proteins were identified, while for control samples 1,389 proteins were identified. After manual curation of these two datasets to remove proteins corresponding to contaminants and reverse proteins, we identified 715 proteins that were shared between the two conditions, 95 proteins present only in WT-infected samples, and 160 proteins present only in control samples, as shown in **Figure 14A**. Among the proteins present only in WT-infected samples we found proteins related to trafficking such as Trappc1-1 (Trafficking protein particle complex subunit 1), Q54TH4 (Golgi to ER traffic protein 4 homolog DDB_G0281815), Q55FM0 (ER membrane protein complex subunit 8/9 homolog DDB_G0268048) and SybA (Synaptobrevin-A); the GTPase guanidine exchanging factor GefQ; proteins involved in multivesicular bodies formation such as Chmp3 (Charged multivesicular body protein 3) and Chmp2a1 (Charged multivesicular body protein 2a homolog 1); a putative phosphatidylinositol phosphate kinase DDB_G0267588; motor proteins such as Kif13 (Kinesin-related protein 13); and actin related proteins Washc2 (WASH complex subunit 2), Actin-18 and ArpA (Centractin). Interestingly, we also found proteins involved in degradative compartments such as the E3 ubiquitin ligases Bre1 and Q54QS0 (E3 UFM1-protein ligase 1 homolog DDB_G0283667), the E2 ubiquitin ligase Ube2v (Probable ubiquitin-conjugating enzyme E2 variant); and different subunits of the COP9 signalosome: Csn2, Csn7 and Cns8 (COP9 signalosome complex subunits 2, 7 and 8). The complete list of proteins present exclusively in WT-infected samples is detailed in **Supplementary Table 1**.

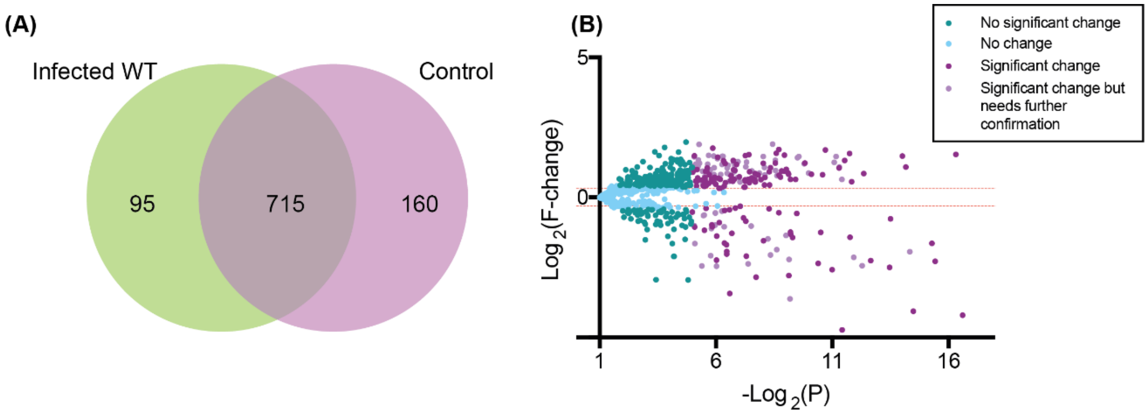


Figure 14 - Proteomic analysis of WT-infected and control samples. (A) Venn diagram showing the distribution of proteins identified in samples from cells infected with the WT strain or control samples. **(B)** Volcano plot generated using the PatternLab for Proteomics TFold module. Each dot represents a protein identified in 3 replicates of all conditions, plotted according to its P-value ($\log_2(P)$) and fold change ($\log_2$(F-change)).

Next, we decided to analyse the differential distribution of proteins found in both datasets. To do this, we used the PatternLab TFold module to generate a Volcano plot (**Figure 13B**) according to the fold change (F-change) and P-value of each protein. We then used the TFold module from PatternLab to analyse the common proteins between the two conditions. This module used the following parameters to generate a volcano plot of these samples: a False Discovery Rate (FDR) of 0.05, an F-stringency of 0.03 and a Q-value of 0.05. After that, for each comparison this module empirically determines an F-change value that maximizes the number of proteins detected for the established FDR and

Q-values. For this particular dataset, when a protein presented an F-change >1.25 and a P-value < 0.05 it was considered to be enriched, and when it presented an F-change < -1.24 and a P-value < 0.05 it was defined as underrepresented in WT-infected samples. Each dot in the plot represents a protein identified in 3 replicates of all conditions, plotted according to its P-value ($-Log_2(P)$) and F-change (Log_2(F-change)). Light blue dots (NC in **Supplementary Table 1**) represent proteins that do not satisfy neither F-change nor statistic criteria, and thus are considered as unchanged between the two conditions. Teal dots (NS in **Supplementary Table 1**) satisfy the F-change criterion, but not the statistical one. Light purple dots (C in **Supplementary Table 1**) correspond to low abundant proteins satisfying both the F-change and Q-value criteria, but due to the low number of spectra they deserved further validation. Finally, purple dots (SC in **Supplementary Table 1**) correspond to proteins satisfying all statistical filters and represent the differentially expressed proteins between WT-infected and control samples.

Using these parameters, we determined the number of proteins specifically enriched in WT-infected samples: 90 proteins in the SC category and 62 in the C category. Among them, we found the trafficking related proteins: Vti1A (Vesicle transport through interaction with t-SNAREs homolog 1A), Syn7A (syntaxin-7A), Syn8A (syntaxin-8A), Syn8B (syntaxin-8B), Trappc5 (Trafficking protein particle complex subunit 5), Rab5B (Ras-related protein Rab-5B) and RacE (Rho-related protein); and actin-related proteins such as VASP (Q5TJ65, protein involved in cytoskeleton remodelling), AcpA (F-actin-capping protein subunit beta), AcpB (F-actin-capping protein subunit alpha) and ArpC (Actin-related protein 3). Again, we found proteins related to degradative compartments such as cathepsin D (O76856), GluA (lysosomal beta glucosidase), LmpB (lysosome membrane protein 2-B) and Atg8 (Autophagy-related protein 8). The complete list of proteins differentially expressed in WT-infected and control samples is detailed in **Supplementary Table 2**.

Next, we analysed the data from Δ*sopB* and Δ*sifA* infected samples using the same parameters used for the WT-infected samples. In the case of the Δ*sopB*-infected samples 1,520 proteins were identified, while for control samples 1,414 proteins were identified. After manual curation of these two datasets we identified 782 proteins that were shared between them, 256 proteins present only in Δ*sopB*-infected samples, and 152 proteins present only in control samples, as shown in **Figure 15A**. Among the proteins found only in Δ*sopB*-infected samples, we found proteins related to intracellular trafficking such as Vta1 (vacuolar protein sorting-associated protein VTA1 homolog), SybA (Synaptobrevin-A), Q54TH4 (Golgi to ER traffic protein 4 homolog DDB_G0281815), PitC (Phosphatidylinositol transfer protein 3), components of the Exocyst complex (ExoC1, ExoC5 and ExoC4), Chmp2a1 (Charged multivesicular body protein 2a homolog 1), Kif13 (Kinesin-related protein 13) and Q55GN6 (Probable phosphatidylinositol phosphate kinase DDB_G0267588); the Ras guanine nucleotide exchange factors GefQ, GefE, GefR, GxcJJ (Rac guanine nucleotide exchange factor JJ) and the Rho GTPase-activating proteins (GAPs) GacJ GacI, GacG and GacT; motor proteins such as Kif8, Kif3, DicA (Cytoplasmic dynein 1 intermediate chain) and putative myosin light chain kinase DDB_G0271550; Ubiquitin related enzymes Ube2V (Probable ubiquitin-conjugating enzyme E2 variant), Bre1 (Probable E3 ubiquitin-protein ligase) and Pex4 (Ubiquitin-conjugating enzyme E2); autophagy related proteins Atg3 and Atg12; and different subunits of the COP9 signalosome (Csn3, Csn4, Csn6 and Csn8). The complete list of proteins present exclusively in Δ*sopB*-infected samples is detailed in **Supplementary Table 3**.

When we used the TFold module to analyse the common proteins between these two conditions (FDR of 0.05, an F-stringency of 0.03 and a Q-value of 0.05), we determined that 95 proteins in the SC category and 40 in the C category were specifically enriched in Δ*sopB*-infected samples. For this comparison, when a protein presented an F-change >1.19 and a P-value < 0.05 it was considered to be enriched and when it presented an F-change < -1.27 and a P-value < 0.05 it was defined as underrepresented in Δ*sopB*-infected samples (**Figure 15B**). We found proteins from the same pathways as those found only in Δ*sopB*-infected samples to be specifically enriched in Δ*sopB*-infected samples, such as Syntaxin 7, Vti1A (Vesicle transport through interaction with t-SNAREs homolog 1A), Vps35 (Vacuolar protein sorting-associated protein), ExoC7 (component of the exocyst complex); GefH (Ras guanine nucleotide exchange factor H); Rho-related proteins RacC, RacE; Ras-related protein RapA and Rab14; actin-related proteins AcpA, AcpB, ArpC, ArcB, ArcE; and Myosin components (mlcE). Noteworthy, several Rab GTPases were found to be underrepresented in Δ*sopB*-infected samples, such as Rab1, Rab2, Rab5, Rab6 and Rab8. The complete list of proteins differentially expressed between *sopB*-infected and control samples is detailed in **Supplementary Table 4**.

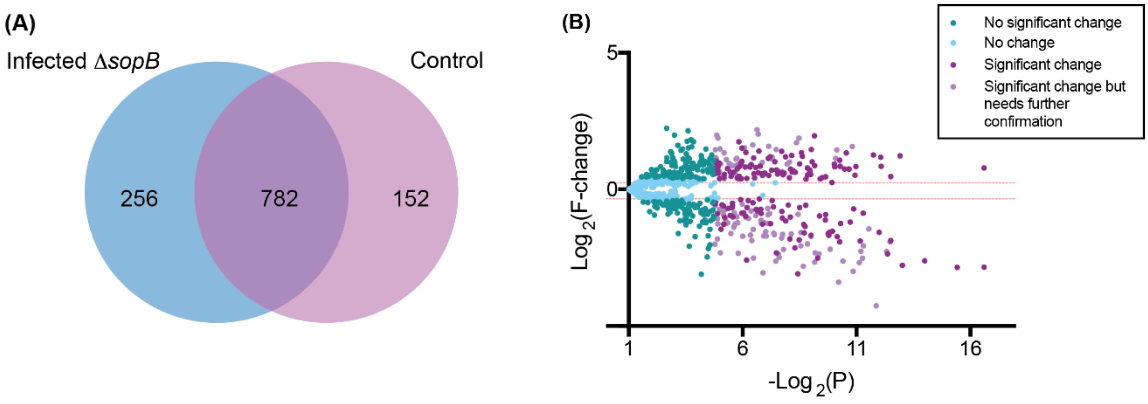


Figure 15 - Proteomic analysis of Δ*sopB*-infected and control samples. (A) Venn diagram showing the distribution of proteins identified in samples from cells infected with the Δ*sopB* mutant or control samples. **(B)** Volcano plot generated using the PatternLab for Proteomics TFold module. Each dot represents a protein identified in 4 replicates of all conditions, plotted according to its P-value ($\log_2$(P)) and fold change ($\log_2$(F-change)).

In the case of the Δ*sifA*-infected samples 1,542 proteins were identified, while for control samples 1,423 proteins were identified. By comparing these two datasets (**Figure 16A**) after manual curation, we identified 750 proteins that were shared between them, 229 proteins present only in Δ*sifA*-infected samples, and 112 proteins present only in control samples. Among the proteins present only in

Δ*sifA*-infected samples, we found the autophagy related proteins Atg5 and Atg3; the vacuolar proteins Vps37 and Vps51; the GAPs GacI, GacJ, GacT and GacG; and the guanidine nucleotide exchanging factor GefE. Of note, we only found one Actin-related protein (Actin 17) and no motor proteins were found in this group. The complete list of proteins present exclusively in *sopB*-infected samples is detailed in **Supplementary Table 5.**

Using the TFold module to analyse the different distribution between proteins in these two conditions (FDR of 0.05, an F-stringency of 0.04 and a Q-value of 0.05) we determined that 88 proteins in the SC category and 63 in the C category were specifically enriched in Δ*sifA*-infected samples. For this dataset, when a protein presented an F-change > 1.32 and a P-value < 0.05 it was considered to be enriched, and when it presented an F-change < -1.32 and a P-value < 0.05 it was considered as underrepresented in Δ*sifA*-infected samples (**Figure 16B**). We also found proteins related to the same pathways as the ones found in proteins only present in Δ*sifA*-infected samples, when we analysed the results of enrichment analysis, such as the trafficking protein particle complex subunit 13 homolog (DDB_G0269062), Syntaxin-7A; the GTPases RapA and RacE; the guanine nucleotide binding protein GpbB; GefH (Ras guanine nucleotide exchange factor H); and actin-related proteins ArcC, ArcE, ArpB, AcpA and AcpB. As in the case of Δ*sopB*-infected samples, several Rab GTPases were found to be underrepresented, including Rab1, Rab2, Rab5 and Rab8. The complete list of proteins differentially expressed in Δ*sifA*-infected and control samples is detailed in **Supplementary Table 6**.

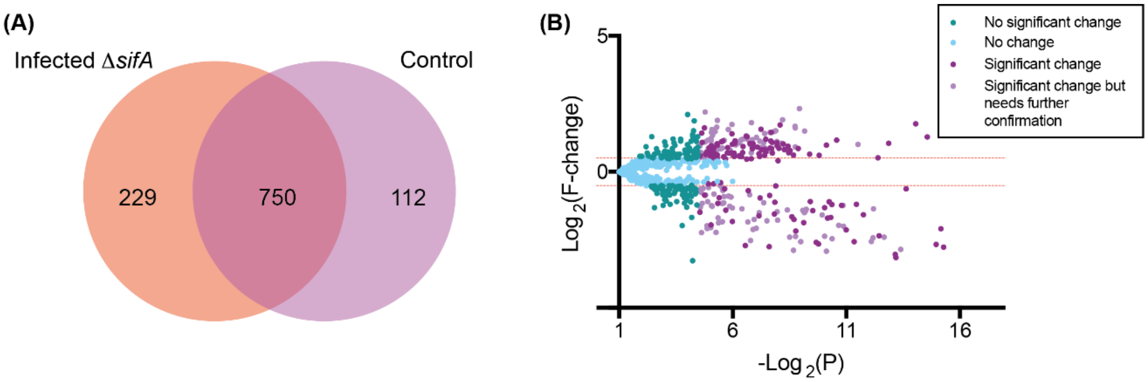


Figure 16 - Proteomic analysis of Δ*sifA*-infected and control samples. (A) Venn Diagram showing the distribution of proteins identified in samples from cells infected with the Δ*sifA* mutant or control samples. **(B)** Volcano plot generated using the PatternLab for Proteomics TFold module. Each dot represents a protein identified in 4 replicates of all conditions, plotted according to its P-value (log$_2$(P)) and fold change (log$_2$(F-change)).

Overall, our proteomic approach allowed us to characterize the fractions enriched in vacuoles containing different strains of *S*. Typhimurium in *D. discoideum*. After analysing the differences observed in relative levels of proteins from controls and samples infected with wild-type and mutant strains (**Table 4**), we can describe for the first time the proteome of the SCV in this model host.

Table 4 – Comparative analysis of functions associated to selected proteins enriched in each sample.

WT	Δ*sopB*	Δ*sifA*
Golgi/ER trafficking	Golgi/ER trafficking	Vacuolar sorting proteins
GTPase exchanging factors	Vacuolar sorting proteins	GTPase exchanging factors
MVB	MVB	RapA and RacE
Motor proteins	GTPase exchanging factors	Autophagy (Atg5 and Atg13)
Actin related proteins	Motor proteins	
Rab5B and RacE	Actin related proteins	
Autophagy (Atg8)	Autophagy (Atg3 and Atg12)	

11.3.3 Infection assays using a PI3K inhibitor

As a strategy to evaluate the role of lipid species in this compartment, we decided to use a pharmacological inhibitor. PI3P is a key component of the SCV in other cellular models and is produced by a PI3K from other phosphoinositide species. It is important to note that the formation of degradative vacuolar compartments requires the presence of this lipid. Thus, we decided to evaluate if inhibition of PI3K activity affects the intracellular survival of *S*. Typhimurium in the amoeba. For this, we performed infection assays up to 6 h, in which we treated amoeba cells with the PI3K inhibitor LY294002 (10 μM) or with an equivalent volume of the vehicle (DMSO) as control. As shown in **Figure 17A**, the survival levels of wild-type and mutant strains were not affected by the presence of the inhibitor. Of note, the inhibitor did not affect cell viability of infected (**Figure 17B**) or uninfected amoeba cells (**Figure 17C**), indicationg that it does not have a toxic effect on *D. discoideum* cells at the times tested.

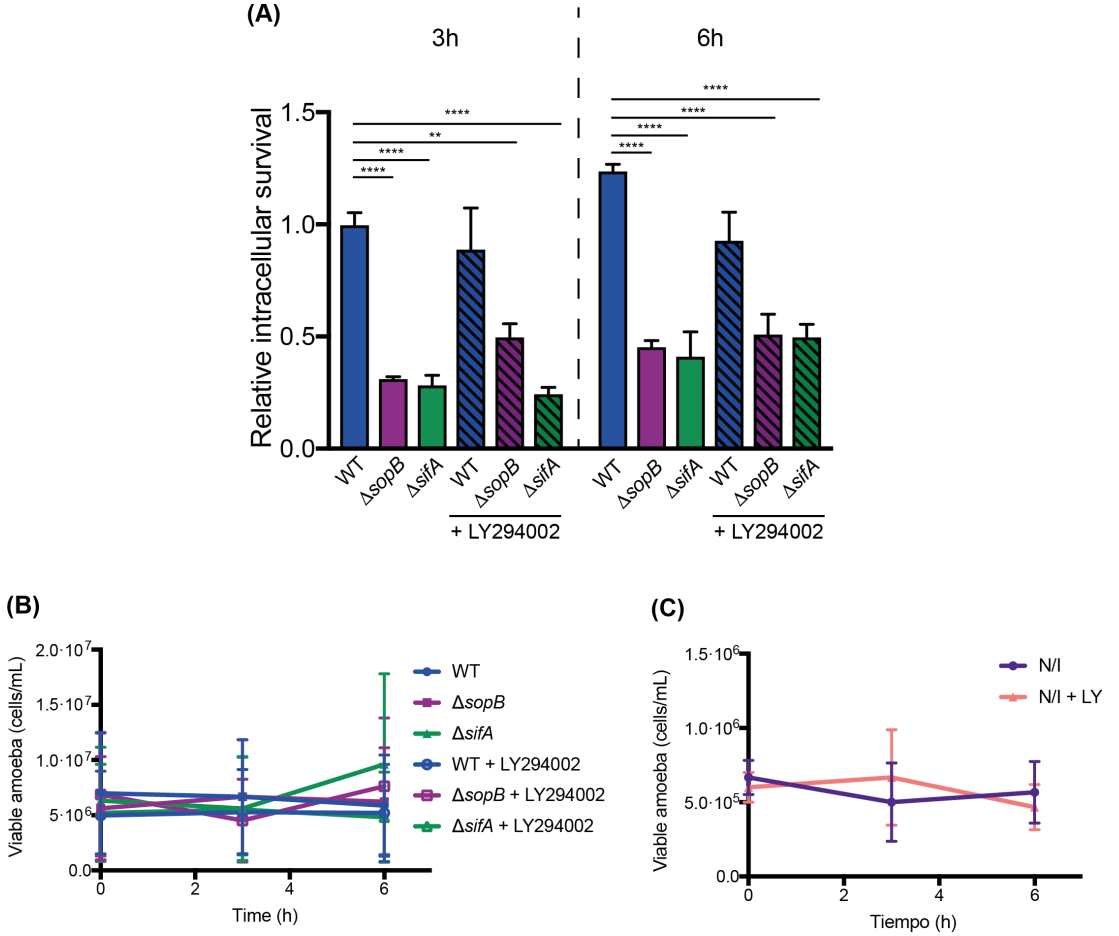


Figure 17 - Intracellular survival of *S.* Typhimurium 14028s and derived mutants in *D. discoideum* AX2 in the presence of a PI3K inhibitor. (A) Relative intracellular survival was calculated as CFU/cell at t=3 or t=6 divided by the CFU/cell at t=0. **(B)** Population of viable amoeba at each time post infection. **(C)** Effect of LY294002 on uninfected amoeba at each time. Statistical significance was determined using two-way ANOVA with Dunnet's test (** = p<0.01, **** = p<0.0001). All graphs show the mean values +/- SEM of three independent assays.

12. DISCUSSION

12.1 *S*. Typhimurium requires effectors SopB and SifA to survive intracellularly in *D. discoideum*

We first decided to analyse the effect of deleting genes encoding essential components of the two T3SS present in *S*. Typhimurium: *invA* (encoding a structural component of $\mathrm{T3SS}_{\mathrm{SPI\text{-}1}}$), *ssaV* (encoding a structural component of $\mathrm{T3SS}_{\mathrm{SPI\text{-}2}}$) and two effectors: *sopB* (encoding an effector protein secreted by $\mathrm{T3SS}_{\mathrm{SPI\text{-}1}}$) and *sifA* (encoding an effector protein secreted by $\mathrm{T3SS}_{\mathrm{SPI\text{-}2}}$). Our results replicated previous results obtained by our group (Riquelme et al., 2016), demonstrating that impairment of T3SS secretion results in defects in intracellular survival at 6 h post infection in *D. discoideum* (**Figure 3C**). We also observed that deletion of genes encoding *sopB* and *sifA* results in similar defects in intracellular survival of *S*. Typhimurium in *D. discoideum* and the phenotype of each mutant was reversed by the presence of a wild-type copy of the corresponding gene in a plasmid (**Figure 3C** and **4C**), demonstrating that *sopB* and *sifA* are required to survive intracellularly in this host.

The role of these effector proteins in the intracellular survival of *Salmonella* in other hosts has been widely reported. *In vivo*, SopB is not required for systemic colonization by *S*. Dublin, but contributes to inflammation in bovine ligated ileal loops (Wood et al., 1998). In the case of *S*. Typhimurium, SopB is not needed to produce colitis in the streptomycin-treated mice model (Hapfelmeier et al., 2004). *In vitro*, it has been shown that SopB contributes to invasion of HeLa cells (Mallo et al., 2008), but is dispensable for intracellular replication in intestinal Henle-407 cells (Hernández et al., 2004). On the other hand, it is required for intracellular growth in bone marrow-derived macrophages (Hernández et al., 2004), which is similar to the phenotype we observe in *D. discoideum*. In the case of SifA, it has been shown that *sifA* mutants are strongly attenuated in mice (Beuzón et al., 2002), but they show a higher percentage of scape from the SCV and hyperreplicate in the cytosol of HeLa cells (Brumell et al., 2002). In restrictive cell lines such as Swiss 3T3 fibroblasts and in RAW 264.7 macrophages, a *sifA* mutant is defective for intracellular replication (Beuzón et al., 2002). Hyperreplication of *Salmonella* has not been described in *D. discoideum* and we have no evidence of this particular phenotype in this model. As described in the literature, SopB and SifA are required to survive and growth intracellularly in mammalian phagocytic cells. Consistently with these phenotypes, our results show that they play a role in the intracellular survival of *S*. Typhimurium in the amoeba *D. discoideum*. To our knowledge, this is the first report on the requirement of effectors SopB and SifA for *Salmonella* survival within protozoa. It is important to note that these effectors are involved in key steps during the biogenesis of the SCV (Reviewed in Ramos-Morales, 2012; Knuff & Finlay, 2017), so we decided to look into this process to understand the role they played in the intracellular survival of *S*. Typhimurium in *D. discoideum*.

12.2 *S*. Typhimurium resides in a vacuolar compartment in *D. discoideum*

We first analysed the presence of a vacuolar compartment that contained *S*. Typhimurium in infected *D. discoideum* cells using two types of microscopy. We first tried to perform ultrastructure studies using transmission electron microscopy of infected cells. Unfortunately, due to the low number of infected cells detected in the samples used for TEM experiments this analysis resulted in only one image of an infected cell carrying a single bacterium. Furthermore, because of the relatively low preservation of endomembranes in the samples we were not able to further characterise the nature of the membranes surrounding the bacterium. In spite of this, in the captured image (**Figure 5**) we observe a double membrane enclosing the bacterium, although it is not possible to determine if the whole compartment is composed by a double membrane or if these membranes correspond to a branch of the ER. Double membranes are a characteristic feature of autophagosomes and structures needed for the formation of these compartments involved in the process of autophagy. Autophagy is defined as a catabolic process that is conserved among all eukaryotic organisms that allows recycling of aged organelles and proteins, and acts as a defence mechanism against pathogens. It has been described that *S*. Typhimurium infection in HeLa cells induces autophagy in order to restrict *Salmonella* intracellular replication (Huang & Brumell, 2014). Also, this process has been linked to the repair of SCV membranes damaged by the $T3SS_{SPI\text{-}1}$ (Kreibich et al., 2015). The role of autophagy in the SCV will be discussed in detail in the next section, along with our proteome results.

As another strategy, we decided to use confocal microscopy in order to evaluate the presence of such compartment using a *D. discoideum* reporter strain that expresses the vATPase VatM fused to GFP. This strain was originally generated to understand vATPase dynamics in this model (Clarke et al., 2002). These enzymes use ATP hydrolysis to transport protons across membranes and are composed of two complexes: V_1 and V_0. V_1 is the outer complex composed of eight subunits and responsible for ATP hydrolysis, while V_0 is the integral membrane complex of at least five subunits that carries protons across the membrane (Clarke et al., 2002). VatM is part of the V_0 complex and has been localized to the membranes of two types of compartments: (1) in the contractile vacuole complex, an organelle that regulates osmolarity in which vATPase energizes water movement from the cytosol into the vacuole complex (Heuser et al., 1993); and (2) in membranes of the endolysosomal system (Adessi et al., 1995), in which vATPase acidifies the lumen of endosomes. The authors of the study (Clarke et al., 2002), showed that VatM-GFP is targeted to the proper endomembranes, and that the delivery of VatM to phagosomes occurs predominantly through fusion of pre-existing endosomes and phagosomes with the new phagosome. This process takes place within a few minutes after the uptake of yeast particles used in this study to evaluate phagocytosis (Clarke et al., 2002). It is also important to note that the vATPase protein is recruited to phagosomal and endolysosomal membranes of other cellular models, such as epithelial cells and macrophages. It has been also described to be present in the SCV in HeLa and macrophage cells infected with *Salmonella* (Dreacktrah et al., 2007; Steele-Mortimer, 2008; Knuff & Finlay, 2017). With this idea, we tested for the presence of the vATPase in *D. discoideum* VatM-GFP infected with *S*. Typhimurium constitutively expressing mCherry. Our experiments showed the presence of the VatM-GFP marker in vacuoles containing *S*. Typhimurium at 3 and 4.5 h post infection (**Figures 3** and **4A**). This confirmed that *S*. Typhimurium is contained in a vacuolar compartment in *D. discoideum* as described by other groups (Skriwan et al., 2002), and that this compartment is a VatM$^+$ vacuole.

Overall, these results show that *S*. Typhimurium is able to survive in *D. discoideum* in a vacuolar compartment that has features of the SCV, such as the presence of vATPase. Other possible markers to evaluate in a future characterization of this SCV-like compartment include Rab proteins involved in the endolysosomal pathway and autophagy related proteins.

12.3 The proteome of the vacuolar compartment containing *S*. Typhimurium in *D. discoideum*

To gain further insight into the cellular components of this compartment, we decided to determine its proteome by obtaining a subcellular fraction containing intact vacuoles and analysing this fraction by quantitative proteomics. Our enrichment protocol allowed us to obtain a fraction enriched in intact vacuoles from amoeba cells infected with the wild-type strain and derived mutants Δ*sopB* and Δ*sifA* (**Figures 9** to **12**), as described in the original protocol we used as starting point (Santos et al., 2015).

The SCV has been predominantly characterized in HeLa cells. The proteome of the compartment in this cell line has been published by at least two groups (Santos et al., 2015; Vorwerk et al., 2014). These proteomic studies identified between 280 and 400 proteins, and their data shows a significant enrichment in proteins from several organelles, incluiding the ER, early and late endosomes, the trans-Golgi network, cytoskeleton proteins that may act stabilizing SIFs, lysosomes, and vesicle-transport related proteins. In fact, both studies were the first to describe the importance of the ER and ER-contacting points in defining the fate of intracellular *S*. Typhimurium in HeLa cells.

HeLa cells are used as a model for epithelial cells mainly because of their easy manipulation for cell biology studies. *Salmonella* replication in these cells is highly permissive, in contrast to replication in macrophages and other non-permissive cell types. Our analysis of the compartment containing *Salmonella* in *D. discoideum* is comparable to SCV studies performed in macrophages and other bacteria-containing compartments in phagocytic cells. Only recently, the isolation of SCVs from human THP-1 macrophages was published (Singh et al., 2018). Unfortunately, only an initial characterization was performed and no proteome has been published.

In contrast, another study determined the proteome of the *Legionella*-containing vacuole (LCV) both in *D. discoideum* and RAW264.7 macrophages (Hoffmann et al., 2014). This particular study is of great interest as it highlights the similarities between these compartments in macrophages and in amoeba. In this study, numerous LCV proteins identified from infected macrophages were already described in the literature. These include several small GTPases such as ArfA, Rab1A, Rab1D, Rab5A, Rab7A, Rab8A, Rab14, RanA, RasG and SarA. In addition, they also identified novel LCV components such as the small GTPases Rab2A, Rab6, Rab11A, Rab18, Rab32A, RacB, RacE and RapA; some GTPase modulators (Rab, Ras and Rho GAPs); SNARE proteins (syntaxin, synaptobrevin, Vamp7); and Ser/Thr kinases. When compared to the proteins identified in the *D. discoideum* LCVs, they found a considerable number of proteins implicated in the same signalling pathways, including Ser/Thr and Tyr protein kinases and phosphatases, cyclin-dependent kinases, small GTPases of the Rho/Rac, Ras or Ran families, GTPase modulators, ubiquitin-dependent factors, multivesicular body (MVB) proteins, cargo receptors, dynamin-like GTPases, sorting nexins (SNXs), syntaxins, motor proteins (dynein, kinesin and myosin), and factors implicated in microtubule dynamics.

Interestingly, our proteome results are similar regarding the type of proteins identified and the biological processes involved, as we found SNARE proteins, motor proteins, ubiquitin ligases, Ser/Thr kinases and phosphatases, and MVB proteins, among others. On the other hand, they differ particularly in the Rab

GTPases enriched in the LCV proteome, as we found that these proteins are not enriched in our SCVs proteomes. In the case of the vacuoles obtained form cells infected with *S*. Typhimurium wild-type, this could be due to limitations of the substractive proteomic approach used. Our enrichment protocol uses an arbitrary fraction that is compared to the same subcellular fraction of the control samples. Therefore, it is possible that some of the common proteins shared between infected and control samples can be discarded during our analysis. Nevertheless, this approach allowed us to obtain a panoramic view of the cellular components present in this compartment.

On the other hand, in the case of vacuoles obtained from Δ*sopB*-infected cells, Rab1, Rab2, Rab5, Rab6 and Rab8 were found to be underrepresented. In HeLa cells it has been described that SopB is needed to recruit cellular factors such as Rab5 in early stages of the SCV biogenesis (Mallo et al., 2008; Ramos-Morales, 2012). The production of PI3P in endosomes and early phagosomes occurs mainly via phosphorylation of phosphatidylinositol by Vps34, a class III PI3K whose recruitment is mediated by the interaction between SopB and Rab5 (Mallo et al., 2008). The authors of this study also determined that a *sopB* mutant is impaired in the recruitment of Rab5 to the SCV. Therefore, the Rab5 underrepresentation that we observed in the proteome of SCV obtained from Δ*sopB*-infected cells can be explained by the lack of SopB activity, which in turn affects the repertoire of Rab GTPases that are retained during the maturation of the compartment.

In the case of SifA, much less is known about the potential targets of this protein in *D. discoideum*. In HeLa cells, SifA is known to avoid kinesin overload at the SCV by interacting with SKIP (SifA and Kinesin-Interacting Protein) (Boucrot et al., 2005), and that its absence generates membrane instability in the SCV allowing the scape of bacteria to the cytosol were they hyperreplicate. It was also reported that SifA interacts with the lysosomal tethering factor HOPS (HOmotypic fusion and Protein Sorting) in HeLa cells, subverting the host late endosomal and lysosomal membrane fusion machinery to obtain host membrane and nutrients (Sindhwani et al., 2017). As discussed before, in murine macrophages *sifA* mutants are defective for intracellular replication (Beuzón et al., 2002) and not much is known about other specific cellular proteins that interact with SifA in phagocytic cells.

In the proteomes SCVs obtained from amoeba infected with all the strains characterized in this work we found several proteins involved in degradative pathways, such as ubiquitin ligases, COP9 signalosome (a type of proteasome that cleaves ubiquitin conjugates and ubiquitin-like protein conjugates, among other targets) (Wei et al., 2008) and autophagy related proteins. As described before, autophagy is a highly-conserved process from yeast to mammals, and many genes associated with autophagy (Atg) are conserved in amoebae, plants, worms and mammals, emphasizing the importance of this process. Autophagy also controls infections caused by intracellular pathogens, as they can be sequestered in autophagosome for degradation. This selective elimination of invading pathogens through autophagy is called xenophagy, and its induction requires ubiquitination of proteins present in the pathogen or in their phagosomes (Saha et al., 2018). In *D. discoideum*, autophagy is the main process that allows this organism to fight intracellular pathogens that escape the endolysosomal degradation pathway (Calvo-Garrido et al., 2010; Dunn et al., 2017). Pathogens such as *Mycobacterium marinum* have been described to subvert autophagy in *D. discoideum* by inducing the autophagy pathway by the transient inhibition of TORC1 activity at the early stages of the interaction, and avoiding being killed inside autolysosomes by blocking the autophagic flux (Cardenal-Muñoz et al., 2017). This results in the accumulation of membranes and cytoplasmic material in the vacuole, which might support bacterial survival within this niche.

In *Salmonella*, similar mechanisms have been described, as ruptured SCVs are recognized by galectins (cytoplasmic lectins that bind specific carbohydrate modifications within the ruptured SCV), which subsequently recruit adaptors and autophagosomes (Thurston et al., 2012). Moreover, several reports indicate that autophagy targets cytoplasmic *Salmonella* for degradation (Thurston et al., 2009; Thurston et al., 2012; Zheng et al., 2009). However, other study (Kreibich et al. 2015) demonstrates that the autophagic machinery can repair damaged SCV membranes caused by $T3SS_{SPI-1}$, allowing the maturation of this compartment and subsequent expression of $T3SS_{SPI-2}$, which together promote intracellular survival. SCV membrane repairing requires regulators (mTOR), recruitment factors (galectins and Optineurin), and initiation factors (ULK1, PI3-kinase C3, Beclin1, ATG2A and ATG9), as well as the ATG12- and ATG8-conjugation systems (Krieger et al., 2015). Current studies by our group show that *S*. Typhimurium activates the autophagy machinery in both *D. discoideum* and RAW264.7 macrophages, and mutants in different $T3SS_{SPI-1}$ and $T3SS_{SPI-2}$ effector proteins are involved in this process (Urrutia, personal communication). Of note, a Δ*sopB* mutant increases the accumulation of autophagosomes when compared to the WT strain while inhibits Akt phosphorylation, one of the main pathways leading to autophagy induction. Other study determined that autophagy is necessary to avoid intracellular replication of *S*. Typhimurium in *D. discoideum*, as amoebae with mutations in genes linked to the autophagy pathway infected with *S*. Typhimurium show a decrease in lifespan and an increased bacterial intracellular replication (Jia et al., 2009). Overall, our proteomic analysis highlights the importance of the autophagic machinery in the fate of the vacuolar compartment involved in *S*. Typhimurium survival in *D. discoideum*.

As any study, our approach also have limitations, for example the use of subcellular fractions enriched in vacuoles instead of isolated vacuoles can produce a higher level of contaminants proteins detected in these fractions. This can be addressed by identifying contaminant membranes from other organelles in the different fractions through: detecting specific markers by Western blot (once suitable antibodies are made available) or measuring enzymatic activities associated to some of these markers. Other option to explore is the future validation of the proteins found in the proteomic analysis using fluorescent markers and confocal microscopy, or TEM coupled with specific immunogold labelling. Furthermore, another limitation of substractive proteomics is that some proteins of interest present in the vacuoles can be excluded from our analysis, if they are also present in other cellular components migrating at the same density in control samples. This can also be addressed by using confocal microscopy of infected cells following those proteins of interest with suitable fluorescent reporters.

Finally, we decided to analyse the effect of PI3K in the intracellular survival of *S*. Typhimurium within *D. discoideum*. PI3P is one of the main signalling lipids involved in the SCV biogenesis in other cell types (Scott et al., 2002), and is needed for the recruitment of the autophagy machinery (Nascimbeni et al., 2017). As shown in **Figure 17**, the use of the PI3K inhibitor LY294002 did not affect the intracellular survival of wild-type *S*. Typhimurium or the ∆*sopB* and ∆*sifA* mutants in *D. discoideum*, so it seems that PI3K activity is dispensable for *S*. Typhimurium survival in this amoeba. This PI3K inhibitor is reported to have no effect in *L. pneumophila* phagocytosis by *D. discoideum*, when compared with untreated cells, indicating that this process does not require functional PI3Ks. On the other hand, amoba cells treated with LY294002 showed an increase in the intracellular replication of *L. pneumophila* in *D. discoideum*, indicating that functional PI3Ks restrict intracellular replication of this pathogen. In RAW264.7 macrophages, the use of this inhibitor only had a minor effect decreasing the intracellular replication of *L. pneumophila* (Weber et al., 2006). Other possibility to consider is that, due to the poor specificity of this inhibitor in *D. discoideum*, we might not be inhibiting the class III PI3K involved in the autophagy process, as very few known chemical inhibitors have an effect in this organism.

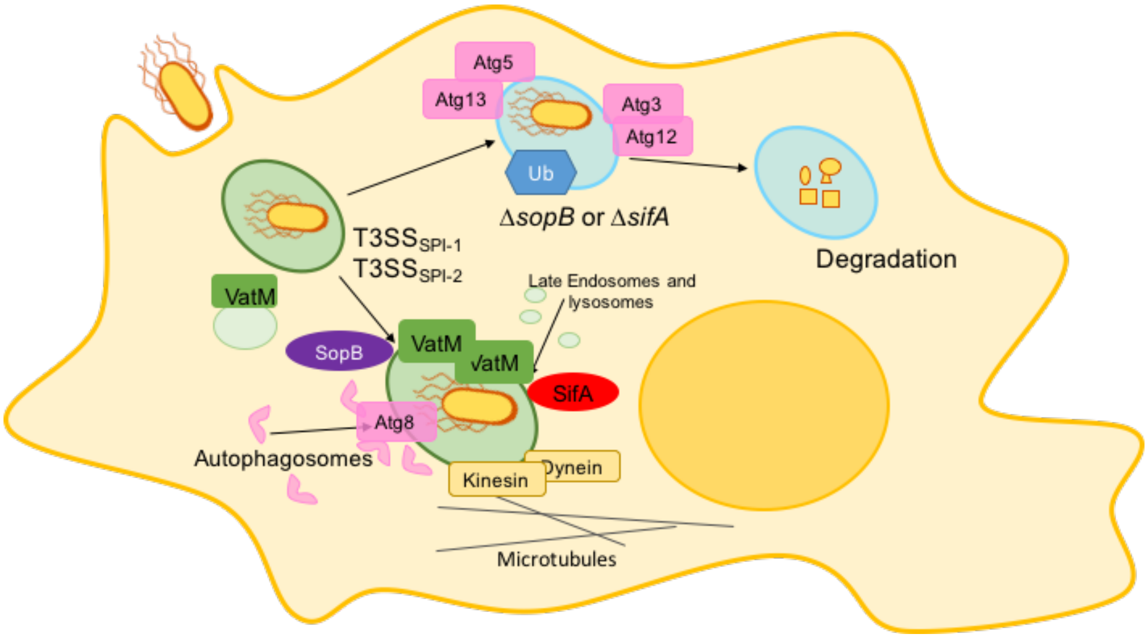


Figure 18 - Model for the biogenesis of the SCV-like compartment in *Dictyostelium discoideum* AX2.

As depicted on **Figure 18**, we propose a model in which *Salmonella* is internalized by *D. discoideum*, using both T3SS$_{SPI-1}$ and T3SS$_{SPI-2}$ in order to diverge the fate of the phagosome in which the pathogen is contained in order to escape the endolysosomal pathway. This vacuole is modified by the action of effector proteins such as SopB and SifA, allowing the recruitment of the autophagy machinery and probably membranes. This hijack of the autophagy pathway allows the survival of *S*. Typhimurium within *D. discoideum*, and its replication at later times of infection (Urrutia et al., 2018). The specific role and the way *Salmonella* can use autophagy to subvert this cellular self-defense response is being currently dilucidated in our laboratory. Additionaly, effectors SopB and SifA could contribute directly to the recruitment of certain cellular factors such as Rab5 to the SCV-like compartment in *D. discoideum*. Altogether our results indicate that the vacuole that contains *S*. Typhimurium in *D. discoideum* present similarities with other pathogen-containing vacuoles, both in this model host and in other phagocytic cells, such as macrophages. This highlights the importance of using *D. discoideum* as a model organism to study the interaction of *Salmonella* with eukaryotic phagocytic cells. To the best of our knowledge, this is the first description of a SCV-like compartment in this host. In the future, the data generated in this Thesis can be further explored as a starting point to determine other cellular and bacterial proteins involved in biological processes related to the interaction of *S*. Typhimurium with *D. discoideum*.

12. CONCLUSIONS

I. SopB and SifA are required for the intracellular survival of *S*. Typhimurium in *D. discoideum*, suggesting that these effectors play a role in the molecular mechanisms involved in this process.

II. Our results indicate that *S*. Typhimurium resides in *D. discoideum* within a membrane-bound compartment that carries the vacuolar ATPase VatM in its membrane.

III. By determining the proteome of a subcellular fraction enriched in intact vacuoles from *D. discoideum* cells infected with *S*. Typhimurium strains, we identified host proteins present in these compartments that are associated to cellular organelles such as endosomes, lysosomes, multivesicular bodies (MVBs) and the ER.

IV. The proteome of these vacuolar compartments also showed the presence of proteins related to vesicular trafficking and autophagy that have been linked to the repair of SCV membranes and the maintenance of this compartment in other cell hosts.

V. The proteome from ∆*sopB* and ∆*sifA* vacuoles is enriched in proteins related to degradative compartments, suggesting that the fate of these mutants is their degradation in these types of compartments. This is in line with the defects in intracellular survival observed for both mutants.

VI. The use of LY294002 to inhibit the production of PI3P did not affect the intracellular survival of *S*. Typhimurium WT or ∆*sopB* and ∆*sifA* mutants in *D. discoideum*, suggesting that this process does not require functional PI3Ks.

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14.- AWARDS AND PUBLICATIONS

14.1 - Fellowships and Grants awarded

CONICYT Doctoral Fellowship 2014. Fellowship for PhD studies in Chile.

ASM Travel Award. Fellowship for 20 PhD students and Post-Doctoral Fellows to attend "5th ASM Conference on *Salmonella*" Potsdam, Germany August 29 to September 1st, 2016.

CONICYT Travel Award 2017. Fellowship for PhD students to attend scientific meetings.

DICTY 2017 Conference Travel Grant. Fellowship for PhD students to attend the 41st Annual International *Dictyostelium* Conference (Dicty 2017), August 20 to 24, 2017. Geneva, Switzerland.

14.2 - Presentations in scientific meetings directly related to this thesis

Camila Valenzuela, Andrea Sabag, Sebastián Riquelme and Carlos A. Santiviago. *Salmonella* Typhimurium Δ*sopB* and Δ*sifA* Mutants Are Impaired in Intracellular Survival in the Amoeba *Dictyostelium discoideum*. ASM Microbe 2016, June 16 to 20, 2016. Boston, Massachusetts, USA.

Camila Valenzuela, Andrea Sabag, Macarena Varas, Ítalo Urrutia, Constanza Morgado, Bayron Labra, Francisco P. Chávez and Carlos A. Santiviago. *Salmonella* Typhimurium requires SopB and SifA to survive intracellularly in a vacuolar compartment in *Dictyostelium discoideum.* 5th ASM Conference on *Salmonella*, August 29 to September 1st, 2016. Potsdam, Germany.

Camila Valenzuela, Andrea Sabag, Macarena Varas, Ítalo Urrutia, Constanza Morgado, Bayron Labra, Francisco P. Chávez y Carlos A. Santiviago. *Salmonella* Typhimurium requiere a los efectores SopB y SifA para sobrevivir intracelularmente en un compartimento vacuolar en *Dictyostelium discoideum*. XXXVIII Congreso Chileno de Microbiología, November 22 to 25, 2016. Valdivia, Chile.

Camila Valenzuela, Andrea Sabag, Ítalo M. Urrutia, Macarena Varas, Carlos A. Santiviago. *Salmonella* Typhimurium requires SopB and SifA to survive intracellularly in a SCV-like compartment in *Dictyostelium discoideum*. FEMS 2017, July 9 to 13, 2017. Valencia, Spain. Work presented as brief talk in a discussion session and also in poster format.

Camila Valenzuela, Andrea Sabag, Ítalo M. Urrutia, Magdalena Gil, Macarena Varas, Jost Enninga and Carlos A. Santiviago. *Salmonella* Typhimurium requires SopB and SifA to survive intracellularly in a SCV-like compartment in *Dictyostelium discoideum.* 41st Annual International *Dictyostelium* Conference

(Dicty 2017), August 20 to 14, 2017. Geneva, Switzerland. Work presented in a flash talk session and also in poster format.

Camila Valenzuela, Magdalena Gil, Andrea Sabag, Ítalo M. Urrutia, Jost Enninga and Carlos A. Santiviago. Proteomic analysis of the *Salmonella*-Containing Vacuole in the social amoeba *Dictyostelium discoideum*. XXIV Congreso Latinoamericano de Microbiología November 13 to 16, 2018. Santiago, Chile.

Supplementary Table 1 – Proteins present only in WT-infected samples.

Locus ID	Description
P42526	Hisactophilin-2 OS=*Dictyostelium discoideum* OX=44689 GN=hatB PE=1 SV=2
P07828	Actin-18 OS=*Dictyostelium discoideum* OX=44689 GN=act18 PE=3 SV=3
Q6TMJ9	Synaptobrevin-A OS=*Dictyostelium discoideum* OX=44689 GN=sybA PE=2 SV=1
Q54LW6	Uncharacterized protein DDB_G0286463 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286463 PE=4 SV=1
Q54P63	Charged multivesicular body protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=chmp3 PE=3 SV=1
Q86HW7	Nuclear transport factor 2 OS=*Dictyostelium discoideum* OX=44689 GN=nutf2 PE=1 SV=1
Q54B20	Succinate dehydrogenase assembly factor 2, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0293946 PE=3 SV=1
Q54LB9	Ponticulin-like protein C5 OS=*Dictyostelium discoideum* OX=44689 GN=ponC5 PE=3 SV=1
A0A0F6B856	Uncharacterized protein OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=STM14_4316 PE=4 SV=1
Q55FM0	ER membrane protein complex subunit 8/9 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268048 PE=3 SV=1
Q54K33	RING-box protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=rbx1 PE=3 SV=1
Q54BN4	40S ribosomal protein S21 OS=*Dictyostelium discoideum* OX=44689 GN=rps21 PE=3 SV=1
Q86HS0	Probable ubiquinone biosynthesis protein coq9, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=coq9 PE=3 SV=2
Q86KL1	Probable E3 ubiquitin-protein ligase bre1 OS=*Dictyostelium discoideum* OX=44689 GN=bre1 PE=3 SV=1
Q54Q05	Elongin-C OS=*Dictyostelium discoideum* OX=44689 GN=tceb1 PE=3 SV=1
Q54I79	Centractin OS=*Dictyostelium discoideum* OX=44689 GN=arpA PE=1 SV=1
Q553W9	Ceroid-lipofuscinosis neuronal protein 5 homolog OS=*Dictyostelium discoideum* OX=44689 GN=cln5 PE=3 SV=1
Q54P40	Iron-sulfur cluster assembly 2 homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=isca2 PE=3 SV=1
Q54VB3	5-demethoxyubiquinone hydroxylase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=coq7 PE=2 SV=1
Q7M438	Ribonuclease DdI OS=*Dictyostelium discoideum* OX=44689 GN=ddiA PE=1 SV=3
Q55BD5	COP9 signalosome complex subunit 7 OS=*Dictyostelium discoideum* OX=44689 GN=csn7 PE=1 SV=1
Q54J86	Dictomallein-1 OS=*Dictyostelium discoideum* OX=44689 GN=dtmlA PE=3 SV=1
Q54D06	Probable ubiquitin-conjugating enzyme E2 variant OS=*Dictyostelium discoideum* OX=44689 GN=ube2v PE=3 SV=1
A0A0F6AXW0	Uncharacterized protein OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=ybaM PE=4 SV=1
O21038	Ribosomal protein S13, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps13 PE=3 SV=1
Q54NZ0	Mitochondrial import inner membrane translocase subunit Tim10 OS=*Dictyostelium discoideum* OX=44689 GN=timm10 PE=3 SV=1
Q54XD0	Ubiquinone biosynthesis O-methyltransferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=coq3 PE=3 SV=1
Q54GK9	Charged multivesicular body protein 2a homolog 1 OS=*Dictyostelium discoideum* OX=44689 GN=chmp2a1 PE=3 SV=2
Q54WY5	Ribosomal RNA processing protein 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=rrp1 PE=3 SV=1
Q552E2	WASH complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=washc2 PE=1 SV=1
Q86CR6	Ubiquitin-like protein atg12 OS=*Dictyostelium discoideum* OX=44689 GN=atg12 PE=3 SV=1

Q86HB8	Counting factor-associated protein C OS=*Dictyostelium discoideum* OX=44689 GN=cfaC PE=3 SV=1
Q54BC8	Proteasome subunit beta type-5 OS=*Dictyostelium discoideum* OX=44689 GN=psmB5 PE=1 SV=1
Q6RZZ9	Kinesin-related protein 13 OS=*Dictyostelium discoideum* OX=44689 GN=kif13 PE=1 SV=1
Q95ZG8	Guanine nucleotide-binding protein subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=gpgA PE=1 SV=1
A0A0F6AXX0	Uncharacterized protein OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=STM14_0575 PE=4 SV=1
Q55GN6	Probable phosphatidylinositol phosphate kinase DDB_G0267588 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267588 PE=1 SV=1
Q556N5	Proteasomal ubiquitin receptor ADRM1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=adrm1-1 PE=1 SV=1
Q54HL6	COP9 signalosome complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=csn2 PE=1 SV=1
Q54MX8	Uncharacterized protein DDB_G0285615 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0285615 PE=3 SV=1
Q55DP8	Aminoacylase-1 OS=*Dictyostelium discoideum* OX=44689 GN=acy1 PE=2 SV=1
Q54T40	Uncharacterized protein DDB_G0282021 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282021 PE=4 SV=1
Q54KT7	General transcription factor IIF subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=gtf2f2 PE=3 SV=2
Q54ES8	Putative synaptobrevin homolog YKT6 OS=*Dictyostelium discoideum* OX=44689 GN=ykt6 PE=1 SV=1
Q54S59	WD repeat-containing protein 61 homolog OS=*Dictyostelium discoideum* OX=44689 GN=wdr61 PE=4 SV=1
Q556I2	Probable 2-aminoethanethiol dioxygenase OS=*Dictyostelium discoideum* OX=44689 GN=ado-1 PE=4 SV=2
Q54QR2	Proteasome subunit beta type-7 OS=*Dictyostelium discoideum* OX=44689 GN=psmB7 PE=3 SV=1
Q86H49	Succinate dehydrogenase assembly factor 3, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=acn9 PE=3 SV=1
Q75JP5	Calponin homology domain-containing protein DDB_G0272472 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272472 PE=4 SV=1
Q557G3	Trafficking protein particle complex subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=trappc1-1 PE=3 SV=1
P34122	cAMP-binding protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=capB PE=1 SV=2
Q55GC7	Sphingomyelinase phosphodiesterase D OS=*Dictyostelium discoideum* OX=44689 GN=sgmD PE=3 SV=1
A0A0F6B552	Phage replication protein O OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=STM14_3214 PE=4 SV=1
Q54CV3	Coiled-coil domain-containing protein 93 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292680 PE=3 SV=1
Q54W07	EKC/KEOPS complex subunit bud32 OS=*Dictyostelium discoideum* OX=44689 GN=bud32 PE=3 SV=1
Q54Z23	Integrator complex subunit 6 homolog OS=*Dictyostelium discoideum* OX=44689 GN=ints6 PE=3 SV=2
Q54KG7	Probable NADPH:adrenodoxin oxidoreductase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=fdxr PE=3 SV=1
Q54TH4	Golgi to ER traffic protein 4 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0281815 PE=3 SV=1
Q86IW8	COMM domain-containing protein 5 OS=*Dictyostelium discoideum* OX=44689 GN=commd5 PE=4 SV=1
Q54WZ0	Cell division cycle 5-like protein OS=*Dictyostelium discoideum* OX=44689 GN=cdc5l PE=3 SV=1
Q54KR1	Cysteine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=cysS PE=3 SV=1
Q8T133	Protein tortoise OS=*Dictyostelium discoideum* OX=44689 GN=torA PE=2 SV=1
Q54LV0	Structural maintenance of chromosomes protein 4 OS=*Dictyostelium discoideum* OX=44689 GN=smc4 PE=3 SV=1
Q55BM0	Succinate dehydrogenase assembly factor 1B, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sdhaf1B PE=3 SV=1

Q54VU7	Methionine aminopeptidase 1D, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=metap1d PE=3 SV=1
Q54QN1	Mitochondrial import inner membrane translocase subunit TIM14 OS=*Dictyostelium discoideum* OX=44689 GN=dnajc19 PE=3 SV=1
Q54UF5	Putative uncharacterized transmembrane protein DDB_G0281105 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0281105 PE=4 SV=1
Q54HX6	Myb-like protein I OS=*Dictyostelium discoideum* OX=44689 GN=mybI PE=3 SV=1
Q54KX4	Probable U6 snRNA-associated Sm-like protein LSm4 OS=*Dictyostelium discoideum* OX=44689 GN=lsm4 PE=3 SV=1
Q54QM0	Mitochondrial import inner membrane translocase subunit tim22 OS=*Dictyostelium discoideum* OX=44689 GN=timm22 PE=3 SV=1
Q54QS0	E3 UFM1-protein ligase 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283667 PE=3 SV=1
Q54ZB3	Conserved oligomeric Golgi complex subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=cog1 PE=3 SV=1
Q8MML5	Paxillin-B OS=*Dictyostelium discoideum* OX=44689 GN=paxB PE=2 SV=1
Q556L1	Signal recognition particle 14 kDa protein OS=*Dictyostelium discoideum* OX=44689 GN=srp14-1 PE=3 SV=1
Q86AD2	Component of gems protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=gemin1 PE=3 SV=1
Q54QK4	COMM domain-containing protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=commd3 PE=4 SV=1
Q86G47	Ras guanine nucleotide exchange factor Q OS=*Dictyostelium discoideum* OX=44689 GN=gefQ PE=2 SV=1
Q75K24	COP9 signalosome complex subunit 8 OS=*Dictyostelium discoideum* OX=44689 GN=csn8 PE=1 SV=1
Q8T293	Probable di-N-acetylchitobiase 2 OS=*Dictyostelium discoideum* OX=44689 GN=ctbs2 PE=3 SV=1
P20425	UMP-CMP kinase OS=*Dictyostelium discoideum* OX=44689 GN=pyrK PE=1 SV=2
Q54VI4	Putative glutathione S-transferase alpha-3 OS=*Dictyostelium discoideum* OX=44689 GN=gsta3 PE=1 SV=1
Q86I14	COMM domain-containing protein 7 OS=*Dictyostelium discoideum* OX=44689 GN=commd7 PE=4 SV=1
Q1ZXQ1	Fumarylacetoacetase OS=*Dictyostelium discoideum* OX=44689 GN=fah PE=3 SV=1
Q86H43	Alanine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=malaS PE=3 SV=1
Q55FT5	Conserved oligomeric Golgi complex subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=cog4 PE=3 SV=1
Q8T2I8	Serine/threonine-protein kinase sepA OS=*Dictyostelium discoideum* OX=44689 GN=sepA PE=2 SV=1
Q555D2	Nuclear pore complex protein DDB_G0274915 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274915 PE=4 SV=2
Q9U7C9	Nucleomorphin OS=*Dictyostelium discoideum* OX=44689 GN=numA PE=1 SV=2
Q556Z0	SWI/SNF complex component SNF12 homolog OS=*Dictyostelium discoideum* OX=44689 GN=snf12-1 PE=3 SV=1
Q55E13	Zinc finger protein ZPR1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=zpr1 PE=3 SV=1
Q555L9	Transcription initiation factor TFIID subunit 12 OS=*Dictyostelium discoideum* OX=44689 GN=TAF12 PE=3 SV=2
Q55GF9	Inner centromere protein A OS=*Dictyostelium discoideum* OX=44689 GN=icpA PE=1 SV=1
Q55DP9	Myb-like protein P OS=*Dictyostelium discoideum* OX=44689 GN=mybP PE=3 SV=1
P0CD65	PAN2-PAN3 deadenylation complex subunit pan3 OS=*Dictyostelium discoideum* OX=44689 GN=pan3 PE=3 SV=1
Q559T8	Probable serine/threonine-protein kinase DDB_G0272282 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272282 PE=3 SV=1

Supplementary Table 2 – Proteins differentially expressed in WT-infected and control samples. Proteins are ordered in descending order according to their Fold change value. Classification is as follows: **SC**: Identifications satisfied both, the automatic fold and statistical criteria. **NSC**: These identifications satisfied the fold criteria but, most likely, this happened by chance. **NC**: These identifications did not meet the fold and P-value criteria. **C**: These identifications were filtered out by the L-stringency and so deserve further experimentation to verify if they are indeed differentially expressed.

Locus ID	Fold change	P-value	Classification	Description
Q55B10	3,937742508	0,0381	NSC	Probable alpha-galactosidase OS=*Dictyostelium discoideum* OX=44689 GN=melA PE=3 SV=1
Q54GJ7	3,741128169	0,0029	C	Probable hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=adhfe1 PE=3 SV=1
Q54VQ0	3,717114703	0,0258	C	Uncharacterized protein DDB_G0280205 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0280205 PE=4 SV=2
Q54JP5	3,445574656	0,0721	NSC	Probable ornithine aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=oatA PE=3 SV=1
Q54HM2	3,399202242	0,0171	SC	Uncharacterized protein DDB_G0289357 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289357 PE=4 SV=1
P10733	3,277383857	0,0024	SC	Severin OS=*Dictyostelium discoideum* OX=44689 GN=sevA PE=1 SV=1
Q54WN8	3,236527923	0,0006	SC	Uncharacterized protein DDB_G0279527 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0279527 PE=1 SV=1
Q552L5	3,093244239	0,0966	NSC	THO complex subunit 7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=thoc7 PE=3 SV=1
Q75JL2	3,070792068	0,0475	NSC	Mitochondrial DNA repair protein recA homolog OS=*Dictyostelium discoideum* OX=44689 GN=recA PE=3 SV=1
Q54YZ4	2,984634204	0,0026	SC	Electron transfer flavoprotein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=etfb PE=3 SV=1
Q55BJ9	2,96635055	0,0003	SC	Superoxide dismutase [Mn], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sod2 PE=3 SV=1
Q23915	2,904144556	0,0000	SC	Probable serine/threonine-protein kinase kinX OS=*Dictyostelium discoideum* OX=44689 GN=kinX PE=3 SV=2
Q54LP8	2,888362464	0,0059	SC	Histone H2B.v3 OS=*Dictyostelium discoideum* OX=44689 GN=H2Bv3 PE=3 SV=1
Q54FD7	2,856453864	0,0020	SC	Electron transfer flavoprotein subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=etfa PE=3 SV=1
Q54ST6	2,830718434	0,0194	C	ER membrane protein complex subunit 7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282229 PE=3 SV=2
Q54VN2	2,823246506	0,0850	NSC	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=coq5 PE=3 SV=1
Q54F42	2,820325204	0,0065	SC	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=*Dictyostelium discoideum* OX=44689 GN=ndufa6 PE=3 SV=1
Q54HI5	2,806473208	0,0296	SC	Lamin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=lmnB PE=1 SV=1

Q54BC2	2,79221024	0,0167	C	Histone H2B.v1 OS=*Dictyostelium discoideum* OX=44689 GN=H2Bv1 PE=3 SV=1
P54872	2,781608861	0,0001	SC	Hydroxymethylglutaryl-CoA synthase A OS=*Dictyostelium discoideum* OX=44689 GN=hgsA PE=1 SV=2
Q54F07	2,778208843	0,0126	C	S-adenosylmethionine synthase OS=*Dictyostelium discoideum* OX=44689 GN=metK PE=1 SV=1
Q27562	2,770391062	0,0130	C	Proteasome subunit alpha type-1 OS=*Dictyostelium discoideum* OX=44689 GN=psmA1 PE=3 SV=1
Q55D12	2,7629067	0,0038	C	Probable histidine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mhisS PE=3 SV=1
Q54M22	2,756630238	0,0004	C	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=bkdA PE=3 SV=1
Q94504	2,756246288	0,0013	C	Cysteine proteinase 7 OS=*Dictyostelium discoideum* OX=44689 GN=cprG PE=1 SV=1
Q54CK6	2,744086039	0,0298	C	Vesicle transport through interaction with t-SNAREs homolog 1A OS=*Dictyostelium discoideum* OX=44689 GN=vti1A PE=1 SV=1
Q54UJ0	2,713875528	0,0148	SC	26S proteasome non-ATPase regulatory subunit 12 OS=*Dictyostelium discoideum* OX=44689 GN=psmD12 PE=2 SV=1
Q54X86	2,675584346	0,0014	C	Probable syntaxin-7B OS=*Dictyostelium discoideum* OX=44689 GN=syn7B PE=3 SV=1
Q54N80	2,615645495	0,0150	C	FK506-binding protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp3 PE=2 SV=1
Q54WD9	2,609715803	0,0591	NSC	Probable tyrosine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mtyrS PE=3 SV=1
O61122	2,577186143	0,0447	NSC	Serine/threonine-protein kinase svkA OS=*Dictyostelium discoideum* OX=44689 GN=svkA PE=1 SV=1
Q55GE2	2,550240239	0,0558	NSC	Probable mitochondrial 2-oxodicarboxylate carrier OS=*Dictyostelium discoideum* OX=44689 GN=mcfT PE=3 SV=1
Q54NZ5	2,545466144	0,0496	NSC	Cullin-3 OS=*Dictyostelium discoideum* OX=44689 GN=culC PE=3 SV=1
Q54CX6	2,530856137	0,0556	NSC	Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=hibA PE=3 SV=1
Q54K47	2,530448804	0,0263	C	Proliferating cell nuclear antigen OS=*Dictyostelium discoideum* OX=44689 GN=pcna PE=3 SV=1
P0C7B6	2,513239869	0,0027	C	Type-1 glutamine synthetase 2 OS=*Dictyostelium discoideum* OX=44689 GN=glnA2 PE=1 SV=1
Q54NS1	2,499246856	0,0003	SC	Putative transferase caf17 homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=caf17 PE=3 SV=1
Q54TY5	2,495539146	0,0093	SC	Probable 39S ribosomal protein L17, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl17 PE=3 SV=1
O15819	2,477562276	0,0125	SC	Histone H3.3 type a OS=*Dictyostelium discoideum* OX=44689 GN=H3a PE=1 SV=1
P26310	2,430984522	0,0081	C	Cytochrome c oxidase polypeptide 6, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cxfA PE=1 SV=2
Q54KB8	2,430677911	0,1372	NSC	Probable glutamate--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=gluS PE=2 SV=1
Q555L8	2,428696975	0,0425	NSC	SH3 and F-BAR domain-containing protein DDB_G0274695 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274695 PE=4 SV=1

Q54ZI6	2,416634274	0,0488	NSC	Phospholipase B-like protein E OS=*Dictyostelium discoideum* OX=44689 GN=plbE PE=3 SV=1
Q54X04	2,401550268	0,0093	C	Probable cysteine desulfurase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=nfs1 PE=1 SV=1
Q557J6	2,394851507	0,0063	C	Drebrin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=abpE-1 PE=2 SV=1
Q869W6	2,387885999	0,0005	C	Probable myosin light chain kinase DDB_G0275057 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275057 PE=3 SV=1
P34123	2,372248028	0,0343	NSC	26S proteasome regulatory subunit 6B homolog OS=*Dictyostelium discoideum* OX=44689 GN=psmC4 PE=1 SV=1
P34124	2,350417068	0,0594	NSC	26S proteasome regulatory subunit 8 OS=*Dictyostelium discoideum* OX=44689 GN=psmC5 PE=1 SV=2
Q54RQ1	2,349091337	0,0027	SC	Extracellular superoxide dismutase [Cu-Zn] 3 OS=*Dictyostelium discoideum* OX=44689 GN=sodC PE=2 SV=1
P27685	2,34826426	0,0011	SC	40S ribosomal protein S2 OS=*Dictyostelium discoideum* OX=44689 GN=rps2 PE=1 SV=1
Q54NS3	2,334854665	0,0254	C	TPR repeat-containing protein DDB_G0285095 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0285095 PE=4 SV=1
Q54TW3	2,331986431	0,0038	SC	60S ribosomal protein L29 OS=*Dictyostelium discoideum* OX=44689 GN=rpl29 PE=3 SV=1
Q54LV3	2,32043674	0,0119	SC	Elongation factor Ts, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=tsfm PE=3 SV=1
P34115	2,310697406	0,0011	C	Cell surface glycoprotein gp138A OS=*Dictyostelium discoideum* OX=44689 GN=GP138A PE=1 SV=1
Q55FR8	2,307833682	0,0704	NSC	Probable carboxypeptidase S-like 2 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267984 PE=3 SV=1
Q54DF1	2,282649033	0,0449	NSC	ATP synthase subunit gamma, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5C1 PE=1 SV=1
Q54QF9	2,28180088	0,0200	C	GrpE protein homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=grpE PE=3 SV=1
Q54G42	2,273108127	0,0287	C	Chitinase domain-containing protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=chid1 PE=3 SV=1
Q86AD5	2,264656786	0,0085	SC	Pyruvate dehydrogenase complex subunit homolog DDB_G0271564, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhX PE=3 SV=1
Q54IX6	2,260642899	0,0130	C	Probable syntaxin-8B OS=*Dictyostelium discoideum* OX=44689 GN=syn8B PE=3 SV=1
Q553R3	2,255627616	0,0394	NSC	Eukaryotic translation initiation factor 4 gamma OS=*Dictyostelium discoideum* OX=44689 GN=eif4g PE=3 SV=1
Q54K91	2,217434894	0,0109	C	Acetyl-CoA hydrolase OS=*Dictyostelium discoideum* OX=44689 GN=ach1 PE=3 SV=1
Q54F10	2,199666886	0,0089	C	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufv2 PE=3 SV=1
P02889	2,170019981	0,0308	C	Probable 26S proteasome non-ATPase regulatory subunit 8 OS=*Dictyostelium discoideum* OX=44689 GN=psmD8-1 PE=2 SV=2
Q54SM3	2,151084534	0,0268	C	Peptidyl-prolyl cis-trans isomerase A OS=*Dictyostelium discoideum* OX=44689 GN=ppiA PE=1 SV=1
Q54YG5	2,137335564	0,0064	C	Trafficking protein particle complex subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=trappc5 PE=3 SV=1

P54680	2,13013962	0,1631	NSC	Fimbrin OS=*Dictyostelium discoideum* OX=44689 GN=fimA PE=2 SV=2
Q8T2J9	2,126098456	0,0001	SC	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mccb PE=3 SV=2
Q54DD3	2,119448823	0,0004	C	Aminomethyltransferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcvT PE=3 SV=1
Q55EX9	2,117323453	0,0608	NSC	Putative methyltransferase DDB_G0268948 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268948 PE=1 SV=2
P19198	2,115264325	0,0316	NSC	cAMP-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=capA-1 PE=2 SV=2
Q54DS3	2,101759752	0,0037	C	Transmembrane protein DDB_G0292058 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292058 PE=2 SV=1
Q54XX1	2,098321873	0,1114	NSC	Signal recognition particle receptor subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=srprb PE=3 SV=1
Q54LN4	2,091144775	0,0322	NSC	Gamma-glutamyl hydrolase A OS=*Dictyostelium discoideum* OX=44689 GN=gghA PE=3 SV=1
Q54YD2	2,086968374	0,0165	C	Putative phosphatidylglycerol/phosphatidylinositol transfer protein DDB_G0278295 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0278295 PE=2 SV=1
Q54NI6	2,086083264	0,0031	SC	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufs7 PE=3 SV=1
Q54VI6	2,079053152	0,0202	SC	Translocon-associated protein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=ssr2 PE=2 SV=2
Q6TMK3	2,077443887	0,0774	NSC	Heat shock protein 88 OS=*Dictyostelium discoideum* OX=44689 GN=hspH PE=1 SV=1
Q54P71	2,073465182	0,0111	C	Probable acid phosphatase DDB_G0284755 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284755 PE=3 SV=2
Q54VA2	2,070578132	0,0004	SC	Fumarate hydratase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=fumH PE=3 SV=1
Q86H98	2,010519192	0,0564	NSC	Charged multivesicular body protein 4 OS=*Dictyostelium discoideum* OX=44689 GN=chmp4 PE=3 SV=1
Q55EQ3	2,004373836	0,0019	SC	Uncharacterized abhydrolase domain-containing protein DDB_G0269086 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0269086 PE=1 SV=2
Q76P23	1,997134628	0,0274	SC	Mitochondrial substrate carrier family protein Q OS=*Dictyostelium discoideum* OX=44689 GN=mcfQ PE=2 SV=1
Q8T1V6	1,988985072	0,0184	C	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufs4 PE=3 SV=2
Q8IS15	1,980707565	0,2288	NSC	Ras guanine nucleotide exchange factor I OS=*Dictyostelium discoideum* OX=44689 GN=gefI PE=2 SV=1
Q869S7	1,97889648	0,0093	SC	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=scsB PE=3 SV=1
Q1ZXF5	1,973797001	0,0453	NSC	Probable cytochrome P450 508A4 OS=*Dictyostelium discoideum* OX=44689 GN=cyp508A4 PE=3 SV=1
Q54EW3	1,953896516	0,0090	C	Probable importin-5 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0291650 PE=3 SV=1
Q54UB5	1,952981105	0,0366	NSC	26S proteasome non-ATPase regulatory subunit 11 OS=*Dictyostelium discoideum* OX=44689 GN=psmD11 PE=2 SV=1
P53766	1,948394513	0,0026	C	Uracil-DNA glycosylase OS=*Dictyostelium discoideum* OX=44689 GN=uglA PE=2 SV=2

Q54DU9	1,946477092	0,0359	NSC	Probable protein tyrosine phosphatase type IVA A OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292024 PE=3 SV=1
Q55AI5	1,946442669	0,0089	SC	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=scsC PE=3 SV=1
Q54E48	1,943744989	0,0892	NSC	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0291852 PE=3 SV=1
Q5XM24	1,938111401	0,1902	NSC	Autocrine proliferation repressor protein A OS=*Dictyostelium discoideum* OX=44689 GN=aprA PE=1 SV=1
Q1ZXQ8	1,924520068	0,0744	NSC	Centrosomal protein 224 OS=*Dictyostelium discoideum* OX=44689 GN=mtaA PE=1 SV=1
Q54NX0	1,922197817	0,0054	C	Putative rRNA methyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=fsjC PE=3 SV=1
Q558Z9	1,92079703	0,0397	NSC	Exocyst complex component 7 OS=*Dictyostelium discoideum* OX=44689 GN=exoc7 PE=3 SV=1
P54660	1,920766306	0,0022	SC	Ponticulin OS=*Dictyostelium discoideum* OX=44689 GN=ponA PE=1 SV=1
Q55F42	1,915574583	0,0206	SC	ATP synthase subunit delta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5D PE=3 SV=1
Q54CL0	1,915082014	0,0233	C	Apoptosis inhibitor 5 homolog OS=*Dictyostelium discoideum* OX=44689 GN=api5 PE=3 SV=1
Q869Z4	1,912736681	0,0020	SC	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pck2 PE=3 SV=1
P36413	1,898941109	0,0213	SC	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhC PE=1 SV=2
Q94464	1,893353852	0,0032	SC	Dynamin-A OS=*Dictyostelium discoideum* OX=44689 GN=dymA PE=1 SV=2
P34136	1,892340774	0,0058	SC	3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 OS=*Dictyostelium discoideum* OX=44689 GN=hmgB PE=2 SV=2
Q54UU6	1,890563879	0,0091	C	KRR1 small subunit processome component homolog OS=*Dictyostelium discoideum* OX=44689 GN=krr1 PE=3 SV=1
Q54U07	1,890041396	0,0465	NSC	Nascent polypeptide-associated complex subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=nacA PE=3 SV=1
Q23889	1,889739884	0,0369	NSC	Ribosomal protein S19, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps19 PE=3 SV=1
Q9NGQ2	1,880178159	0,0795	NSC	Kinesin-related protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=kif1 PE=1 SV=1
Q54EX7	1,876596825	0,0311	SC	Glutaredoxin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=grxB PE=3 SV=1
Q54M21	1,843985296	0,1709	NSC	DnaJ homolog subfamily C member 3 homolog OS=*Dictyostelium discoideum* OX=44689 GN=dnajc3 PE=3 SV=1
Q54D07	1,842152928	0,0729	NSC	Cytochrome c1, heme protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cyc1 PE=3 SV=1
Q54Q48	1,834487747	0,0018	SC	Putative uncharacterized protein DDB_G0284097 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284097 PE=1 SV=1
Q54WP3	1,832525581	0,0043	C	Probable 39S ribosomal protein L22, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl22 PE=3 SV=1
Q54JY7	1,825086367	0,0010	C	Syntaxin-7A OS=*Dictyostelium discoideum* OX=44689 GN=syn7A PE=1 SV=1

Q556U6	1,8185332	0,0490	NSC	Luminal-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=bip1-1 PE=3 SV=1
Q54XK0	1,816936631	0,0112	C	Probable 39S ribosomal protein L27, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl27 PE=3 SV=1
Q54S60	1,815877697	0,0351	NSC	Translation machinery-associated protein 16 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282655 PE=3 SV=1
Q54XS2	1,808042377	0,0002	SC	Probable aconitate hydratase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aco2 PE=3 SV=1
Q1ZXA8	1,806577354	0,0049	SC	Uncharacterized protein DDB_G0292160 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292160 PE=3 SV=1
P54639	1,804946857	0,0185	C	Cysteine proteinase 4 OS=*Dictyostelium discoideum* OX=44689 GN=cprD PE=2 SV=2
Q869R8	1,80144509	0,0943	NSC	Triosephosphate isomerase OS=*Dictyostelium discoideum* OX=44689 GN=tpiA PE=3 SV=1
Q86H60	1,79825893	0,0048	C	Small heat shock protein hspK OS=*Dictyostelium discoideum* OX=44689 GN=hspK PE=3 SV=1
Q86AD9	1,794075456	0,0442	NSC	Probable acetyl-CoA acetyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271544 PE=2 SV=1
Q964D8	1,793763246	0,0696	NSC	Beta-ureidopropionase OS=*Dictyostelium discoideum* OX=44689 GN=pyd3 PE=1 SV=1
Q54JD2	1,791407324	0,0470	NSC	Putative uncharacterized protein DDB_G0288137 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288137 PE=4 SV=1
Q9TW32	1,778042466	0,0583	NSC	Peptidyl-prolyl cis-trans isomerase B OS=*Dictyostelium discoideum* OX=44689 GN=cypB PE=1 SV=1
Q55FI1	1,777346336	0,0018	SC	4-aminobutyrate aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=gabT PE=3 SV=1
Q54NG2	1,77706026	0,0009	SC	60S ribosomal protein L17 OS=*Dictyostelium discoideum* OX=44689 GN=rpl17 PE=3 SV=1
Q869N6	1,768412576	0,0165	C	3-hydroxybutyryl-CoA dehydratase-like protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271866 PE=3 SV=1
Q54JV8	1,763066466	0,0135	C	Probable glycine cleavage system H protein 1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcvH1 PE=3 SV=1
O77229	1,75985378	0,0007	SC	Catalase-A OS=*Dictyostelium discoideum* OX=44689 GN=catA PE=2 SV=2
Q8MYF0	1,751561794	0,0104	C	Mitochondrial genome maintenance protein mgm101 homolog OS=*Dictyostelium discoideum* OX=44689 GN=mgm101 PE=3 SV=1
Q9NKW1	1,751470667	0,0190	SC	Peroxisomal multifunctional enzyme A OS=*Dictyostelium discoideum* OX=44689 GN=mfeA PE=2 SV=1
Q54J34	1,744780381	0,0036	C	Adenylosuccinate lyase OS=*Dictyostelium discoideum* OX=44689 GN=purB PE=3 SV=1
P13466	1,744499738	0,0044	SC	Gelation factor OS=*Dictyostelium discoideum* OX=44689 GN=abpC PE=1 SV=1
Q54M18	1,740587582	0,0024	SC	Bifunctional protein argC, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=argC PE=1 SV=1
Q55E35	1,73903755	0,0623	NSC	Signal peptidase complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=spcs2 PE=3 SV=2
O60952	1,73400126	0,0583	NSC	LIM domain-containing protein E OS=*Dictyostelium discoideum* OX=44689 GN=limE PE=1 SV=1

P13651	1,723431496	0,1111	NSC	Eukaryotic translation initiation factor 5A OS=*Dictyostelium discoideum* OX=44689 GN=eif5a PE=1 SV=2
Q54IM8	1,720307452	0,0025	C	Isobutyryl-CoA dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=acad8 PE=3 SV=1
Q54D04	1,714349785	0,0099	SC	Probable malate dehydrogenase 2, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mdhB PE=1 SV=1
Q54K35	1,712013498	0,0390	NSC	Mitochondrial import inner membrane translocase subunit tim17 OS=*Dictyostelium discoideum* OX=44689 GN=timm17 PE=3 SV=1
Q54R04	1,711281399	0,1882	NSC	ADP-ribosylation factor-like protein 8 OS=*Dictyostelium discoideum* OX=44689 GN=arl8 PE=3 SV=1
P05095	1,707893133	0,0734	NSC	Alpha-actinin A OS=*Dictyostelium discoideum* OX=44689 GN=abpA PE=1 SV=2
Q869Z0	1,706360321	0,0476	NSC	Putative protein disulfide-isomerase DDB_G0275025 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275025 PE=1 SV=1
Q86KZ5	1,705187763	0,0493	NSC	Ribosome maturation protein SBDS OS=*Dictyostelium discoideum* OX=44689 GN=sbds PE=3 SV=2
P30815	1,699756438	0,0438	NSC	Cytochrome c oxidase subunit 4, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cxdA PE=2 SV=2
Q54QJ9	1,689206724	0,1160	NSC	Adenylate kinase OS=*Dictyostelium discoideum* OX=44689 GN=adkA PE=3 SV=1
Q54UH8	1,688152812	0,0855	NSC	D-3-phosphoglycerate dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=serA PE=1 SV=1
Q558Z0	1,677542938	0,1684	NSC	Probable arginine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=argS1 PE=3 SV=1
Q54XZ0	1,674920625	0,0480	NSC	Probable enoyl-CoA hydratase 2 OS=*Dictyostelium discoideum* OX=44689 GN=mfeB PE=2 SV=1
Q8IS16	1,672263537	0,1278	NSC	Ras guanine nucleotide exchange factor H OS=*Dictyostelium discoideum* OX=44689 GN=gefH PE=1 SV=1
Q553P5	1,669343801	0,0218	C	Syntaxin-8A OS=*Dictyostelium discoideum* OX=44689 GN=syn8A PE=1 SV=1
Q5TJ65	1,667950502	0,0078	SC	Protein VASP homolog OS=*Dictyostelium discoideum* OX=44689 GN=vasp PE=1 SV=1
Q54M70	1,663655586	0,0843	NSC	Aspartyl aminopeptidase OS=*Dictyostelium discoideum* OX=44689 GN=dnpep PE=1 SV=1
Q54DU1	1,660093144	0,2147	NSC	Mitochondrial substrate carrier family protein P OS=*Dictyostelium discoideum* OX=44689 GN=mcfP PE=3 SV=1
Q54JD4	1,656727551	0,0023	SC	Uncharacterized protein DDB_G0288133 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288133 PE=4 SV=1
P02886	1,654761938	0,0372	NSC	Discoidin-1 subunit A OS=*Dictyostelium discoideum* OX=44689 GN=dscA-1 PE=1 SV=3
Q54WH2	1,65015675	0,1794	NSC	Formin-A OS=*Dictyostelium discoideum* OX=44689 GN=forA PE=1 SV=1
Q55BI2	1,643609537	0,0162	SC	Isocitrate dehydrogenase [NAD] regulatory subunit A, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=idhA PE=3 SV=1
Q54R47	1,640709166	0,0214	C	Glutaryl-CoA dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcdh PE=3 SV=1
Q54QG4	1,638918218	0,0369	NSC	Uncharacterized protein DDB_G0283843 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283843 PE=4 SV=1

P02887	1,638133392	0,0397	NSC	Discoidin-1 subunit B/C OS=*Dictyostelium discoideum* OX=44689 GN=dscC-1 PE=1 SV=1
Q556Y4	1,637297343	0,0083	C	Casein kinase I OS=*Dictyostelium discoideum* OX=44689 GN=cak1-1 PE=1 SV=1
Q55AH5	1,636176448	0,0036	SC	V-type proton ATPase subunit F OS=*Dictyostelium discoideum* OX=44689 GN=vatF PE=3 SV=1
O00780	1,627604653	0,0358	NSC	V-type proton ATPase subunit E OS=*Dictyostelium discoideum* OX=44689 GN=vatE PE=1 SV=1
Q54IT3	1,626593802	0,0218	SC	Probable flavin-containing monoamine oxidase A OS=*Dictyostelium discoideum* OX=44689 GN=maoA PE=3 SV=1
Q8T2K9	1,626032352	0,0465	NSC	Malate synthase OS=*Dictyostelium discoideum* OX=44689 GN=masA PE=2 SV=2
Q54JE4	1,621737682	0,0054	SC	2-oxoglutarate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ogdh PE=3 SV=1
Q54CE4	1,617296423	0,1024	NSC	Probable isoleucine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mileS PE=3 SV=1
Q54SF7	1,616725939	0,0268	SC	Aspartate aminotransferase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=aatB PE=3 SV=1
Q9GPM4	1,615539944	0,1556	NSC	Phosphoglycerate kinase OS=*Dictyostelium discoideum* OX=44689 GN=pgkA PE=1 SV=2
P09402	1,614842447	0,0146	SC	Myosin, essential light chain OS=*Dictyostelium discoideum* OX=44689 GN=mlcE PE=2 SV=2
Q54I58	1,612612534	0,0430	NSC	Protein NipSnap homolog OS=*Dictyostelium discoideum* OX=44689 GN=nipsnap PE=3 SV=1
Q54TR1	1,610114374	0,0973	NSC	Counting factor associated protein D OS=*Dictyostelium discoideum* OX=44689 GN=cfaD PE=1 SV=1
P02888	1,606649623	0,0379	NSC	Discoidin-1 subunit D OS=*Dictyostelium discoideum* OX=44689 GN=dscD-1 PE=1 SV=2
Q86JD4	1,606329142	0,1508	NSC	Signal peptidase complex catalytic subunit sec11 OS=*Dictyostelium discoideum* OX=44689 GN=sec11 PE=3 SV=1
Q55D66	1,603672162	0,0966	NSC	Proteasome subunit beta type-3 OS=*Dictyostelium discoideum* OX=44689 GN=psmB3 PE=3 SV=1
Q54CT8	1,592362119	0,1005	NSC	Probable adenylate kinase B OS=*Dictyostelium discoideum* OX=44689 GN=adkB PE=3 SV=1
Q9NKX1	1,591550057	0,0584	NSC	Endoplasmin homolog OS=*Dictyostelium discoideum* OX=44689 GN=grp94 PE=2 SV=2
Q54SV6	1,590828319	0,0444	NSC	Mitochondrial import inner membrane translocase subunit tim16 OS=*Dictyostelium discoideum* OX=44689 GN=timm16 PE=3 SV=1
O96042	1,587133348	0,2775	NSC	Differentiation-associated protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=dia2 PE=2 SV=1
Q54SR7	1,579625547	0,0701	NSC	FK506-binding protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp2 PE=3 SV=1
Q23858	1,578166968	0,0179	SC	Calreticulin OS=*Dictyostelium discoideum* OX=44689 GN=crtA PE=1 SV=3
Q54PX7	1,576075661	0,0462	NSC	PCI domain-containing protein 2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=pcid2 PE=3 SV=1
Q54LV1	1,575317807	0,1401	NSC	UV excision repair protein RAD23 homolog OS=*Dictyostelium discoideum* OX=44689 GN=rcbA PE=1 SV=1
Q54RX9	1,573757408	0,0097	C	Putative ras-related protein Rab-5B OS=*Dictyostelium discoideum* OX=44689 GN=rab5B PE=5 SV=1

Q54HB4	1,571646999	0,0841	NSC	Transcription and mRNA export factor ENY2 OS=*Dictyostelium discoideum* OX=44689 GN=eny2 PE=3 SV=1
Q8T191	1,567375643	0,0635	NSC	Probable UDP-glucose:glycoprotein glucosyltransferase A OS=*Dictyostelium discoideum* OX=44689 GN=ggtA PE=1 SV=2
Q869Y7	1,566661803	0,0090	SC	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=odhB PE=1 SV=1
Q86CR8	1,566282227	0,0004	C	Autophagy-related protein 8 OS=*Dictyostelium discoideum* OX=44689 GN=atg8 PE=2 SV=1
Q9BKJ9	1,56381405	0,0017	SC	Lysosome membrane protein 2-B OS=*Dictyostelium discoideum* OX=44689 GN=lmpB PE=1 SV=1
Q23862	1,563445269	0,0015	SC	Rho-related protein racE OS=*Dictyostelium discoideum* OX=44689 GN=racE PE=1 SV=1
Q55F21	1,563385515	0,0138	SC	Aspartate aminotransferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aatA PE=3 SV=1
Q54GI9	1,562232088	0,0869	NSC	Prohibitin-1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=phbA PE=3 SV=1
Q54RB9	1,561350149	0,0060	SC	Calcium-binding mitochondrial carrier protein OS=*Dictyostelium discoideum* OX=44689 GN=mcfO PE=3 SV=1
Q8TA03	1,560737545	0,0049	SC	6-phosphogluconate dehydrogenase, decarboxylating OS=*Dictyostelium discoideum* OX=44689 GN=gnd PE=1 SV=1
Q54B68	1,556874771	0,0041	SC	Isocitrate dehydrogenase [NAD] regulatory subunit B, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=idhB PE=3 SV=1
Q54PV8	1,556701146	0,2168	NSC	Inorganic pyrophosphatase OS=*Dictyostelium discoideum* OX=44689 GN=ppa1 PE=1 SV=1
Q54Q31	1,554994857	0,0763	NSC	Prohibitin-2 OS=*Dictyostelium discoideum* OX=44689 GN=phbB PE=3 SV=1
P02599	1,554711591	0,0454	NSC	Calmodulin OS=*Dictyostelium discoideum* OX=44689 GN=calA PE=1 SV=3
Q9UA41	1,552570172	0,0224	SC	Peptidyl-prolyl cis-trans isomerase D, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cypD PE=1 SV=1
O77257	1,550833301	0,0494	NSC	Protein gp17 OS=*Dictyostelium discoideum* OX=44689 GN=p17 PE=2 SV=1
Q54SG3	1,549860452	0,1228	NSC	Uncharacterized transmembrane protein DDB_G0282483 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282483 PE=4 SV=1
Q54PN7	1,549774251	0,2644	NSC	26S proteasome regulatory subunit 6A homolog OS=*Dictyostelium discoideum* OX=44689 GN=psmC3 PE=1 SV=1
Q54Z26	1,546110497	0,0571	NSC	Serine hydroxymethyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=shmt1 PE=1 SV=1
Q54RK5	1,544211922	0,1056	NSC	Enolase A OS=*Dictyostelium discoideum* OX=44689 GN=enoA PE=3 SV=1
P42520	1,543347676	0,0066	SC	40S ribosomal protein S17 OS=*Dictyostelium discoideum* OX=44689 GN=rps17 PE=3 SV=2
O21036	1,543270805	0,1093	NSC	Ribosomal protein S8, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps8 PE=3 SV=1
Q54KE6	1,541570074	0,0234	SC	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mccA PE=3 SV=1
Q5V9F0	1,541321276	0,0253	C	Cytosol aminopeptidase OS=*Dictyostelium discoideum* OX=44689 GN=lap PE=1 SV=1

Q54R45	1,540508498	0,1184	NSC	Translocon-associated protein subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=ssr1 PE=3 SV=1
Q54SE2	1,533949051	0,0424	NSC	1-Cys peroxiredoxin OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282517 PE=3 SV=1
Q54WR9	1,525442184	0,1625	NSC	Type-3 glutamine synthetase OS=*Dictyostelium discoideum* OX=44689 GN=glnA3 PE=1 SV=1
Q54XB5	1,522873666	0,0538	NSC	60S ribosomal protein L31 OS=*Dictyostelium discoideum* OX=44689 GN=rpl31 PE=3 SV=1
Q8I0H7	1,522135667	0,0101	SC	Heat shock 70 kDa protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mhsp70 PE=1 SV=1
Q4W6B5	1,521611665	0,0216	SC	Mitochondrial-processing peptidase subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=mppB PE=1 SV=1
P25323	1,521522347	0,2076	NSC	Myosin light chain kinase A OS=*Dictyostelium discoideum* OX=44689 GN=mlkA PE=1 SV=2
P34116	1,521358943	0,0576	NSC	Cell surface glycoprotein gp138B OS=*Dictyostelium discoideum* OX=44689 GN=GP138B PE=1 SV=1
Q7KWQ2	1,517734425	0,2191	NSC	Serine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=serS PE=1 SV=1
Q54BQ3	1,509826887	0,0166	SC	60S ribosomal protein L23a OS=*Dictyostelium discoideum* OX=44689 GN=rpl23a PE=1 SV=1
Q54GW3	1,509336204	0,0273	C	Coiled-coil domain-containing protein 124 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289893 PE=3 SV=1
P13021	1,50763379	0,0271	SC	F-actin-capping protein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=acpA PE=1 SV=1
Q554D9	1,50549082	0,2129	NSC	Asparagine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=asnS1 PE=1 SV=1
Q54D99	1,502319892	0,0173	C	Probable 39S ribosomal protein L53, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl53 PE=3 SV=1
Q54J23	1,501736763	0,0285	SC	60S ribosomal protein L35 OS=*Dictyostelium discoideum* OX=44689 GN=rpl35 PE=3 SV=1
Q55C70	1,500946437	0,0829	NSC	Mitochondrial import inner membrane translocase subunit tim50 OS=*Dictyostelium discoideum* OX=44689 GN=timm50 PE=3 SV=1
Q54N17	1,499197931	0,0049	SC	40S ribosomal protein S15 OS=*Dictyostelium discoideum* OX=44689 GN=rps15 PE=3 SV=1
O96552	1,498657697	0,0736	NSC	Charged multivesicular body protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=chmp1 PE=3 SV=1
P13022	1,496082916	0,0065	SC	F-actin-capping protein subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=acpB PE=1 SV=1
Q54XM6	1,495276585	0,1181	NSC	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=etfdh PE=3 SV=1
Q54RA8	1,495268081	0,1191	NSC	ATP synthase subunit O, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5O PE=3 SV=1
Q95VZ3	1,493656656	0,2019	NSC	Protein CARMIL OS=*Dictyostelium discoideum* OX=44689 GN=carmil PE=1 SV=1
O76856	1,492447945	0,0094	SC	Cathepsin D OS=*Dictyostelium discoideum* OX=44689 GN=ctsD PE=1 SV=1
Q869Q8	1,49117466	0,0495	NSC	Probable serine carboxypeptidase CPVL OS=*Dictyostelium discoideum* OX=44689 GN=cpvl PE=3 SV=1

Q23892	1,490667318	0,0105	C	Lysosomal beta glucosidase OS=*Dictyostelium discoideum* OX=44689 GN=gluA PE=1 SV=2
Q1ZXF1	1,485978463	0,1593	NSC	Probable enoyl-CoA hydratase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=echs1 PE=3 SV=1
Q54M82	1,483840895	0,0171	SC	Probable cytochrome b-c1 complex subunit 7 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286171 PE=3 SV=1
P28178	1,479685245	0,0843	NSC	Protein kinase 2 OS=*Dictyostelium discoideum* OX=44689 GN=pkgB PE=1 SV=2
Q553V1	1,479021021	0,0003	SC	Citrate synthase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cs PE=3 SV=1
Q54RN1	1,474422922	0,0690	NSC	Extracellular superoxide dismutase [Cu-Zn] 2 OS=*Dictyostelium discoideum* OX=44689 GN=sodB PE=2 SV=1
Q54NB6	1,472366799	0,0800	NSC	FK506-binding protein 4 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp4 PE=1 SV=1
Q54PR9	1,472084821	0,0076	C	Counting factor 60 OS=*Dictyostelium discoideum* OX=44689 GN=cf60 PE=1 SV=1
P29505	1,469103257	0,0048	SC	Cytochrome c oxidase subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=cxeA PE=1 SV=3
Q23911	1,468364565	0,0919	NSC	Protein 29C OS=*Dictyostelium discoideum* OX=44689 GN=29C PE=3 SV=2
P54648	1,467026214	0,0441	NSC	V-type proton ATPase subunit C OS=*Dictyostelium discoideum* OX=44689 GN=vatC PE=2 SV=1
P29447	1,462913486	0,1020	NSC	Thioredoxin-3 OS=*Dictyostelium discoideum* OX=44689 GN=trxC PE=3 SV=2
Q9NH03	1,462023843	0,0338	NSC	Farnesyl diphosphate synthase OS=*Dictyostelium discoideum* OX=44689 GN=fps PE=2 SV=1
Q54QN4	1,462023623	0,1146	NSC	Uncharacterized transmembrane protein DDB_G0283731 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283731 PE=4 SV=1
Q86HX0	1,461449934	0,0818	NSC	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhB PE=1 SV=1
Q559Z4	1,459950321	0,0728	NSC	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=ndufa5 PE=3 SV=1
Q555C8	1,457293551	0,0823	NSC	Monothiol glutaredoxin-5, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=grx5 PE=3 SV=1
Q76NV5	1,448161672	0,1262	NSC	4-hydroxyphenylpyruvate dioxygenase OS=*Dictyostelium discoideum* OX=44689 GN=hpd PE=1 SV=1
P34093	1,444413947	0,0058	SC	Nucleoside diphosphate kinase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndkM PE=1 SV=2
P42528	1,441851356	0,0118	SC	Actin-related protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=arpC PE=1 SV=1
P24639	1,438404496	0,1301	NSC	Annexin A7 OS=*Dictyostelium discoideum* OX=44689 GN=nxnA PE=1 SV=1
Q54C70	1,438105268	0,0693	NSC	Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhA PE=1 SV=1
Q54E22	1,436437234	0,0206	C	Acyl carrier protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufab1 PE=3 SV=1
Q54DD2	1,434682151	0,1533	NSC	Thimet-like oligopeptidase OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292362 PE=3 SV=1

P34149	1,43276393	0,0699	NSC	Rho-related protein racC OS=*Dictyostelium discoideum* OX=44689 GN=racC PE=1 SV=1
P46794	1,43217139	0,0699	NSC	Cystathionine beta-synthase OS=*Dictyostelium discoideum* OX=44689 GN=cysB PE=2 SV=2
P22685	1,422368523	0,0193	SC	60S acidic ribosomal protein P0 OS=*Dictyostelium discoideum* OX=44689 GN=rplp0 PE=1 SV=2
Q7Z2B8	1,416333575	0,1607	NSC	Myosin-ID light chain OS=*Dictyostelium discoideum* OX=44689 GN=mlcD PE=1 SV=1
Q554H5	1,415030624	0,1669	NSC	Phospholipase B-like protein F OS=*Dictyostelium discoideum* OX=44689 GN=plbF PE=3 SV=1
Q86IV5	1,409937483	0,0201	C	Countin-1 OS=*Dictyostelium discoideum* OX=44689 GN=ctnA PE=1 SV=1
Q54VG0	1,407295236	0,0160	C	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1 homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=odhA PE=3 SV=1
Q86AV5	1,404913573	0,2498	NSC	Mitochondrial substrate carrier family protein X OS=*Dictyostelium discoideum* OX=44689 GN=mcfX PE=3 SV=1
Q54YT4	1,404899215	0,0712	NSC	Enoyl-[acyl-carrier-protein] reductase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mecr PE=3 SV=1
Q54DK1	1,399454737	0,1718	NSC	Sulfide:quinone oxidoreductase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sqor PE=3 SV=1
Q55BV5	1,398191101	0,0528	NSC	26S proteasome regulatory subunit 4 homolog OS=*Dictyostelium discoideum* OX=44689 GN=psmC1 PE=1 SV=1
Q8MML6	1,391503833	0,0455	NSC	V-type proton ATPase subunit H OS=*Dictyostelium discoideum* OX=44689 GN=vatH PE=1 SV=1
Q54WA4	1,39026633	0,0545	NSC	Probable 28S ribosomal protein S10, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps10 PE=3 SV=1
Q58A42	1,387179268	0,0157	SC	Protein DD3-3 OS=*Dictyostelium discoideum* OX=44689 GN=DD3-3 PE=2 SV=1
Q86I43	1,384901523	0,1744	NSC	Uncharacterized protein DDB_G0275161 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275161 PE=2 SV=1
P22683	1,384138935	0,0581	NSC	60S acidic ribosomal protein P2 OS=*Dictyostelium discoideum* OX=44689 GN=rplp2 PE=1 SV=3
Q86AV6	1,380901603	0,0231	C	Citrate synthase OS=*Dictyostelium discoideum* OX=44689 GN=gltA PE=3 SV=1
Q76NW2	1,379877833	0,0724	NSC	Histone H4 OS=*Dictyostelium discoideum* OX=44689 GN=H4a PE=1 SV=1
Q869U7	1,372207155	0,0377	NSC	40S ribosomal protein S18 OS=*Dictyostelium discoideum* OX=44689 GN=rps18 PE=3 SV=1
P36967	1,369835657	0,1396	NSC	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=scsA PE=1 SV=3
Q86A77	1,367691564	0,1171	NSC	V-type proton ATPase subunit D OS=*Dictyostelium discoideum* OX=44689 GN=atp6v1d PE=1 SV=1
P32255	1,367241892	0,0637	NSC	Tubulin alpha chain OS=*Dictyostelium discoideum* OX=44689 GN=tubA PE=1 SV=1
P42530	1,36131785	0,0843	NSC	Discoidin-2 OS=*Dictyostelium discoideum* OX=44689 GN=dscE PE=1 SV=1
Q54MA6	1,360753267	0,0037	SC	40S ribosomal protein S5 OS=*Dictyostelium discoideum* OX=44689 GN=rps5 PE=1 SV=1

Q54JD9	1,359904603	0,0032	SC	Probable succinyl-CoA:3-ketoacid coenzyme A transferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=oxct1 PE=3 SV=1
P36408	1,358534043	0,0605	NSC	Guanine nucleotide-binding protein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=gpbA PE=1 SV=1
O77082	1,358055309	0,0333	NSC	40S ribosomal protein S10 OS=*Dictyostelium discoideum* OX=44689 GN=rps10 PE=1 SV=3
Q54KD9	1,358036264	0,2704	NSC	Ran-specific GTPase-activating protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=ranbp1 PE=1 SV=1
Q54ME1	1,357487219	0,2244	NSC	Gamete and mating-type specific protein A OS=*Dictyostelium discoideum* OX=44689 GN=gmsA PE=2 SV=1
Q54EW1	1,357099406	0,0666	NSC	Serine hydroxymethyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=shmt2 PE=3 SV=1
Q54I10	1,356887904	0,0575	NSC	Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mmsdh PE=3 SV=1
Q54BC6	1,356870469	0,1632	NSC	26S proteasome non-ATPase regulatory subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=psmD2 PE=1 SV=1
O00897	1,353449182	0,0364	NSC	Calmodulin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=calB PE=2 SV=1
Q54J47	1,351599003	0,2060	NSC	Probable pyridoxal 5'-phosphate synthase subunit pdx1 OS=*Dictyostelium discoideum* OX=44689 GN=pdx1 PE=1 SV=1
Q54TR8	1,350877353	0,0492	NSC	Nascent polypeptide-associated complex subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=nacB PE=3 SV=1
Q54EN4	1,349697961	0,0678	NSC	Protein disulfide-isomerase 2 OS=*Dictyostelium discoideum* OX=44689 GN=pdi2 PE=3 SV=1
Q54RA2	1,348036987	0,0430	NSC	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283293 PE=3 SV=1
B0G104	1,346763713	0,2069	NSC	60S ribosome subunit biogenesis protein NIP7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=nip7 PE=3 SV=1
Q54PX9	1,345982381	0,0208	SC	40S ribosomal protein S12 OS=*Dictyostelium discoideum* OX=44689 GN=rps12 PE=1 SV=1
Q550R2	1,343289402	0,0342	NSC	Cortexillin-2 OS=*Dictyostelium discoideum* OX=44689 GN=ctxB PE=1 SV=1
Q54KZ8	1,338603801	0,2073	NC	Eukaryotic translation initiation factor 3 subunit M OS=*Dictyostelium discoideum* OX=44689 GN=eif3m PE=1 SV=1
Q54HG2	1,338182826	0,0813	NSC	Cortexillin-1 OS=*Dictyostelium discoideum* OX=44689 GN=ctxA PE=1 SV=1
Q54G86	1,33715294	0,0227	SC	60S ribosomal protein L23 OS=*Dictyostelium discoideum* OX=44689 GN=rpl23 PE=1 SV=1
Q54NZ8	1,33611014	0,1097	NSC	Isochorismatase family protein 1B OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284901 PE=3 SV=1
P54651	1,334470328	0,0278	SC	Heat shock cognate 90 kDa protein OS=*Dictyostelium discoideum* OX=44689 GN=hspD PE=1 SV=2
Q54CY2	1,333552271	0,1537	NSC	Putative uncharacterized protein DDB_G0292556 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292556 PE=4 SV=1
Q54QB1	1,333185176	0,2780	NC	Extracellular signal-regulated kinase 2 OS=*Dictyostelium discoideum* OX=44689 GN=erkB PE=1 SV=1

Q54NQ0	1,332510937	0,2995	NC	26S proteasome non-ATPase regulatory subunit 13 OS=*Dictyostelium discoideum* OX=44689 GN=psmD13 PE=2 SV=1
Q55C21	1,330841356	0,0976	NSC	Methionine aminopeptidase 2 OS=*Dictyostelium discoideum* OX=44689 GN=metap2 PE=3 SV=3
Q23887	1,326064873	0,2184	NC	Ribosomal protein S7, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps7 PE=3 SV=1
Q01501	1,323280968	0,1762	NC	Mitochondrial outer membrane protein porin OS=*Dictyostelium discoideum* OX=44689 GN=porA PE=1 SV=1
Q54KB7	1,322595355	0,0122	SC	Glutamate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gluD PE=1 SV=1
Q54UI0	1,320757576	0,1904	NC	Uncharacterized transmembrane protein DDB_G0281067 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0281067 PE=1 SV=1
Q54KA7	1,319777173	0,3508	NC	Ankyrin repeat, PH and SEC7 domain containing protein secG OS=*Dictyostelium discoideum* OX=44689 GN=secG PE=2 SV=1
P34112	1,31924884	0,2926	NC	Cyclin-dependent kinase 1 OS=*Dictyostelium discoideum* OX=44689 GN=cdk1 PE=2 SV=1
Q55CS9	1,31806876	0,0220	SC	ATP synthase subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5b PE=1 SV=1
Q55DV9	1,317847094	0,1780	NC	Cystathionine gamma-lyase OS=*Dictyostelium discoideum* OX=44689 GN=cysA PE=1 SV=1
P36410	1,313405058	0,0513	NSC	Ras-related protein Rab-14 OS=*Dictyostelium discoideum* OX=44689 GN=rab14 PE=1 SV=2
P27133	1,301663515	0,0420	NSC	Coronin-A OS=*Dictyostelium discoideum* OX=44689 GN=corA PE=1 SV=2
P14326	1,297658429	0,2487	NC	Vegetative-specific protein H5 OS=*Dictyostelium discoideum* OX=44689 GN=cinB PE=2 SV=2
Q8T869	1,296172407	0,1674	NC	Luminal-binding protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=bip2 PE=1 SV=1
Q55GU3	1,295880619	0,1209	NC	Probable mitochondrial pyruvate carrier 2 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268478 PE=3 SV=1
P09556	1,294940584	0,0880	NC	Uridine 5'-monophosphate synthase OS=*Dictyostelium discoideum* OX=44689 GN=pyr56 PE=1 SV=2
Q54QR9	1,294696307	0,1856	NC	Protein phosphatase 2A scaffold subunit OS=*Dictyostelium discoideum* OX=44689 GN=pppA PE=1 SV=1
Q55ED1	1,292378833	0,2119	NC	Probable nucleosome assembly protein OS=*Dictyostelium discoideum* OX=44689 GN=nap1 PE=2 SV=1
Q54UD0	1,292273663	0,2677	NC	Eukaryotic translation initiation factor 3 subunit H OS=*Dictyostelium discoideum* OX=44689 GN=eif3H PE=3 SV=1
Q54VZ4	1,291826761	0,0066	SC	60S ribosomal protein L18 OS=*Dictyostelium discoideum* OX=44689 GN=rpl18 PE=1 SV=1
P14132	1,291557778	0,0067	SC	40S ribosomal protein S9 OS=*Dictyostelium discoideum* OX=44689 GN=rps9 PE=1 SV=1
O96626	1,290191805	0,0391	NSC	Actin-related protein 2/3 complex subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=arcE PE=1 SV=1
Q54FG5	1,286763621	0,2030	NC	Rho GTPase-activating protein gacJJ OS=*Dictyostelium discoideum* OX=44689 GN=gacJJ PE=3 SV=1
Q54C24	1,283426677	0,1370	NC	Vacuolar protein sorting-associated protein 35 OS=*Dictyostelium discoideum* OX=44689 GN=vps35 PE=3 SV=1

Q54I90	1,281586589	0,0765	NC	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufv1 PE=2 SV=1
Q75JI3	1,271283034	0,0604	NC	Vesicle-fusing ATPase OS=*Dictyostelium discoideum* OX=44689 GN=nsfA PE=1 SV=1
P51405	1,270597073	0,0558	NC	40S ribosomal protein S4 OS=*Dictyostelium discoideum* OX=44689 GN=rps4 PE=1 SV=3
Q54NC1	1,267824913	0,1793	NC	NADH-cytochrome b5 reductase 1 OS=*Dictyostelium discoideum* OX=44689 GN=cyb5r1 PE=3 SV=1
P13723	1,266054654	0,1541	NC	Beta-hexosaminidase subunit A1 OS=*Dictyostelium discoideum* OX=44689 GN=hexa1 PE=1 SV=1
P08796	1,265180166	0,3662	NC	Contact site A protein OS=*Dictyostelium discoideum* OX=44689 GN=csaA PE=1 SV=3
Q54N00	1,265155123	0,3430	NC	Formin-H OS=*Dictyostelium discoideum* OX=44689 GN=forH PE=1 SV=1
P54647	1,262250726	0,0478	NC	V-type proton ATPase catalytic subunit A OS=*Dictyostelium discoideum* OX=44689 GN=vatA PE=1 SV=2
Q55F94	1,261708501	0,1482	NC	Dynamin-like protein A OS=*Dictyostelium discoideum* OX=44689 GN=dlpA PE=2 SV=1
Q54MK8	1,257668979	0,0143	SC	60S ribosomal protein L18a OS=*Dictyostelium discoideum* OX=44689 GN=rpl18a PE=3 SV=2
Q54S03	1,25750797	0,0132	SC	Probable ATP-dependent RNA helicase ddx18 OS=*Dictyostelium discoideum* OX=44689 GN=ddx18 PE=3 SV=1
Q54VG1	1,254819308	0,2700	NC	Guanine nucleotide-binding protein alpha-12 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaL PE=1 SV=1
Q8T2H0	1,253205864	0,1451	NC	Protein FAM49 homolog OS=*Dictyostelium discoideum* OX=44689 GN=fam49 PE=3 SV=2
Q54WR2	1,251919611	0,1949	NC	eIF-2-alpha kinase activator GCN1 OS=*Dictyostelium discoideum* OX=44689 GN=gcn1 PE=3 SV=1
Q54Q99	1,248758636	0,0678	NC	Serine/threonine-protein phosphatase 2A regulatory subunit phr2AB OS=*Dictyostelium discoideum* OX=44689 GN=phr2aB PE=3 SV=1
Q75JR2	1,247611699	0,0863	NC	Isocitrate dehydrogenase [NADP], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=idhM PE=3 SV=1
O96623	1,246960321	0,0676	NC	Actin-related protein 2/3 complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=arcB PE=1 SV=1
Q9GRF8	1,244094273	0,1999	NC	Elongation factor 1-beta OS=*Dictyostelium discoideum* OX=44689 GN=efa1B PE=1 SV=1
Q54H97	1,240949603	0,1230	NC	CBS domain-containing protein DDB_G0289609 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289609 PE=2 SV=1
Q94490	1,240887742	0,3230	NC	Ubiquitin conjugating enzyme E2 B OS=*Dictyostelium discoideum* OX=44689 GN=ubcB PE=1 SV=1
Q95YL5	1,240596856	0,0857	NC	Penta-EF hand domain-containing protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=pefA PE=1 SV=1
Q54BM2	1,23953767	0,0470	NC	Polyadenylate-binding protein 1-A OS=*Dictyostelium discoideum* OX=44689 GN=pabpc1A PE=1 SV=1
P33519	1,235459022	0,1783	NC	GTP-binding nuclear protein Ran OS=*Dictyostelium discoideum* OX=44689 GN=ranA PE=1 SV=1
Q54U31	1,235305019	0,3700	NC	Dual specificity protein kinase shkD OS=*Dictyostelium discoideum* OX=44689 GN=shkD PE=3 SV=1

Q554Z5	1,233545344	0,1731	NC	Acyl-CoA synthetase short-chain family member B, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aslB PE=3 SV=1
Q8I8U2	1,228215332	0,0987	NC	AP-1 complex subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=ap1g1 PE=1 SV=1
Q54PJ1	1,228201134	0,2130	NC	26S proteasome regulatory subunit 10B OS=*Dictyostelium discoideum* OX=44689 GN=psmC6 PE=1 SV=1
Q869N1	1,226250357	0,2247	NC	Cytochrome c OS=*Dictyostelium discoideum* OX=44689 GN=cytC PE=3 SV=1
Q54JC2	1,223866161	0,2136	NC	Uncharacterized protein DDB_G0288155 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288155 PE=1 SV=1
Q553V2	1,223129149	0,1458	NC	Methylmalonyl-CoA epimerase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mcee PE=3 SV=1
P52285	1,220386708	0,2231	NC	SCF ubiquitin ligase complex protein SKP1a OS=*Dictyostelium discoideum* OX=44689 GN=fpaA PE=1 SV=1
P34098	1,21974908	0,0444	NC	Lysosomal alpha-mannosidase OS=*Dictyostelium discoideum* OX=44689 GN=manA PE=1 SV=2
Q54X51	1,2180235	0,1381	NC	40S ribosomal protein S19 OS=*Dictyostelium discoideum* OX=44689 GN=rps19 PE=3 SV=1
Q556Y1	1,214827963	0,3408	NC	40S ribosomal protein S30 OS=*Dictyostelium discoideum* OX=44689 GN=rps30-1 PE=3 SV=1
Q55G75	1,210429907	0,3187	NC	PH domain-containing protein DDB_G0267786 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267786 PE=4 SV=1
Q55AQ9	1,209771533	0,2024	NC	60S ribosomal protein L36 OS=*Dictyostelium discoideum* OX=44689 GN=rpl36 PE=3 SV=1
Q9GRX6	1,208897547	0,2126	NC	Apoptosis-inducing factor 1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aif PE=2 SV=1
Q03409	1,20393936	0,0799	NC	40S ribosomal protein S25 OS=*Dictyostelium discoideum* OX=44689 GN=rps25 PE=3 SV=1
Q556J0	1,200600099	0,3233	NC	Transketolase OS=*Dictyostelium discoideum* OX=44689 GN=tkt-1 PE=1 SV=1
Q55BZ5	1,200085655	0,3156	NC	Protein dcd1A OS=*Dictyostelium discoideum* OX=44689 GN=dcd1A PE=2 SV=1
Q55G04	1,200036498	0,3313	NC	Proteasome subunit alpha type-5 OS=*Dictyostelium discoideum* OX=44689 GN=psmA5 PE=3 SV=1
Q54DR1	1,199547799	0,3559	NC	Squalene synthase OS=*Dictyostelium discoideum* OX=44689 GN=fdfT PE=3 SV=1
Q54T46	1,197199532	0,3025	NC	Probable Xaa-Pro aminopeptidase 3 OS=*Dictyostelium discoideum* OX=44689 GN=xpnpep3 PE=2 SV=1
Q54J50	1,19529771	0,1748	NC	60S ribosomal protein L12 OS=*Dictyostelium discoideum* OX=44689 GN=rpl12 PE=1 SV=1
P46800	1,195198838	0,1117	NC	Guanine nucleotide-binding protein subunit beta-like protein OS=*Dictyostelium discoideum* OX=44689 GN=gpbB PE=1 SV=2
Q54DS8	1,194964492	0,2704	NC	Protein SEC13 homolog OS=*Dictyostelium discoideum* OX=44689 GN=sec13 PE=3 SV=1
P22887	1,194659634	0,1706	NC	Nucleoside diphosphate kinase, cytosolic OS=*Dictyostelium discoideum* OX=44689 GN=ndkC-1 PE=1 SV=1
P0C7W5	1,193815294	0,2315	NC	Uncharacterized protein DDB_G0281707 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0281707 PE=4 SV=1

Q54FD6	1,190949372	0,2971	NC	Transcription initiation factor IIB OS=*Dictyostelium discoideum* OX=44689 GN=gtf2b PE=3 SV=1
Q55BN7	1,186628071	0,1664	NC	60S ribosomal protein L35a OS=*Dictyostelium discoideum* OX=44689 GN=rpl35a PE=3 SV=1
Q54Q94	1,184337082	0,3054	NC	Probable ATP-dependent RNA helicase ddx10 OS=*Dictyostelium discoideum* OX=44689 GN=ddx10 PE=3 SV=1
Q86A67	1,183860477	0,0274	NC	Fructose-bisphosphate aldolase OS=*Dictyostelium discoideum* OX=44689 GN=fba PE=3 SV=1
Q55GJ7	1,182093938	0,0730	NC	60S ribosomal protein L38 OS=*Dictyostelium discoideum* OX=44689 GN=rpl38 PE=3 SV=1
Q86L04	1,181052821	0,1698	NC	TNF receptor-associated protein 1 homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=trap1 PE=2 SV=1
P54632	1,180639138	0,1650	NC	14-3-3-like protein OS=*Dictyostelium discoideum* OX=44689 GN=fttB PE=1 SV=2
Q54HF1	1,179461968	0,0298	NC	Putative actin-24 OS=*Dictyostelium discoideum* OX=44689 GN=act24 PE=3 SV=1
Q54GB3	1,17574958	0,2860	NC	Synaptobrevin-B OS=*Dictyostelium discoideum* OX=44689 GN=sybB PE=3 SV=1
P22684	1,175461087	0,2174	NC	60S acidic ribosomal protein P1 OS=*Dictyostelium discoideum* OX=44689 GN=rplp1 PE=3 SV=1
Q55CC2	1,170262036	0,2840	NC	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sdhB PE=3 SV=1
Q86IC8	1,168320478	0,2222	NC	Probable caffeoyl-CoA O-methyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=omt6 PE=1 SV=1
O00909	1,168244395	0,1920	NC	ADP-ribosylation factor 1 OS=*Dictyostelium discoideum* OX=44689 GN=arfA PE=1 SV=3
Q54NR3	1,167352335	0,3502	NC	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=*Dictyostelium discoideum* OX=44689 GN=ndufb9 PE=3 SV=1
P21900	1,166882633	0,1040	NC	Adenylosuccinate synthetase OS=*Dictyostelium discoideum* OX=44689 GN=purA PE=1 SV=1
Q54BM3	1,165345997	0,3670	NC	Mitochondrial substrate carrier family protein G OS=*Dictyostelium discoideum* OX=44689 GN=mcfG PE=2 SV=1
P34121	1,161809059	0,2879	NC	Coactosin OS=*Dictyostelium discoideum* OX=44689 GN=coaA PE=1 SV=1
Q869Q2	1,1596477	0,2376	NC	Ribosome biogenesis regulatory protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=rrs1 PE=3 SV=1
P32254	1,158622339	0,3692	NC	Ras-like protein rasS OS=*Dictyostelium discoideum* OX=44689 GN=rasS PE=2 SV=1
Q54MR6	1,157974725	0,3334	NC	Heat shock 70-related protein 5 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0285709 PE=3 SV=1
Q54DF7	1,153171971	0,1756	NC	Probable serine/threonine-protein kinase DDB_G0292354 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292354 PE=3 SV=1
Q55GH8	1,152803867	0,2758	NC	Small heat shock protein hspL OS=*Dictyostelium discoideum* OX=44689 GN=hspL PE=3 SV=1
Q554S6	1,149650462	0,0364	NC	Actin-17 OS=*Dictyostelium discoideum* OX=44689 GN=act17 PE=3 SV=1
P54638	1,147509539	0,2090	NC	Acetylornithine deacetylase OS=*Dictyostelium discoideum* OX=44689 GN=argE PE=1 SV=2

Q55FE0	1,145682154	0,3761	NC	Eukaryotic translation initiation factor 4E OS=*Dictyostelium discoideum* OX=44689 GN=eif4e PE=3 SV=1
Q54WG0	1,132934666	0,3953	NC	Density-regulated protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=denr PE=3 SV=1
O96621	1,131725772	0,0123	NC	Actin-related protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=arpB PE=1 SV=1
P54657	1,131685631	0,2135	NC	Calcium-dependent cell adhesion molecule 1 OS=*Dictyostelium discoideum* OX=44689 GN=cadA PE=1 SV=1
Q86K94	1,131317567	0,2965	NC	Trafficking protein particle complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=trappc3 PE=3 SV=2
Q86L14	1,131083649	0,3921	NC	Bifunctional purine biosynthesis protein purH OS=*Dictyostelium discoideum* OX=44689 GN=purH PE=1 SV=1
Q54T27	1,130160298	0,2351	NC	Eukaryotic translation initiation factor 2 subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=eif2s2 PE=3 SV=1
P07829	1,129173772	0,0166	NC	Actin-3 OS=*Dictyostelium discoideum* OX=44689 GN=act3 PE=3 SV=3
P11874	1,127520547	0,1924	NC	60S ribosomal protein L7 OS=*Dictyostelium discoideum* OX=44689 GN=rpl7 PE=1 SV=3
Q54CC5	1,119691976	0,2945	NC	Eukaryotic translation initiation factor 3 subunit E OS=*Dictyostelium discoideum* OX=44689 GN=eif3E PE=3 SV=1
Q54ZW5	1,117756793	0,2062	NC	40S ribosomal protein S3a OS=*Dictyostelium discoideum* OX=44689 GN=rps3a PE=3 SV=1
Q7KWL3	1,116709997	0,3428	NC	DDB1- and CUL4-associated factor 13 OS=*Dictyostelium discoideum* OX=44689 GN=wdsof1 PE=3 SV=1
Q55C75	1,11271939	0,3887	NC	26S proteasome non-ATPase regulatory subunit 6 OS=*Dictyostelium discoideum* OX=44689 GN=psmD6 PE=1 SV=1
Q55CW0	1,109452476	0,2602	NC	rRNA 2'-O-methyltransferase fibrillarin OS=*Dictyostelium discoideum* OX=44689 GN=fbl PE=3 SV=1
Q54PQ4	1,108811578	0,3666	NC	Ras guanine nucleotide exchange factor A OS=*Dictyostelium discoideum* OX=44689 GN=gefA PE=1 SV=1
Q54X53	1,105577974	0,0889	NC	60S ribosomal protein L21 OS=*Dictyostelium discoideum* OX=44689 GN=rpl21 PE=3 SV=1
Q55EK2	1,10168271	0,4206	NC	Probable cytochrome P450 524A1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp524A1 PE=3 SV=1
Q55DR6	1,100594413	0,0998	NC	Fatty acyl-CoA synthetase A OS=*Dictyostelium discoideum* OX=44689 GN=fcsA PE=1 SV=1
Q54W90	1,100162613	0,3370	NC	Protein SEY1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_0206311 PE=3 SV=1
Q54NP6	1,098972116	0,3324	NC	Alpha-soluble NSF attachment protein OS=*Dictyostelium discoideum* OX=44689 GN=snpA PE=1 SV=1
Q54TU8	1,096925314	0,3453	NC	Calcium load-activated calcium channel homolog OS=*Dictyostelium discoideum* OX=44689 GN=tmco1 PE=2 SV=1
P18613	1,09666933	0,2741	NC	Ras-related protein rapA OS=*Dictyostelium discoideum* OX=44689 GN=rapA PE=1 SV=1
Q75K27	1,094153625	0,2629	NC	40S ribosomal protein S24 OS=*Dictyostelium discoideum* OX=44689 GN=rps24 PE=3 SV=1
Q54XC4	1,092868226	0,4288	NC	Myeloid-derived growth factor homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0279047 PE=3 SV=2

Q54Y41	1,092819254	0,2051	NC	40S ribosomal protein S20 OS=*Dictyostelium discoideum* OX=44689 GN=rps20 PE=3 SV=1
Q65YR7	1,091511925	0,3636	NC	Cystatin-A2 OS=*Dictyostelium discoideum* OX=44689 GN=cpiB PE=2 SV=1
Q54I98	1,091318829	0,3376	NC	Probable cycloartenol-C-24-methyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=smt1 PE=1 SV=1
P11872	1,090977045	0,4020	NC	cAMP-regulated M3R protein OS=*Dictyostelium discoideum* OX=44689 GN=prtB PE=2 SV=4
C7G046	1,090540206	0,3669	NC	von Willebrand factor A domain-containing protein DDB_G0286969 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286969 PE=4 SV=1
Q23921	1,090529635	0,3880	NC	Protein pkiA OS=*Dictyostelium discoideum* OX=44689 GN=pkiA PE=1 SV=2
P13833	1,088182115	0,1924	NC	Myosin regulatory light chain OS=*Dictyostelium discoideum* OX=44689 GN=mlcR PE=2 SV=1
P36416	1,088087942	0,3402	NC	N-terminal acetyltransferase complex ARD1 subunit homolog OS=*Dictyostelium discoideum* OX=44689 GN=natA PE=2 SV=1
P52922	1,087699614	0,4204	NC	Leukotriene A-4 hydrolase homolog OS=*Dictyostelium discoideum* OX=44689 GN=lkhA PE=2 SV=2
Q54K74	1,087680209	0,2792	NC	Endoplasmic reticulum transmembrane protein YET-like OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0287543 PE=3 SV=2
P34046	1,087647882	0,3985	NC	Guanine nucleotide-binding protein alpha-8 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaH PE=2 SV=2
Q65YR8	1,086471115	0,3786	NC	Cystatin-A1 OS=*Dictyostelium discoideum* OX=44689 GN=cpiA PE=2 SV=1
Q54U94	1,08120595	0,3602	NC	RNA exonuclease 4 OS=*Dictyostelium discoideum* OX=44689 GN=rexo4 PE=3 SV=1
Q556M4	1,079413215	0,3943	NC	Probable cytochrome P450 508A2 OS=*Dictyostelium discoideum* OX=44689 GN=cyp508A2-1 PE=3 SV=1
Q54PH8	1,076633926	0,1220	NC	40S ribosomal protein S13 OS=*Dictyostelium discoideum* OX=44689 GN=rps13 PE=3 SV=1
Q75JR3	1,076238744	0,3814	NC	Isocitrate dehydrogenase [NADP] cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=idhC PE=1 SV=1
Q55CV5	1,075166011	0,4042	NC	Probable tetraspanin tspA OS=*Dictyostelium discoideum* OX=44689 GN=tspA PE=2 SV=1
P46793	1,067727015	0,3261	NC	40S ribosomal protein S15a OS=*Dictyostelium discoideum* OX=44689 GN=rps15a PE=2 SV=3
Q54N47	1,066698204	0,3811	NC	Branched-chain-amino-acid aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=bcaA PE=3 SV=1
Q54YA0	1,065924599	0,3509	NC	Probable ATP-citrate synthase OS=*Dictyostelium discoideum* OX=44689 GN=acly PE=1 SV=1
P15808	1,058980286	0,4437	NC	Flavin-dependent thymidylate synthase OS=*Dictyostelium discoideum* OX=44689 GN=thyA PE=3 SV=2
Q86A84	1,057199154	0,4606	NC	Mitochondrial-processing peptidase subunit alpha-1 OS=*Dictyostelium discoideum* OX=44689 GN=mppA1 PE=1 SV=1
Q54UF3	1,056432423	0,4051	NC	Probable ornithine decarboxylase OS=*Dictyostelium discoideum* OX=44689 GN=odc PE=3 SV=1
Q54HG7	1,056078521	0,4422	NC	Methylglutaconyl-CoA hydratase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=auh PE=3 SV=1

O15757	1,052331216	0,4228	NC	Serine/threonine-protein phosphatase PP1 OS=*Dictyostelium discoideum* OX=44689 GN=pppB PE=1 SV=1
Q54PA9	1,052298791	0,4114	NC	Ribose-phosphate pyrophosphokinase A OS=*Dictyostelium discoideum* OX=44689 GN=prsA PE=1 SV=1
Q86KC1	1,048777235	0,4669	NC	Probable GH family 25 lysozyme 2 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274181 PE=3 SV=1
P36415	1,048504596	0,3285	NC	Heat shock cognate 70 kDa protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=hspB PE=1 SV=2
Q54QQ0	1,043217851	0,3569	NC	Inosine-5'-monophosphate dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=impdh PE=1 SV=1
Q54VN6	1,04104135	0,1402	NC	60S ribosomal protein L24 OS=*Dictyostelium discoideum* OX=44689 GN=rpl24 PE=1 SV=1
Q23883	1,039150168	0,4351	NC	NADH-ubiquinone oxidoreductase 49 kDa subunit OS=*Dictyostelium discoideum* OX=44689 GN=nad7 PE=1 SV=1
Q54IN6	1,036400945	0,4337	NC	Uncharacterized protein DDB_G0288629 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288629 PE=4 SV=1
O96624	1,031385958	0,3772	NC	Actin-related protein 2/3 complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=arcC PE=1 SV=1
Q54EQ1	1,031075282	0,4508	NC	Eukaryotic translation initiation factor 3 subunit K OS=*Dictyostelium discoideum* OX=44689 GN=eif3K PE=3 SV=2
Q86B05	1,030548842	0,4721	NC	Probable ribosome biogenesis protein RLP24 OS=*Dictyostelium discoideum* OX=44689 GN=rlp24 PE=2 SV=1
Q54JN0	1,029388458	0,4264	NC	Ribosome biogenesis protein BRX1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=bxdc2 PE=3 SV=1
Q54Z13	1,028484253	0,4482	NC	V-type proton ATPase subunit G OS=*Dictyostelium discoideum* OX=44689 GN=atp6v1g PE=1 SV=2
Q54J68	1,026972369	0,4346	NC	10 kDa heat shock protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=hspe1 PE=3 SV=1
Q1ZXD3	1,026825868	0,4424	NC	26S proteasome non-ATPase regulatory subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=psmD3 PE=1 SV=1
Q54F47	1,023548238	0,4734	NC	Probable cytochrome P450 513C1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp513C1 PE=3 SV=1
Q9U3X4	1,020934466	0,4251	NC	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sdhA PE=3 SV=1
Q54DJ0	1,020872415	0,4127	NC	Ribosome production factor 2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=bxdc1 PE=3 SV=1
Q9GS21	1,020835595	0,4282	NC	60S ribosomal protein L28 OS=*Dictyostelium discoideum* OX=44689 GN=rpl28 PE=2 SV=1
Q75JD5	1,018350014	0,4809	NC	Phosphoenolpyruvate carboxykinase (ATP) OS=*Dictyostelium discoideum* OX=44689 GN=pckA PE=1 SV=1
Q54B67	1,018071085	0,4746	NC	Mitochondrial substrate carrier family protein Z OS=*Dictyostelium discoideum* OX=44689 GN=mcfZ PE=2 SV=1
Q54I41	1,016582253	0,3655	NC	40S ribosomal protein S7 OS=*Dictyostelium discoideum* OX=44689 GN=rps7 PE=1 SV=1
P13023	1,014376433	0,4438	NC	60S ribosomal protein L8 OS=*Dictyostelium discoideum* OX=44689 GN=rpl8 PE=1 SV=2
Q559R0	1,013963772	0,4356	NC	GTP-binding protein Sar1A OS=*Dictyostelium discoideum* OX=44689 GN=sarA PE=1 SV=1

Q86IA3	1,012896909	0,4735	NC	Protein disulfide-isomerase 1 OS=*Dictyostelium discoideum* OX=44689 GN=pdi1 PE=1 SV=2
Q54JT7	1,012576213	0,4897	NC	Nicastrin OS=*Dictyostelium discoideum* OX=44689 GN=ncstn PE=3 SV=2
Q86JA1	1,012242796	0,4915	NC	26S proteasome regulatory subunit 7 OS=*Dictyostelium discoideum* OX=44689 GN=psmC2 PE=1 SV=1
Q9U9A3	1,008634824	0,4833	NC	Serine/threonine-protein phosphatase 6 catalytic subunit OS=*Dictyostelium discoideum* OX=44689 GN=ppp6c PE=2 SV=2
Q55BY1	1,007606976	0,4755	NC	40S ribosomal protein SA OS=*Dictyostelium discoideum* OX=44689 GN=rpsA PE=1 SV=1
Q557E0	1,007016245	0,4716	NC	Heat shock cognate 70 kDa protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=hspE-1 PE=1 SV=1
Q54Y72	1,000334726	0,4990	NC	Rho GTPase-activating protein gacA OS=*Dictyostelium discoideum* OX=44689 GN=gacA PE=3 SV=1
Q54Z69	-1,000021375	0,4999	NC	60S ribosomal protein L4 OS=*Dictyostelium discoideum* OX=44689 GN=rpl4 PE=1 SV=1
Q54YZ0	-1,000021937	0,5000	NC	UTP--glucose-1-phosphate uridylyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=ugpB PE=2 SV=1
Q54MB5	-1,000215218	0,4999	NC	Adenosine kinase OS=*Dictyostelium discoideum* OX=44689 GN=adk PE=3 SV=2
Q54CL2	-1,007073771	0,4832	NC	T-complex protein 1 subunit delta OS=*Dictyostelium discoideum* OX=44689 GN=cct4 PE=3 SV=1
Q551M2	-1,008855725	0,4901	NC	Eukaryotic translation initiation factor 6 OS=*Dictyostelium discoideum* OX=44689 GN=eif6 PE=1 SV=1
Q54F93	-1,009275206	0,4769	NC	Mitochondrial-processing peptidase subunit alpha-2 OS=*Dictyostelium discoideum* OX=44689 GN=mppA2 PE=1 SV=1
Q54ZD1	-1,01100817	0,4359	NC	60S ribosomal protein L7a OS=*Dictyostelium discoideum* OX=44689 GN=rpl7a PE=1 SV=1
Q559Z0	-1,012260469	0,4652	NC	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufa9 PE=3 SV=1
Q6UK63	-1,014804136	0,4880	NC	Protein pirA OS=*Dictyostelium discoideum* OX=44689 GN=pirA PE=1 SV=1
Q557D2	-1,019348521	0,4809	NC	Glucose-6-phosphate 1-dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=g6pd-1 PE=3 SV=1
Q55FN7	-1,020004336	0,4379	NC	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=bkdB PE=3 SV=1
Q54Y55	-1,029924943	0,4273	NC	Dual specificity protein kinase shkC OS=*Dictyostelium discoideum* OX=44689 GN=shkC PE=3 SV=1
Q54J97	-1,030218962	0,4132	NC	60 kDa heat shock protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=hspA PE=2 SV=1
Q54GK6	-1,030643407	0,3675	NC	60S ribosomal protein L22 2 OS=*Dictyostelium discoideum* OX=44689 GN=rpl22a PE=3 SV=1
Q54MD4	-1,032596405	0,4445	NC	Probable replication factor C subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=rfc4 PE=3 SV=1
Q54EG3	-1,035049289	0,3659	NC	40S ribosomal protein S14 OS=*Dictyostelium discoideum* OX=44689 GN=rps14 PE=3 SV=1
Q86L05	-1,036457902	0,4126	NC	60S ribosomal protein L10a OS=*Dictyostelium discoideum* OX=44689 GN=rpl10a PE=1 SV=1
Q552P9	-1,037062467	0,4523	NC	Uncharacterized protein DDB_G0275933 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275933 PE=3 SV=1

Q54HP3	-1,038217335	0,3998	NC	Developmentally-regulated GTP-binding protein 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=drg1 PE=3 SV=1
Q54C49	-1,041346123	0,4125	NC	Eukaryotic translation initiation factor 3 subunit F OS=*Dictyostelium discoideum* OX=44689 GN=eif3f PE=3 SV=1
P08800	-1,042328458	0,4110	NC	UTP--glucose-1-phosphate uridylyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=uppA PE=2 SV=2
Q54J69	-1,045066648	0,0719	NC	60S ribosomal protein L10 OS=*Dictyostelium discoideum* OX=44689 GN=rpl10 PE=1 SV=2
Q76NU1	-1,045637255	0,3642	NC	V-type proton ATPase subunit B OS=*Dictyostelium discoideum* OX=44689 GN=vatB PE=1 SV=1
P26199	-1,049943979	0,2159	NC	Profilin-1 OS=*Dictyostelium discoideum* OX=44689 GN=proA PE=2 SV=1
P14329	-1,050343211	0,2537	NC	60S ribosomal protein L19 OS=*Dictyostelium discoideum* OX=44689 GN=rpl19 PE=1 SV=1
Q54BN3	-1,053954267	0,3842	NC	Probable replication factor C subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=rfc3 PE=3 SV=1
Q86HV4	-1,058217393	0,3722	NC	Oxysterol-binding protein 6 OS=*Dictyostelium discoideum* OX=44689 GN=osbF PE=3 SV=1
P16168	-1,05905697	0,3502	NC	60S ribosomal protein L11 OS=*Dictyostelium discoideum* OX=44689 GN=rpl11 PE=1 SV=2
Q54CE0	-1,059792879	0,3946	NC	Probable ATP-dependent RNA helicase ddx17 OS=*Dictyostelium discoideum* OX=44689 GN=ddx17 PE=3 SV=1
Q54EW8	-1,062854877	0,3328	NC	Dihydrolipoyl dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=lpd PE=3 SV=1
Q54JH4	-1,071403188	0,3689	NC	P2X receptor E OS=*Dictyostelium discoideum* OX=44689 GN=p2xE PE=3 SV=2
Q54NU2	-1,079715497	0,3670	NC	Ras-related protein Rab-1D OS=*Dictyostelium discoideum* OX=44689 GN=rab1D PE=1 SV=1
P15064	-1,081376994	0,3896	NC	Ras-like protein rasG OS=*Dictyostelium discoideum* OX=44689 GN=rasG PE=1 SV=1
Q550U9	-1,085559945	0,3733	NC	Phospholipase B-like protein A OS=*Dictyostelium discoideum* OX=44689 GN=plbA PE=1 SV=1
Q54XF7	-1,086641809	0,3881	NC	Cullin-5 OS=*Dictyostelium discoideum* OX=44689 GN=culE PE=3 SV=1
Q55BS9	-1,088010738	0,3636	NC	60S ribosomal protein L30 OS=*Dictyostelium discoideum* OX=44689 GN=rpl30 PE=3 SV=1
Q54KM7	-1,089432323	0,3888	NC	Glycine dehydrogenase (decarboxylating), mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcvP PE=3 SV=1
Q54KS4	-1,09299799	0,1142	NC	Guanine nucleotide-binding protein-like 3 homolog OS=*Dictyostelium discoideum* OX=44689 GN=gnl3 PE=3 SV=1
Q54BF6	-1,093413396	0,3750	NC	Mitochondrial substrate carrier family protein N OS=*Dictyostelium discoideum* OX=44689 GN=mcfN PE=1 SV=2
Q54WM4	-1,09379566	0,3939	NC	Eukaryotic translation initiation factor 3 subunit G OS=*Dictyostelium discoideum* OX=44689 GN=eif3G PE=3 SV=1
Q54QM8	-1,09950249	0,2093	NC	60S ribosomal protein L26 OS=*Dictyostelium discoideum* OX=44689 GN=rpl26 PE=3 SV=1
Q55BE6	-1,100351675	0,1397	NC	60S ribosomal protein L27 OS=*Dictyostelium discoideum* OX=44689 GN=rpl27 PE=3 SV=1

Q54BN0	-1,102155447	0,1294	NC	Transmembrane emp24 domain-containing protein B OS=*Dictyostelium discoideum* OX=44689 GN=empB PE=3 SV=1
Q555L5	-1,104666334	0,3133	NC	Peroxiredoxin-4 OS=*Dictyostelium discoideum* OX=44689 GN=prdx4 PE=1 SV=2
Q54K93	-1,110153561	0,2544	NC	Putative uncharacterized protein DDB_G0287517 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0287517 PE=4 SV=1
Q54HB2	-1,113037176	0,2671	NC	Elongation factor Tu, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=tufm PE=1 SV=2
Q54E20	-1,11566107	0,1544	NC	60S ribosomal protein L13 OS=*Dictyostelium discoideum* OX=44689 GN=rpl13 PE=1 SV=1
Q54BK2	-1,117813137	0,3151	NC	Neutral ceramidase A OS=*Dictyostelium discoideum* OX=44689 GN=dcd2A PE=1 SV=1
Q54P23	-1,123460513	0,4080	NC	Stromal cell-derived factor 2-like protein OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284847 PE=3 SV=1
Q54RR5	-1,130590281	0,2529	NC	Probable short/branched chain specific acyl-CoA dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=acadsb PE=3 SV=1
Q75JD4	-1,141710494	0,3721	NC	SH3 and F-BAR domain-containing protein DDB_G0271676 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271676 PE=4 SV=1
Q54V77	-1,149460744	0,2195	NC	CTP synthase OS=*Dictyostelium discoideum* OX=44689 GN=ctps PE=3 SV=1
P32256	-1,151632491	0,1034	NC	Tubulin beta chain OS=*Dictyostelium discoideum* OX=44689 GN=tubB PE=1 SV=2
Q76P29	-1,152464751	0,1819	NC	Importin subunit alpha-B OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272318 PE=3 SV=1
Q86HD3	-1,161755961	0,1255	NC	Ribosome assembly factor mrt4 OS=*Dictyostelium discoideum* OX=44689 GN=mrt4 PE=3 SV=1
Q7YXD4	-1,164785829	0,3316	NC	Protein P80 OS=*Dictyostelium discoideum* OX=44689 GN=p80 PE=2 SV=1
Q54JE3	-1,165519902	0,1075	NC	60S ribosomal protein L22 1 OS=*Dictyostelium discoideum* OX=44689 GN=rpl22 PE=3 SV=1
Q55AB5	-1,168082152	0,0210	NC	60S ribosomal protein L32 OS=*Dictyostelium discoideum* OX=44689 GN=rpl32 PE=3 SV=1
B0G159	-1,183153128	0,3530	NC	Mitochondrial substrate carrier family protein C OS=*Dictyostelium discoideum* OX=44689 GN=mcfC PE=2 SV=1
Q54G21	-1,183317227	0,3475	NC	FK506-binding protein 5 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp5 PE=1 SV=1
Q54YJ6	-1,188935259	0,2881	NC	Eukaryotic translation initiation factor 1A OS=*Dictyostelium discoideum* OX=44689 GN=eif1a PE=3 SV=1
Q54UG4	-1,19011904	0,2781	NC	60S ribosomal protein L37a OS=*Dictyostelium discoideum* OX=44689 GN=rpl37A PE=3 SV=1
P34144	-1,190133278	0,0977	NC	Rho-related protein rac1A OS=*Dictyostelium discoideum* OX=44689 GN=rac1A PE=1 SV=2
Q54R41	-1,193803723	0,2839	NC	Guanine nucleotide-binding protein alpha-9 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaI PE=2 SV=1
O00899	-1,200514569	0,2390	NC	Ras GTPase-activating-like protein gapA OS=*Dictyostelium discoideum* OX=44689 GN=gapA PE=1 SV=1
Q54XE6	-1,204420527	0,2085	NC	Probable H/ACA ribonucleoprotein complex subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=gar1 PE=3 SV=1

Q54LV8	-1,206056187	0,0634	NC	60S ribosomal protein L34 OS=*Dictyostelium discoideum* OX=44689 GN=rpl34 PE=3 SV=1
Q94469	-1,206432856	0,2311	NC	Glyceraldehyde-3-phosphate dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=gpdA PE=1 SV=2
Q54K32	-1,209037516	0,2923	NC	Ras GTPase-activating-like protein rgaA OS=*Dictyostelium discoideum* OX=44689 GN=rgaA PE=1 SV=1
Q02720	-1,209086546	0,3533	NC	Casein kinase II subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=casK PE=2 SV=1
P83401	-1,209460439	0,3264	NC	Putative aldehyde dehydrogenase family 7 member A1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0276821 PE=3 SV=2
P08799	-1,209681809	0,0677	NC	Myosin-2 heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=mhcA PE=1 SV=3
Q54UU3	-1,217388465	0,1310	NC	40S ribosomal protein S6 OS=*Dictyostelium discoideum* OX=44689 GN=rps6 PE=1 SV=1
Q554U9	-1,224219661	0,1687	NC	Eukaryotic translation initiation factor 3 subunit D OS=*Dictyostelium discoideum* OX=44689 GN=eif3d PE=3 SV=1
Q03380	-1,224824399	0,2354	NC	Comitin OS=*Dictyostelium discoideum* OX=44689 GN=comA PE=1 SV=1
Q550H6	-1,229674632	0,1055	NC	Ras-related protein Rab-11C OS=*Dictyostelium discoideum* OX=44689 GN=rab11C PE=1 SV=1
Q54UP4	-1,230061529	0,2981	NC	Probable transaldolase OS=*Dictyostelium discoideum* OX=44689 GN=tal PE=3 SV=1
P90526	-1,233738841	0,0149	NC	40S ribosomal protein S3 OS=*Dictyostelium discoideum* OX=44689 GN=rps3 PE=1 SV=1
Q557H1	-1,237236222	0,2959	NC	Dipeptidyl peptidase 3 OS=*Dictyostelium discoideum* OX=44689 GN=dpp3-1 PE=3 SV=1
Q54LT7	-1,242010984	0,3481	NC	Probable cytochrome P450 519E1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp519E1 PE=3 SV=1
P34139	-1,242546725	0,0286	NC	Ras-related protein Rab-1A OS=*Dictyostelium discoideum* OX=44689 GN=rab1A PE=2 SV=2
Q8T2T5	-1,243336627	0,2140	NC	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sdhC PE=3 SV=1
Q9U641	-1,243438773	0,0076	SC	Conditioned medium factor receptor 1 OS=*Dictyostelium discoideum* OX=44689 GN=cmfB PE=1 SV=1
Q23884	-1,244414075	0,2984	NC	60S ribosomal protein L11, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl11 PE=3 SV=1
Q54ZM4	-1,245748767	0,2709	NC	Probable cytochrome P450 518A1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp518A1 PE=3 SV=1
Q54QS3	-1,249693433	0,1405	NC	Probable ATP-dependent RNA helicase ddx3 OS=*Dictyostelium discoideum* OX=44689 GN=ddx3 PE=3 SV=1
Q55BU8	-1,256273178	0,2134	NC	Protein erg2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=erg2 PE=3 SV=1
Q86AQ7	-1,262161641	0,0870	NC	Vesicle-associated membrane protein 7B OS=*Dictyostelium discoideum* OX=44689 GN=vamp7B PE=3 SV=1
Q54JA5	-1,271973569	0,1115	NC	Integrin beta-like protein C OS=*Dictyostelium discoideum* OX=44689 GN=sibC PE=1 SV=1
Q54JV6	-1,274005259	0,2278	NC	Protein transport protein Sec61 subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=sec61g PE=3 SV=1

Q54WU3	-1,274367438	0,1146	NC	Methionine aminopeptidase 1 OS=*Dictyostelium discoideum* OX=44689 GN=metap1 PE=3 SV=1
Q54S90	-1,279336092	0,0480	NC	40S ribosomal protein S11 OS=*Dictyostelium discoideum* OX=44689 GN=rps11 PE=1 SV=1
P16894	-1,280487454	0,0615	NC	Guanine nucleotide-binding protein alpha-1 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaA PE=2 SV=1
P0CE94	-1,282010914	0,3257	NC	Talin-A OS=*Dictyostelium discoideum* OX=44689 GN=talA PE=3 SV=1
Q54QK7	-1,288591816	0,0987	NC	Probable dimethyladenosine transferase OS=*Dictyostelium discoideum* OX=44689 GN=dimt1 PE=3 SV=1
Q553M7	-1,289054072	0,0758	NC	60S ribosomal protein L13a OS=*Dictyostelium discoideum* OX=44689 GN=rpl13a PE=1 SV=1
Q54Z09	-1,28983603	0,0932	NC	60S ribosomal protein L14 OS=*Dictyostelium discoideum* OX=44689 GN=rpl14 PE=3 SV=1
Q54Q51	-1,299527864	0,0088	SC	40S ribosomal protein S16 OS=*Dictyostelium discoideum* OX=44689 GN=rps16 PE=3 SV=1
P54641	-1,306030952	0,0210	SC	V-type proton ATPase subunit d OS=*Dictyostelium discoideum* OX=44689 GN=vatD-1 PE=1 SV=2
P36411	-1,322897477	0,0032	SC	Ras-related protein Rab-7A OS=*Dictyostelium discoideum* OX=44689 GN=rab7A PE=1 SV=1
Q54DW2	-1,338855703	0,0743	NSC	Probable endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=ergic3 PE=3 SV=1
O96759	-1,343778543	0,1168	NSC	Alkyldihydroxyacetonephosphate synthase OS=*Dictyostelium discoideum* OX=44689 GN=eapA PE=1 SV=1
P54671	-1,350861582	0,0382	NSC	Histone H1 OS=*Dictyostelium discoideum* OX=44689 GN=H1 PE=1 SV=3
O15706	-1,352390141	0,2126	NSC	Vacuolin-A OS=*Dictyostelium discoideum* OX=44689 GN=vacA PE=1 SV=1
Q54GE3	-1,355395639	0,1038	NSC	Vacuolar protein sorting-associated protein 45 OS=*Dictyostelium discoideum* OX=44689 GN=vps45 PE=1 SV=1
Q1ZXG4	-1,355888464	0,0104	SC	Proliferation-associated protein A OS=*Dictyostelium discoideum* OX=44689 GN=prlA PE=2 SV=1
O96625	-1,360268332	0,1061	NSC	Actin-related protein 2/3 complex subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=arcD PE=1 SV=1
Q54NW7	-1,36957765	0,1488	NSC	Vesicle-associated membrane protein 7A OS=*Dictyostelium discoideum* OX=44689 GN=vamp7A PE=1 SV=1
P32252	-1,371866059	0,1796	NSC	Ras-like protein rasB OS=*Dictyostelium discoideum* OX=44689 GN=rasB PE=1 SV=1
Q54TL8	-1,374862553	0,0120	SC	40S ribosomal protein S26 OS=*Dictyostelium discoideum* OX=44689 GN=rps26 PE=3 SV=1
Q55BX3	-1,378595444	0,1586	NSC	NDRG-like protein OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0270324 PE=3 SV=1
Q54HW8	-1,392950904	0,2506	NSC	Uncharacterized protein DDB_G0289171 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289171 PE=2 SV=1
P54642	-1,394436622	0,0800	NSC	V-type proton ATPase proteolipid subunit OS=*Dictyostelium discoideum* OX=44689 GN=vatP PE=2 SV=1
Q1ZXL7	-1,40295207	0,1703	NSC	Probable cytochrome P450 508A3 OS=*Dictyostelium discoideum* OX=44689 GN=cyp508A3-1 PE=3 SV=1
P54654	-1,404481848	0,0131	C	Adenylyl cyclase-associated protein OS=*Dictyostelium discoideum* OX=44689 GN=cap PE=1 SV=1

Q54NS7	-1,40881366	0,1699	NSC	PRA1 family protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=prafB PE=3 SV=2
Q86J23	-1,414313524	0,1258	NSC	Ragulator complex protein LAMTOR3 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274833 PE=3 SV=1
P54659	-1,422835778	0,0376	NSC	Major vault protein beta OS=*Dictyostelium discoideum* OX=44689 GN=mvpB PE=1 SV=1
Q54FL2	-1,427270873	0,2115	NSC	Ras-related protein RabG2 OS=*Dictyostelium discoideum* OX=44689 GN=rabG2 PE=3 SV=2
Q54GQ6	-1,432738013	0,2188	NSC	Peroxisomal acyl-coenzyme A oxidase 1 OS=*Dictyostelium discoideum* OX=44689 GN=acox1 PE=3 SV=1
P32253	-1,43374911	0,0855	NSC	Ras-like protein rasC OS=*Dictyostelium discoideum* OX=44689 GN=rasC PE=2 SV=1
Q86A92	-1,435919348	0,0578	NSC	Enhancer of rudimentary homolog OS=*Dictyostelium discoideum* OX=44689 GN=erh PE=3 SV=1
P21837	-1,436449458	0,0316	SC	Crystal protein OS=*Dictyostelium discoideum* OX=44689 GN=cryS PE=1 SV=1
Q54UU8	-1,437008861	0,2054	NSC	Thioredoxin reductase OS=*Dictyostelium discoideum* OX=44689 GN=trrA PE=3 SV=1
Q54DG1	-1,449258529	0,0801	NSC	Aldehyde dehydrogenase family 3 comG OS=*Dictyostelium discoideum* OX=44689 GN=comG PE=3 SV=1
P24005	-1,453694811	0,1394	NSC	Calcium-regulated actin-bundling protein OS=*Dictyostelium discoideum* OX=44689 GN=abpB PE=1 SV=1
Q556J2	-1,456091779	0,1641	NSC	3-ketodihydrosphingosine reductase OS=*Dictyostelium discoideum* OX=44689 GN=ksrA-1 PE=3 SV=1
P14797	-1,460867177	0,0024	SC	Ubiquitin-40S ribosomal protein S27a OS=*Dictyostelium discoideum* OX=44689 GN=ubqC PE=1 SV=2
Q54C27	-1,460923543	0,1722	NSC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=ost1 PE=2 SV=1
Q54WZ2	-1,46490241	0,2151	NSC	Vacuolin-B OS=*Dictyostelium discoideum* OX=44689 GN=vacB PE=1 SV=1
Q554J3	-1,471876776	0,0159	C	FK506-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp1 PE=3 SV=1
Q86I22	-1,471876776	0,0159	C	Acylpyruvase FAHD1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=fahd1 PE=3 SV=1
Q54ST4	-1,474749025	0,1514	NSC	Probable replication factor C subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=rfc5 PE=3 SV=1
Q6IMN8	-1,47927401	0,1474	NSC	Aldose reductase A OS=*Dictyostelium discoideum* OX=44689 GN=alrA PE=2 SV=1
A0A0F6B980	-1,484879369	0,0678	NSC	Thioredoxin OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=trxA PE=3 SV=1
Q54E24	-1,486527958	0,0014	SC	40S ribosomal protein S8 OS=*Dictyostelium discoideum* OX=44689 GN=rps8 PE=1 SV=1
Q55EX6	-1,487570351	0,2117	NSC	Trafficking protein particle complex subunit 13 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0269062 PE=3 SV=2
Q54FB6	-1,491043295	0,0485	NSC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=ost2 PE=3 SV=1
P34142	-1,494511594	0,1421	NSC	Ras-related protein Rab-21 OS=*Dictyostelium discoideum* OX=44689 GN=rab21 PE=1 SV=2
Q54FE6	-1,518515336	0,1610	NSC	Mitochondrial substrate carrier family protein S OS=*Dictyostelium discoideum* OX=44689 GN=mcfS PE=3 SV=1

Q7KWK5	-1,520186763	0,0416	NSC	Pre-mRNA-processing factor 19 OS=*Dictyostelium discoideum* OX=44689 GN=prp19 PE=3 SV=1
Q559X6	-1,521144555	0,0408	NSC	Ras-related protein Rab-2B OS=*Dictyostelium discoideum* OX=44689 GN=rab2B PE=3 SV=1
Q55GW4	-1,523001082	0,1483	NSC	Putative uncharacterized protein DDB_G0267482 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267482 PE=4 SV=1
P34118	-1,538322348	0,0475	NSC	Major vault protein alpha OS=*Dictyostelium discoideum* OX=44689 GN=mvpA PE=1 SV=1
Q55C99	-1,542810356	0,1608	NSC	Aspartate--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=maspS PE=3 SV=1
Q54GE6	-1,544272449	0,0221	C	Probable malate dehydrogenase 1 OS=*Dictyostelium discoideum* OX=44689 GN=mdhA PE=1 SV=1
Q54LY8	-1,550862998	0,1195	NSC	Uncharacterized protein DDB_G0286299 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286299 PE=4 SV=1
Q54IF7	-1,556686462	0,0945	NSC	Vacuolar protein sorting-associated protein 29 OS=*Dictyostelium discoideum* OX=44689 GN=vps29 PE=3 SV=1
B0G180	-1,564387374	0,0227	C	Signal peptidase complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=spcs3 PE=3 SV=1
Q54HG9	-1,593061373	0,1184	NSC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit swp1 OS=*Dictyostelium discoideum* OX=44689 GN=swp1 PE=3 SV=1
Q86K01	-1,607997213	0,0696	NSC	60S ribosomal protein L15 OS=*Dictyostelium discoideum* OX=44689 GN=rpl15-1 PE=1 SV=1
Q54NU0	-1,624880729	0,2426	NSC	Flap endonuclease 1 OS=*Dictyostelium discoideum* OX=44689 GN=repG PE=3 SV=1
Q54XI5	-1,628602024	0,0513	NSC	60S ribosomal protein L9 OS=*Dictyostelium discoideum* OX=44689 GN=rpl9 PE=1 SV=2
Q54LP3	-1,631877952	0,0345	NSC	Dolichol-phosphate mannosyltransferase subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=dpm1 PE=3 SV=1
P48160	-1,657570422	0,0069	SC	60S ribosomal protein L27a OS=*Dictyostelium discoideum* OX=44689 GN=rpl27a PE=3 SV=1
Q54YR4	-1,66684447	0,0600	NSC	Protein transport protein Sec61 subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=sec61b PE=3 SV=1
Q54VI3	-1,685532883	0,0400	NSC	Glutamate dehydrogenase 2 OS=*Dictyostelium discoideum* OX=44689 GN=glud2 PE=1 SV=2
Q54KN7	-1,693620199	0,0001	SC	Putative thioredoxin-5 OS=*Dictyostelium discoideum* OX=44689 GN=trxE PE=3 SV=1
P54661	-1,695928922	0,1973	NSC	Small aggregate formation protein OS=*Dictyostelium discoideum* OX=44689 GN=smlA PE=2 SV=2
Q55FI3	-1,764264382	0,1490	NSC	Probable asparagine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=asnS2 PE=3 SV=1
Q55GJ6	-1,793235833	0,0584	NSC	Proteasome subunit beta type-6 OS=*Dictyostelium discoideum* OX=44689 GN=psmB6 PE=1 SV=1
Q54BU4	-1,798688551	0,1589	NSC	ABC transporter B family member 1 OS=*Dictyostelium discoideum* OX=44689 GN=abcB1 PE=3 SV=1
Q54FW9	-1,801859019	0,0900	NSC	WD repeat-containing protein DDB_G0290555 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0290555 PE=4 SV=1
Q54MG6	-1,801881435	0,0064	SC	60S ribosomal protein L37 OS=*Dictyostelium discoideum* OX=44689 GN=rpl37 PE=3 SV=1

Q9U9R7	-1,810747749	0,0324	NSC	Gamma-soluble NSF attachment protein OS=*Dictyostelium discoideum* OX=44689 GN=snpC PE=1 SV=1
Q55E94	-1,831325801	0,0835	NSC	Elongation factor G, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gfm1 PE=3 SV=1
Q54P26	-1,855276703	0,1313	NSC	Probable serine/threonine-protein kinase samkB OS=*Dictyostelium discoideum* OX=44689 GN=samkB PE=3 SV=1
P36412	-1,858112428	0,0141	SC	Ras-related protein Rab-11A OS=*Dictyostelium discoideum* OX=44689 GN=rab11A PE=1 SV=1
Q55FB8	-1,903794207	0,0656	NSC	Presporeless protein A OS=*Dictyostelium discoideum* OX=44689 GN=pslA PE=1 SV=1
Q54QR3	-1,922574202	0,0329	NSC	Ras-related protein Rab-32A OS=*Dictyostelium discoideum* OX=44689 GN=rab32A PE=1 SV=1
Q8MY12	-1,938730606	0,1279	NSC	Myosin heavy chain kinase C OS=*Dictyostelium discoideum* OX=44689 GN=mhkC PE=1 SV=1
P26200	-1,945787606	0,0937	NSC	Profilin-2 OS=*Dictyostelium discoideum* OX=44689 GN=proB PE=1 SV=1
Q55FK2	-1,975309792	0,0176	SC	Ras-related protein Rab-6 OS=*Dictyostelium discoideum* OX=44689 GN=rab6 PE=3 SV=1
Q55FL5	-1,97739482	0,0813	NSC	Serine palmitoyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=sptA PE=3 SV=1
Q55DT8	-1,977439111	0,0160	C	Probable acetylornithine aminotransferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=argD PE=3 SV=1
Q54I92	-1,999391015	0,0429	NSC	Protein psiI OS=*Dictyostelium discoideum* OX=44689 GN=psiI PE=3 SV=1
Q54GY8	-2,001712513	0,0300	C	Ras-related protein Rab-18 OS=*Dictyostelium discoideum* OX=44689 GN=rab18 PE=3 SV=1
Q86IV4	-2,032319942	0,0054	C	PH domain-containing protein DDB_G0274775 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274775 PE=4 SV=1
Q54JA3	-2,059282089	0,0122	C	Integrin beta-like protein E OS=*Dictyostelium discoideum* OX=44689 GN=sibE PE=1 SV=1
P20790	-2,069020815	0,0173	SC	Ras-related protein Rab-8A OS=*Dictyostelium discoideum* OX=44689 GN=rab8A PE=3 SV=1
Q54QE4	-2,077630608	0,0294	SC	Bifunctional purine synthesis protein purC/E OS=*Dictyostelium discoideum* OX=44689 GN=purC/E PE=1 SV=1
Q54WN5	-2,079133223	0,0386	NSC	U3 small nucleolar RNA-associated protein 6 homolog OS=*Dictyostelium discoideum* OX=44689 GN=utp6 PE=1 SV=1
Q54X82	-2,1593099	0,0179	C	AP-1 complex subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=ap1b1 PE=3 SV=1
Q76P36	-2,204789957	0,0545	NSC	40S ribosomal protein S29 OS=*Dictyostelium discoideum* OX=44689 GN=rps29 PE=3 SV=1
Q54TH8	-2,213240597	0,1208	NSC	T-complex protein 1 subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=cct3 PE=1 SV=1
Q54LT2	-2,249401733	0,0221	SC	Uricase OS=*Dictyostelium discoideum* OX=44689 GN=uox PE=3 SV=1
Q54E04	-2,363280358	0,0017	SC	Vacuolar proton translocating ATPase 100 kDa subunit OS=*Dictyostelium discoideum* OX=44689 GN=vatM PE=1 SV=2
P34140	-2,371085217	0,0007	SC	Ras-related protein Rab-1B OS=*Dictyostelium discoideum* OX=44689 GN=rab1B PE=2 SV=2
Q37315	-2,429256855	0,0097	SC	ATP synthase subunit 9, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp9 PE=3 SV=1

Q54XX3	-2,485328671	0,0017	SC	60S ribosomal protein L5 OS=*Dictyostelium discoideum* OX=44689 GN=rpl5 PE=1 SV=1
Q86LA2	-2,557152168	0,0019	C	Eukaryotic translation initiation factor 3 subunit L OS=*Dictyostelium discoideum* OX=44689 GN=eif3L PE=3 SV=1
Q54E49	-2,594502535	0,0153	SC	Probable ATP-dependent RNA helicase ddx6 OS=*Dictyostelium discoideum* OX=44689 GN=ddx6 PE=3 SV=1
P54644	-2,622588043	0,0653	NSC	RAC family serine/threonine-protein kinase homolog OS=*Dictyostelium discoideum* OX=44689 GN=pkbA PE=1 SV=1
O96622	-2,675128993	0,0003	SC	Actin-related protein 2/3 complex subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=arcA PE=1 SV=1
O15818	-2,699813763	0,0016	SC	Clustered mitochondria protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=clua PE=1 SV=2
Q54TS4	-2,79243775	0,0033	C	Protein YIPF1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=yipf1 PE=3 SV=1
Q55DW4	-2,821613047	0,0393	NSC	ABC transporter G family member 1 OS=*Dictyostelium discoideum* OX=44689 GN=abcG1 PE=3 SV=1
Q55BP5	-2,850068585	0,1284	NSC	Probable DNA topoisomerase 2 OS=*Dictyostelium discoideum* OX=44689 GN=top2 PE=3 SV=1
P18142	-2,922255889	0,0038	SC	cAMP-regulated D2 protein OS=*Dictyostelium discoideum* OX=44689 GN=D2 PE=2 SV=3
Q54E62	-3,098742723	0,0121	SC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=*Dictyostelium discoideum* OX=44689 GN=ddost PE=3 SV=1
Q55A19	-3,118806213	0,0000	SC	40S ribosomal protein S23 OS=*Dictyostelium discoideum* OX=44689 GN=rps23 PE=3 SV=1
Q54MT2	-3,123550746	0,0292	C	Nucleolar protein 56 OS=*Dictyostelium discoideum* OX=44689 GN=nop56 PE=3 SV=1
Q55CT1	-3,13762717	0,0572	NSC	NADPH--cytochrome P450 reductase OS=*Dictyostelium discoideum* OX=44689 GN=redB PE=2 SV=1
Q54XD8	-3,215349655	0,0114	SC	Eukaryotic translation initiation factor 2 subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=eif2s3 PE=2 SV=1
Q86KI1	-3,631911596	0,0025	C	AP-2 complex subunit alpha-2 OS=*Dictyostelium discoideum* OX=44689 GN=ap2a1-1 PE=3 SV=1
Q86JP3	-3,800893624	0,0113	SC	Ras-related protein Rab-5A OS=*Dictyostelium discoideum* OX=44689 GN=rab5A PE=3 SV=1
Q75JK6	-3,830727246	0,0000	C	ATP synthase subunit epsilon, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5e PE=3 SV=1
Q8T1V4	-4,05613178	0,0113	SC	40S ribosomal protein S27 OS=*Dictyostelium discoideum* OX=44689 GN=rps27 PE=3 SV=2
Q555H8	-4,146767454	0,0031	C	E3 ubiquitin-protein ligase listerin OS=*Dictyostelium discoideum* OX=44689 GN=rnf160 PE=3 SV=1
P34092	-4,235808707	0,0183	C	Myosin IB heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=myoB PE=1 SV=2
P34042	-4,265413185	0,0063	SC	Guanine nucleotide-binding protein alpha-4 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaD PE=1 SV=1
Q9U1M8	-4,290380328	0,0543	NSC	Myosin-I heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=myoI PE=1 SV=1
Q54ET0	-4,301930454	0,0551	NSC	Metabotropic glutamate receptor-like protein E OS=*Dictyostelium discoideum* OX=44689 GN=grlE PE=2 SV=2

Q54N72	-4,405086585	0,0003	C	Probable nucleolar GTP-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=nog1 PE=1 SV=1
Q54TJ4	-4,632045963	0,0018	C	Probable ATP-dependent RNA helicase ddx27 OS=*Dictyostelium discoideum* OX=44689 GN=ddx27 PE=3 SV=1
P16051	-4,721415737	0,0153	SC	Guanine nucleotide-binding protein alpha-2 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaB PE=1 SV=3
P34113	-4,778252888	0,0002	SC	60S ribosomal protein L3 OS=*Dictyostelium discoideum* OX=44689 GN=rpl3 PE=1 SV=2
Q54D63	-4,847337198	0,0000	SC	60S ribosomal protein L6 OS=*Dictyostelium discoideum* OX=44689 GN=rpl6 PE=1 SV=1
O97470	-5,112622045	0,0007	SC	Mitochondrial substrate carrier family protein ancA OS=*Dictyostelium discoideum* OX=44689 GN=ancA PE=1 SV=1
Q54I48	-5,163917509	0,0060	C	Choline transporter-like protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=slc44a2 PE=3 SV=1
P54679	-5,40463086	0,0002	C	Probable plasma membrane ATPase OS=*Dictyostelium discoideum* OX=44689 GN=patB PE=2 SV=2
Q55BF2	-5,463695934	0,0237	C	60S ribosomal export protein NMD3 OS=*Dictyostelium discoideum* OX=44689 GN=nmd3 PE=3 SV=1
Q94502	-5,49152847	0,0154	C	Neutral alpha-glucosidase AB OS=*Dictyostelium discoideum* OX=44689 GN=modA PE=3 SV=1
P54678	-5,63505283	0,0001	SC	Calcium-transporting ATPase PAT1 OS=*Dictyostelium discoideum* OX=44689 GN=patA PE=2 SV=2
P15112	-5,97286426	0,0005	SC	Elongation factor 2 OS=*Dictyostelium discoideum* OX=44689 GN=efbA PE=1 SV=2
Q55FI4	-6,890926646	0,0018	SC	Nucleolar protein 58 OS=*Dictyostelium discoideum* OX=44689 GN=nop58 PE=3 SV=1
Q54EW2	-7,207686946	0,0047	SC	Putative bifunctional amine oxidase DDB_G0291301 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0291301 PE=1 SV=1
Q54ET6	-7,653718327	0,0929	NSC	Actin-binding protein F OS=*Dictyostelium discoideum* OX=44689 GN=abpF PE=1 SV=1
Q54B10	-7,694106437	0,0357	NSC	NADPH oxidoreductase A OS=*Dictyostelium discoideum* OX=44689 GN=redA PE=2 SV=1
Q54NM9	-10,79914065	0,0104	SC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 OS=*Dictyostelium discoideum* OX=44689 GN=stt3 PE=3 SV=1
Q55DA0	-12,30415541	0,0017	C	ABC transporter G family member 22 OS=*Dictyostelium discoideum* OX=44689 GN=abcG22 PE=2 SV=1
P34036	-16,66554916	0,0000	SC	Dynein heavy chain, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=dhcA PE=1 SV=2
Q9XPJ9	-18,39834422	0,0000	SC	ATP synthase subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp1 PE=1 SV=1
P20054	-26,56277311	0,0004	SC	Protein PYR1-3 OS=*Dictyostelium discoideum* OX=44689 GN=pyr1-3 PE=1 SV=3

Supplementary Table 3 – Proteins present only in Δ*sopB*-infected samples.

Locus ID	Description
P42526	Hisactophilin-2 OS=*Dictyostelium discoideum* OX=44689 GN=hatB PE=1 SV=2
Q6TMJ9	Synaptobrevin-A OS=*Dictyostelium discoideum* OX=44689 GN=sybA PE=2 SV=1
Q558Y7	Protein costars OS=*Dictyostelium discoideum* OX=44689 GN=cosA PE=2 SV=1
Q54BN4	40S ribosomal protein S21 OS=*Dictyostelium discoideum* OX=44689 GN=rps21 PE=3 SV=1
Q55FM0	ER membrane protein complex subunit 8/9 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268048 PE=3 SV=1
Q55DU1	Actobindin-B/C OS=*Dictyostelium discoideum* OX=44689 GN=abnB PE=3 SV=1
Q54LW6	Uncharacterized protein DDB_G0286463 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286463 PE=4 SV=1
P54658	32 kDa heat shock protein OS=*Dictyostelium discoideum* OX=44689 GN=hspC PE=2 SV=1
Q54GP8	Glutaredoxin OS=*Dictyostelium discoideum* OX=44689 GN=grxA PE=2 SV=1
Q54I79	Centractin OS=*Dictyostelium discoideum* OX=44689 GN=arpA PE=1 SV=1
Q55GN3	Probable prefoldin subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=pfdn2 PE=3 SV=1
Q54LX0	Calcium-binding protein M OS=*Dictyostelium discoideum* OX=44689 GN=cbpM PE=1 SV=1
Q54P14	COMM domain-containing protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=commd2 PE=4 SV=1
Q54HL6	COP9 signalosome complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=csn2 PE=1 SV=1
Q54WY5	Ribosomal RNA processing protein 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=rrp1 PE=3 SV=1
Q54X65	Protein BRICK1 OS=*Dictyostelium discoideum* OX=44689 GN=brk1 PE=1 SV=1
Q1ZXQ1	Fumarylacetoacetase OS=*Dictyostelium discoideum* OX=44689 GN=fah PE=3 SV=1
Q54QX0	Calcium-binding protein B OS=*Dictyostelium discoideum* OX=44689 GN=cbpB PE=4 SV=1
Q54XP2	Small nuclear ribonucleoprotein F OS=*Dictyostelium discoideum* OX=44689 GN=snrpf PE=3 SV=1
Q86HB8	Counting factor-associated protein C OS=*Dictyostelium discoideum* OX=44689 GN=cfaC PE=3 SV=1
Q54JM3	NEDD8-activating enzyme E1 regulatory subunit OS=*Dictyostelium discoideum* OX=44689 GN=nae1 PE=3 SV=1
Q54YX3	CRAL-TRIO domain-containing protein DDB_G0278031 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0278031 PE=4 SV=2
Q55DP8	Aminoacylase-1 OS=*Dictyostelium discoideum* OX=44689 GN=acy1 PE=2 SV=1
Q54D06	Probable ubiquitin-conjugating enzyme E2 variant OS=*Dictyostelium discoideum* OX=44689 GN=ube2v PE=3 SV=1
Q54KX4	Probable U6 snRNA-associated Sm-like protein LSm4 OS=*Dictyostelium discoideum* OX=44689 GN=lsm4 PE=3 SV=1
Q54BC8	Proteasome subunit beta type-5 OS=*Dictyostelium discoideum* OX=44689 GN=psmB5 PE=1 SV=1
Q54DF9	Uroporphyrinogen decarboxylase OS=*Dictyostelium discoideum* OX=44689 GN=hemE PE=1 SV=1
Q54VI4	Putative glutathione S-transferase alpha-3 OS=*Dictyostelium discoideum* OX=44689 GN=gsta3 PE=1 SV=1
Q54X03	Phosphomannomutase 1 OS=*Dictyostelium discoideum* OX=44689 GN=pmmA PE=3 SV=1
Q553W9	Ceroid-lipofuscinosis neuronal protein 5 homolog OS=*Dictyostelium discoideum* OX=44689 GN=cln5 PE=3 SV=1
Q8T293	Probable di-N-acetylchitobiase 2 OS=*Dictyostelium discoideum* OX=44689 GN=ctbs2 PE=3 SV=1
Q86HT3	BolA-like protein DDB_G0274439 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274439 PE=3 SV=1

Q54HF6	Probable U6 snRNA-associated Sm-like protein LSm7 OS=*Dictyostelium discoideum* OX=44689 GN=lsm7 PE=3 SV=1
Q553E8	RNA transcription, translation and transport factor protein OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275847 PE=2 SV=1
Q54PZ2	Copper transport protein ATOX1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=atox1 PE=3 SV=2
A0A0F6BB72	Putative cytoplasmic protein OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=yjiX PE=4 SV=1
Q550G0	Peroxisome biogenesis factor 16 OS=*Dictyostelium discoideum* OX=44689 GN=pex16 PE=3 SV=1
Q86JE1	Recoverin family protein DDB_G0272130 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272130 PE=1 SV=1
P54670	Calfumirin-1 OS=*Dictyostelium discoideum* OX=44689 GN=cafA PE=2 SV=1
Q54RX0	Probable small nuclear ribonucleoprotein G OS=*Dictyostelium discoideum* OX=44689 GN=snrpG PE=3 SV=1
Q556L1	Signal recognition particle 14 kDa protein OS=*Dictyostelium discoideum* OX=44689 GN=srp14-1 PE=3 SV=1
Q54KI0	Eukaryotic translation initiation factor 3 subunit J OS=*Dictyostelium discoideum* OX=44689 GN=eif3J PE=3 SV=1
Q95ZG8	Guanine nucleotide-binding protein subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=gpgA PE=1 SV=1
Q556Z0	SWI/SNF complex component SNF12 homolog OS=*Dictyostelium discoideum* OX=44689 GN=snf12-1 PE=3 SV=1
Q54B20	Succinate dehydrogenase assembly factor 2, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0293946 PE=3 SV=1
Q55CQ7	Transportin OS=*Dictyostelium discoideum* OX=44689 GN=tnpo PE=3 SV=1
Q54U86	Peroxisome biogenesis factor 3 OS=*Dictyostelium discoideum* OX=44689 GN=pex3 PE=3 SV=1
Q552S7	Putative acetyltransferase DDB_G0275913 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275913 PE=3 SV=1
Q55BD5	COP9 signalosome complex subunit 7 OS=*Dictyostelium discoideum* OX=44689 GN=csn7 PE=1 SV=1
Q54TH4	Golgi to ER traffic protein 4 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0281815 PE=3 SV=1
Q86KL1	Probable E3 ubiquitin-protein ligase bre1 OS=*Dictyostelium discoideum* OX=44689 GN=bre1 PE=3 SV=1
Q86IL5	Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=ppp4r2 PE=3 SV=2
A0A0F6B856	Uncharacterized protein OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=STM14_4316 PE=4 SV=1
Q54GT9	Autophagy protein 5 OS=*Dictyostelium discoideum* OX=44689 GN=atg5 PE=3 SV=1
Q54ES6	DNA-directed RNA polymerases I and III subunit rpc19 OS=*Dictyostelium discoideum* OX=44689 GN=rpc19 PE=3 SV=1
Q55F34	3'(2'),5'-bisphosphate nucleotidase OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268652 PE=3 SV=1
Q54N50	Dynactin subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=dynB PE=3 SV=1
Q55C77	GDP-L-fucose synthase OS=*Dictyostelium discoideum* OX=44689 GN=ger PE=3 SV=1
Q86IZ3	Ubiquitin-conjugating enzyme E2 pex4 OS=*Dictyostelium discoideum* OX=44689 GN=pex4 PE=3 SV=1
Q556G4	Deoxyhypusine hydroxylase OS=*Dictyostelium discoideum* OX=44689 GN=dohh-1 PE=3 SV=1
Q86CR6	Ubiquitin-like protein atg12 OS=*Dictyostelium discoideum* OX=44689 GN=atg12 PE=3 SV=1
Q550A8	Autophagy-related protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=atg3 PE=3 SV=3
P20425	UMP-CMP kinase OS=*Dictyostelium discoideum* OX=44689 GN=pyrK PE=1 SV=2
Q54GK9	Charged multivesicular body protein 2a homolog 1 OS=*Dictyostelium discoideum* OX=44689 GN=chmp2a1 PE=3 SV=2
Q54DA8	Protein STIP1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=sti1 PE=3 SV=1
Q54EH2	DNA-directed RNA polymerases I, II, and III subunit rpabc1 OS=*Dictyostelium discoideum* OX=44689 GN=polr2e PE=3 SV=2

Q54D73	Flavohemoprotein B OS=*Dictyostelium discoideum* OX=44689 GN=fhbB PE=1 SV=1
Q54RS2	Uncharacterized protein DDB_G0282957 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282957 PE=4 SV=1
P34122	cAMP-binding protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=capB PE=1 SV=2
Q54XJ0	MOB kinase activator-like 1 homolog A OS=*Dictyostelium discoideum* OX=44689 GN=mobA PE=3 SV=1
Q54KR1	Cysteine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=cysS PE=3 SV=1
Q54C92	COP9 signalosome complex subunit 6 OS=*Dictyostelium discoideum* OX=44689 GN=csn6 PE=1 SV=1
O76187	Darlin OS=*Dictyostelium discoideum* OX=44689 GN=darA PE=1 SV=1
Q55E13	Zinc finger protein ZPR1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=zpr1 PE=3 SV=1
Q550D2	Phenylalanine--tRNA ligase beta subunit OS=*Dictyostelium discoideum* OX=44689 GN=phesB PE=3 SV=2
Q54Q05	Elongin-C OS=*Dictyostelium discoideum* OX=44689 GN=tceb1 PE=3 SV=1
Q75K24	COP9 signalosome complex subunit 8 OS=*Dictyostelium discoideum* OX=44689 GN=csn8 PE=1 SV=1
Q556N5	Proteasomal ubiquitin receptor ADRM1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=adrm1-1 PE=1 SV=1
Q55G87	Calcineurin subunit B type 1 OS=*Dictyostelium discoideum* OX=44689 GN=cnbA PE=1 SV=1
Q54P93	Porphobilinogen deaminase OS=*Dictyostelium discoideum* OX=44689 GN=hemC PE=3 SV=1
Q54X41	SOSS complex subunit B homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0279223 PE=3 SV=1
Q557A2	Uncharacterized protein DDB_G0273701/DDB_G0273221 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0273701 PE=4 SV=1
Q54KT7	General transcription factor IIF subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=gtf2f2 PE=3 SV=2
Q75JP5	Calponin homology domain-containing protein DDB_G0272472 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272472 PE=4 SV=1
Q23919	Phosphoglucomutase-1 OS=*Dictyostelium discoideum* OX=44689 GN=pgmA PE=2 SV=1
Q9NGP4	Sumo-conjugating enzyme ubc9 OS=*Dictyostelium discoideum* OX=44689 GN=ubc9 PE=3 SV=1
Q86IW8	COMM domain-containing protein 5 OS=*Dictyostelium discoideum* OX=44689 GN=commd5 PE=4 SV=1
Q6RZZ9	Kinesin-related protein 13 OS=*Dictyostelium discoideum* OX=44689 GN=kif13 PE=1 SV=1
Q54WR6	Protein transport protein yos1 OS=*Dictyostelium discoideum* OX=44689 GN=yos1 PE=3 SV=1
Q54WZ0	Cell division cycle 5-like protein OS=*Dictyostelium discoideum* OX=44689 GN=cdc5l PE=3 SV=1
Q8T662	ATPase ASNA1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=arsA PE=1 SV=1
Q54IK9	Protein hook homolog OS=*Dictyostelium discoideum* OX=44689 GN=hook PE=3 SV=1
Q55CK2	Mental retardation GTPase activating protein homolog 2 OS=*Dictyostelium discoideum* OX=44689 GN=mgp2 PE=3 SV=1
Q1ZXG8	Probable tyrosine-protein phosphatase DG1060 OS=*Dictyostelium discoideum* OX=44689 GN=DG1060 PE=3 SV=1
Q54HX6	Myb-like protein I OS=*Dictyostelium discoideum* OX=44689 GN=mybI PE=3 SV=1
Q9XZE5	Serine/threonine-protein phosphatase 2A catalytic subunit A OS=*Dictyostelium discoideum* OX=44689 GN=pho2a PE=1 SV=1
Q55GN6	Probable phosphatidylinositol phosphate kinase DDB_G0267588 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267588 PE=1 SV=1
Q8T2I8	Serine/threonine-protein kinase sepA OS=*Dictyostelium discoideum* OX=44689 GN=sepA PE=2 SV=1
Q54ZB3	Conserved oligomeric Golgi complex subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=cog1 PE=3 SV=1
Q54C55	Peroxisomal membrane protein PEX14 OS=*Dictyostelium discoideum* OX=44689 GN=pex14 PE=3 SV=1

Q54ES8	Putative synaptobrevin homolog YKT6 OS=*Dictyostelium discoideum* OX=44689 GN=ykt6 PE=1 SV=1
Q54MR1	Hydroxyacylglutathione hydrolase OS=*Dictyostelium discoideum* OX=44689 GN=hagh PE=3 SV=1
Q8T1G4	Lysozyme A OS=*Dictyostelium discoideum* OX=44689 GN=alyA PE=1 SV=1
Q54BM5	Branchpoint-bridging protein OS=*Dictyostelium discoideum* OX=44689 GN=sf1 PE=3 SV=1
Q55AR8	U5 small nuclear ribonucleoprotein 40 kDa protein OS=*Dictyostelium discoideum* OX=44689 GN=snrnp40 PE=3 SV=1
Q86G47	Ras guanine nucleotide exchange factor Q OS=*Dictyostelium discoideum* OX=44689 GN=gefQ PE=2 SV=1
B0G163	Exocyst complex component 5 OS=*Dictyostelium discoideum* OX=44689 GN=exoc5 PE=3 SV=1
Q550I8	COMM domain-containing protein 4 OS=*Dictyostelium discoideum* OX=44689 GN=commd4 PE=4 SV=1
Q55EX5	Probable U6 snRNA-associated Sm-like protein LSm5 OS=*Dictyostelium discoideum* OX=44689 GN=lsm5 PE=3 SV=1
Q54ST3	DDT domain-containing protein DDB_G0282237 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282237 PE=3 SV=1
Q7M438	Ribonuclease DdI OS=*Dictyostelium discoideum* OX=44689 GN=ddiA PE=1 SV=3
Q54LV0	Structural maintenance of chromosomes protein 4 OS=*Dictyostelium discoideum* OX=44689 GN=smc4 PE=3 SV=1
Q554G7	Signal recognition particle 19 kDa protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=srp19 PE=3 SV=1
Q76NT6	Dolichol-phosphate mannosyltransferase subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=dpm3 PE=3 SV=1
Q54QS0	E3 UFM1-protein ligase 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283667 PE=3 SV=1
Q54MV3	Rho GTPase-activating protein gacJ OS=*Dictyostelium discoideum* OX=44689 GN=gacJ PE=3 SV=1
Q9U7C9	Nucleomorphin OS=*Dictyostelium discoideum* OX=44689 GN=numA PE=1 SV=2
O77033	General transcriptional corepressor trfA OS=*Dictyostelium discoideum* OX=44689 GN=trfA PE=2 SV=1
Q55CU8	Phosphatidylinositol transfer protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=pitC PE=2 SV=1
Q54YQ9	Diphosphomevalonate decarboxylase OS=*Dictyostelium discoideum* OX=44689 GN=mvd PE=3 SV=1
Q55CV0	NAD(P)H-hydrate epimerase OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0269890 PE=3 SV=1
Q8IS18	Ras guanine nucleotide exchange factor E OS=*Dictyostelium discoideum* OX=44689 GN=gefE PE=2 SV=1
Q55BX5	Nuclear pore complex protein nup54 OS=*Dictyostelium discoideum* OX=44689 GN=nup54 PE=3 SV=1
Q54NV1	Exocyst complex component 1 OS=*Dictyostelium discoideum* OX=44689 GN=exoc1 PE=3 SV=1
Q54GZ0	O-methyltransferase 9 OS=*Dictyostelium discoideum* OX=44689 GN=omt9 PE=3 SV=1
Q54EH1	Epsin OS=*Dictyostelium discoideum* OX=44689 GN=epnA PE=3 SV=1
Q54RE8	Kynurenine 3-monooxygenase OS=*Dictyostelium discoideum* OX=44689 GN=kmo PE=3 SV=1
Q54S59	WD repeat-containing protein 61 homolog OS=*Dictyostelium discoideum* OX=44689 GN=wdr61 PE=4 SV=1
Q54E53	COP9 signalosome complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=csn3 PE=1 SV=1
Q54J37	Striatin homolog OS=*Dictyostelium discoideum* OX=44689 GN=strn PE=3 SV=1
A0A0F6B4E5	Histidine kinase OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=pgtB PE=4 SV=1
Q55G31	Expansin-like protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=expl1 PE=2 SV=1
Q54YY1	Protein SCAI homolog OS=*Dictyostelium discoideum* OX=44689 GN=scai PE=3 SV=1
Q86HS0	Probable ubiquinone biosynthesis protein coq9, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=coq9 PE=3 SV=2

Q54I82	Probable cytidine deaminase OS=*Dictyostelium discoideum* OX=44689 GN=cda PE=3 SV=1
Q54CS6	Protein dcd1B OS=*Dictyostelium discoideum* OX=44689 GN=dcd1B PE=2 SV=1
Q55FT5	Conserved oligomeric Golgi complex subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=cog4 PE=3 SV=1
Q54RJ4	Probable serine/threonine-protein kinase iksA OS=*Dictyostelium discoideum* OX=44689 GN=iksA PE=3 SV=1
Q551M4	Zinc finger protein-like 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=zfpl1 PE=3 SV=1
Q54DV3	von Willebrand factor A domain-containing protein DDB_G0292016 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292016 PE=4 SV=1
Q1ZXI2	CCR4-NOT transcription complex subunit 11 OS=*Dictyostelium discoideum* OX=44689 GN=cnot11 PE=3 SV=1
Q54CK9	WAS protein family homolog DDB_G0292878 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292878 PE=1 SV=1
Q54PG1	Dynein light chain Tctex-type OS=*Dictyostelium discoideum* OX=44689 GN=dlcA PE=3 SV=2
Q54NA0	Nuclear pore complex protein nup85 OS=*Dictyostelium discoideum* OX=44689 GN=nup85 PE=3 SV=1
Q54K96	Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66 OS=*Dictyostelium discoideum* OX=44689 GN=jcdg PE=3 SV=1
Q54Z23	Integrator complex subunit 6 homolog OS=*Dictyostelium discoideum* OX=44689 GN=ints6 PE=3 SV=2
Q552E2	WASH complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=washc2 PE=1 SV=1
Q55FK4	Acyl-protein thioesterase 1 homolog 2 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268064 PE=1 SV=1
Q54I54	Putative uncharacterized transmembrane protein DDB_G0288997 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288997 PE=4 SV=2
O60950	Golvesin OS=*Dictyostelium discoideum* OX=44689 GN=gol PE=1 SV=1
Q54QK4	COMM domain-containing protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=commd3 PE=4 SV=1
Q54J86	Dictomallein-1 OS=*Dictyostelium discoideum* OX=44689 GN=dtmlA PE=3 SV=1
Q54BQ5	NSFL1 cofactor p47 homolog OS=*Dictyostelium discoideum* OX=44689 GN=nsfl1c PE=3 SV=1
Q8T197	Dehydrogenase/reductase SDR family protein 7-like OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274201 PE=3 SV=1
Q55E83	NIF3-like protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=nif3 PE=2 SV=1
Q86JM3	DNA-directed RNA polymerase III subunit rpc6 OS=*Dictyostelium discoideum* OX=44689 GN=polr3f PE=3 SV=1
Q553X3	Rho GTPase-activating protein gacI OS=*Dictyostelium discoideum* OX=44689 GN=gacI PE=3 SV=1
P26355	TATA-box-binding protein OS=*Dictyostelium discoideum* OX=44689 GN=tbpA PE=2 SV=2
Q1ZXD9	Sphingomyelinase DDB_G0288017 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288017 PE=3 SV=1
Q54PL2	Integrator complex subunit 7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=ints7 PE=3 SV=1
Q54N83	Leucine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=leuS PE=3 SV=1
Q55GC7	Sphingomyelinase phosphodiesterase D OS=*Dictyostelium discoideum* OX=44689 GN=sgmD PE=3 SV=1
Q54NL0	Rho GTPase-activating protein gacT OS=*Dictyostelium discoideum* OX=44689 GN=gacT PE=3 SV=1
Q54TC3	Probable inactive serine/threonine-protein kinase slob1 OS=*Dictyostelium discoideum* OX=44689 GN=slob1 PE=3 SV=1
Q86A97	EARP-interacting protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=eipr1 PE=1 SV=1
Q54WH7	Putative uncharacterized protein DDB_G0279653 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0279653 PE=4 SV=1
Q54XT8	Ribosomal RNA processing protein 36 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0278751 PE=3 SV=1
Q86A12	Probable serine/threonine-protein kinase sky1 OS=*Dictyostelium discoideum* OX=44689 GN=sky1 PE=3 SV=1

Q54H39	AP-2 complex subunit sigma OS=*Dictyostelium discoideum* OX=44689 GN=ap2s1 PE=3 SV=2
Q55FF3	Putative glutathione S-transferase alpha-1 OS=*Dictyostelium discoideum* OX=44689 GN=gsta1 PE=1 SV=1
Q86AD7	Probable myosin light chain kinase DDB_G0271550 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271550 PE=3 SV=1
Q54B82	COP9 signalosome complex subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=csn4 PE=2 SV=1
Q54NP0	Putative uncharacterized protein DDB_G0285119 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0285119 PE=3 SV=1
Q55D99	Serine/threonine-protein kinase pakA OS=*Dictyostelium discoideum* OX=44689 GN=pakA PE=1 SV=1
Q54TH6	Probable serine/threonine-protein kinase DDB_G0281745 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0281745 PE=3 SV=1
Q54XS1	Phenylalanine-4-hydroxylase OS=*Dictyostelium discoideum* OX=44689 GN=pah PE=1 SV=1
Q54K95	Tyrosine aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=tat PE=3 SV=1
Q54NU5	BTG family protein OS=*Dictyostelium discoideum* OX=44689 GN=btg PE=3 SV=1
Q54CV3	Coiled-coil domain-containing protein 93 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292680 PE=3 SV=1
Q54QR2	Proteasome subunit beta type-7 OS=*Dictyostelium discoideum* OX=44689 GN=psmB7 PE=3 SV=1
Q54ML1	Glutamine-dependent NAD(+) synthetase OS=*Dictyostelium discoideum* OX=44689 GN=nadsyn1 PE=3 SV=1
P42525	Extracellular signal-regulated kinase 1 OS=*Dictyostelium discoideum* OX=44689 GN=erkA PE=2 SV=2
Q54P76	Exocyst complex component 4 OS=*Dictyostelium discoideum* OX=44689 GN=exoc4 PE=3 SV=1
Q54LT4	Uncharacterized protein DDB_G0286423 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286423 PE=4 SV=1
Q54RV3	Serine/threonine-protein kinase pakG OS=*Dictyostelium discoideum* OX=44689 GN=pakG PE=3 SV=1
Q55FE3	Protein FAM45 homolog OS=*Dictyostelium discoideum* OX=44689 GN=fam45 PE=3 SV=1
Q7KWX2	Probable CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=pgs1 PE=3 SV=1
Q54XC1	Cytosolic purine 5'-nucleotidase OS=*Dictyostelium discoideum* OX=44689 GN=nt5c2 PE=3 SV=1
Q54BA2	Ankyrin repeat, bromo and BTB domain-containing protein DDB_G0293800 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0293800 PE=4 SV=1
Q54VX5	Exocyst complex component 2 OS=*Dictyostelium discoideum* OX=44689 GN=exoc2 PE=3 SV=1
Q54G05	Putative leucine-rich repeat-containing protein DDB_G0290503 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0290503 PE=4 SV=1
Q02158	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase OS=*Dictyostelium discoideum* OX=44689 GN=plc PE=2 SV=1
Q54PF1	Casein kinase II subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=csnk2b PE=3 SV=1
Q75K28	Calcium-binding protein NCSA OS=*Dictyostelium discoideum* OX=44689 GN=ncsA PE=1 SV=2
B0G0Y8	cGMP-specific 3',5'-cGMP phosphodiesterase 3 OS=*Dictyostelium discoideum* OX=44689 GN=pde3 PE=1 SV=1
Q54M35	Putative lysozyme-like protein OS=*Dictyostelium discoideum* OX=44689 GN=alyL PE=3 SV=2
Q9XPI8	Ribosomal protein S4, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps4 PE=3 SV=1
Q54X95	Probable methionine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=metS PE=3 SV=1
Q8T133	Protein tortoise OS=*Dictyostelium discoideum* OX=44689 GN=torA PE=2 SV=1
P34099	cAMP-dependent protein kinase catalytic subunit OS=*Dictyostelium discoideum* OX=44689 GN=pkaC PE=1 SV=2
Q54PH5	Pre-mRNA-splicing factor cwc2 OS=*Dictyostelium discoideum* OX=44689 GN=cwc2 PE=3 SV=1
Q54TD7	ATP-dependent RNA helicase ddx24 OS=*Dictyostelium discoideum* OX=44689 GN=ddx24 PE=3 SV=1

Q54SD5	Phosphatidylethanolamine N-methyltransferase A OS=*Dictyostelium discoideum* OX=44689 GN=pemtA PE=3 SV=1
P14325	Probable glutamine--tRNA ligase OS=*Dictyostelium discoideum* OX=44689 GN=glnS PE=2 SV=2
Q54M29	Serine hydrolase-like protein DDB_G0286239 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286239 PE=3 SV=2
Q54ND5	Multiple inositol polyphosphate phosphatase 1 OS=*Dictyostelium discoideum* OX=44689 GN=mipp1 PE=1 SV=1
Q555D2	Nuclear pore complex protein DDB_G0274915 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274915 PE=4 SV=2
Q54CD6	Probable ATP-dependent RNA helicase ddx5 OS=*Dictyostelium discoideum* OX=44689 GN=ddx5 PE=3 SV=1
Q558W0	HIT domain-containing protein DDB_G0272839 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272839 PE=2 SV=1
Q54G43	Dual specificity protein kinase shkE OS=*Dictyostelium discoideum* OX=44689 GN=shkE PE=3 SV=1
Q23917	3',5'-cyclic-nucleotide phosphodiesterase regA OS=*Dictyostelium discoideum* OX=44689 GN=regA PE=1 SV=1
Q55BR7	Protein raptor homolog OS=*Dictyostelium discoideum* OX=44689 GN=raptor PE=1 SV=1
Q54IT1	Putative uncharacterized protein DDB_G0288537 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288537 PE=4 SV=1
P54201	Ubiquitin carboxyl-terminal hydrolase A OS=*Dictyostelium discoideum* OX=44689 GN=ubpA PE=2 SV=2
Q6S003	Kinesin-related protein 8 OS=*Dictyostelium discoideum* OX=44689 GN=kif8 PE=2 SV=1
Q54N40	Putative peroxisome assembly protein 12 OS=*Dictyostelium discoideum* OX=44689 GN=pex12 PE=3 SV=1
Q54IL2	Striatin-interacting protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=fam40 PE=3 SV=1
Q54DY7	Serine carboxypeptidase S10 family member 1 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0291912 PE=3 SV=1
Q54UC9	Kinesin-related protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=kif3 PE=1 SV=1
Q54CL3	Probable peroxisomal membrane protein PEX13 OS=*Dictyostelium discoideum* OX=44689 GN=pex13 PE=3 SV=1
Q554K2	Countin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274609 PE=3 SV=1
P54703	Cytoplasmic dynein 1 intermediate chain OS=*Dictyostelium discoideum* OX=44689 GN=dicA PE=2 SV=2
Q54DF2	Probable serine/threonine-protein kinase MARK-A OS=*Dictyostelium discoideum* OX=44689 GN=mrkA PE=3 SV=1
Q54E33	WD repeat-containing protein 92 homolog OS=*Dictyostelium discoideum* OX=44689 GN=wdr92 PE=4 SV=1
Q86KZ2	General transcription factor IIH subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=gtf2h2 PE=3 SV=2
Q55CP6	Probable ATP-dependent RNA helicase ddx1 OS=*Dictyostelium discoideum* OX=44689 GN=ddx1 PE=3 SV=1
Q7KWN2	Probable cytochrome P450 525A1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp525A1 PE=3 SV=1
Q55BU9	Probable cytochrome P450 513A3 OS=*Dictyostelium discoideum* OX=44689 GN=cyp513A3 PE=3 SV=1
Q54QB9	Rho GTPase-activating protein gacG OS=*Dictyostelium discoideum* OX=44689 GN=gacG PE=3 SV=1
Q54DD0	AMP deaminase OS=*Dictyostelium discoideum* OX=44689 GN=amdA PE=1 SV=1
Q54IJ9	Probable basic-leucine zipper transcription factor Q OS=*Dictyostelium discoideum* OX=44689 GN=bzpQ PE=3 SV=1
Q54CT0	Conserved oligomeric Golgi complex subunit 6 OS=*Dictyostelium discoideum* OX=44689 GN=cog6 PE=3 SV=1
Q54QG9	NEDD8-activating enzyme E1 catalytic subunit OS=*Dictyostelium discoideum* OX=44689 GN=uba3 PE=1 SV=1
Q54MI3	SUN domain-containing protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=sun2 PE=3 SV=1
Q75J96	RapA guanosine triphosphatase-activating protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=rapgap1 PE=2 SV=1

Q54JC0	Calmodulin-binding protein CmbB OS=*Dictyostelium discoideum* OX=44689 GN=cmbB PE=1 SV=1
Q55GH4	Glycogen [starch] synthase OS=*Dictyostelium discoideum* OX=44689 GN=glcS PE=3 SV=1
Q54GV0	Putative mediator of RNA polymerase II transcription subunit 24 OS=*Dictyostelium discoideum* OX=44689 GN=med24 PE=3 SV=2
Q557F4	Probable importin subunit alpha-A OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0273149 PE=3 SV=1
Q54S40	Cyclic GMP-binding protein D OS=*Dictyostelium discoideum* OX=44689 GN=gbpD PE=2 SV=1
Q55GI5	L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=l2hgdh PE=3 SV=1
Q553D3	Rac guanine nucleotide exchange factor JJ OS=*Dictyostelium discoideum* OX=44689 GN=gxcJJ PE=1 SV=1
Q55C84	Bromodomain-containing protein DDB_G0270170 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0270170 PE=4 SV=1
Q869P0	Probable ATP-dependent RNA helicase ddx31 OS=*Dictyostelium discoideum* OX=44689 GN=ddx31 PE=3 SV=2
Q55E98	Probable zinc transporter protein DDB_G0269332 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0269332 PE=3 SV=1
Q555L9	Transcription initiation factor TFIID subunit 12 OS=*Dictyostelium discoideum* OX=44689 GN=TAF12 PE=3 SV=2
Q86H43	Alanine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=malaS PE=3 SV=1
Q55BQ3	Probable inactive serine/threonine-protein kinase scy2 OS=*Dictyostelium discoideum* OX=44689 GN=scy2 PE=3 SV=1
Q55BC0	ABC transporter A family member 8 OS=*Dictyostelium discoideum* OX=44689 GN=abcA8 PE=3 SV=1
Q55B11	Vacuolar protein sorting-associated protein VTA1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=vta1 PE=3 SV=1
Q86I06	Probable serine/threonine-protein kinase nek3 OS=*Dictyostelium discoideum* OX=44689 GN=nek3 PE=3 SV=1
Q8SSQ0	Ras guanine nucleotide exchange factor R OS=*Dictyostelium discoideum* OX=44689 GN=gefR PE=1 SV=1
Q8MXQ3	Transmembrane protein 260 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275853 PE=3 SV=2
Q54XG7	Basic-leucine zipper transcription factor A OS=*Dictyostelium discoideum* OX=44689 GN=dimA PE=1 SV=2
Q556J8	AP-3 complex subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=ap3b-1 PE=3 SV=1
Q54P47	Probable serine/threonine-protein kinase ndrC OS=*Dictyostelium discoideum* OX=44689 GN=ndrC PE=3 SV=1

Supplementary Table 4 – Proteins differentially expressed in Δ*sopB*-infected and control samples. Proteins are ordered in descending order according to their Fold change value. Classification is as follows: **SC**: Identifications satisfied both, the automatic fold and statistical criteria. **NSC**: These identifications satisfied the fold criteria but, most likely, this happened by chance. **NC**: These identifications did not meet the fold and P-value criteria. **C**: These identifications were filtered out by the L-stringency and so deserve further experimentation to verify if they are indeed differentially expressed.

Locus ID	Fold Change	P-value	Classification	Description
Q54LV1	4,721927855	0,1572	NSC	UV excision repair protein RAD23 homolog OS=*Dictyostelium discoideum* OX=44689 GN=rcbA PE=1 SV=1
Q55B10	4,542332259	0,0101	C	Probable alpha-galactosidase OS=*Dictyostelium discoideum* OX=44689 GN=melA PE=3 SV=1
P54680	4,421368155	0,0824	NSC	Fimbrin OS=*Dictyostelium discoideum* OX=44689 GN=fimA PE=2 SV=2
Q8IS16	4,08186857	0,0097	C	Ras guanine nucleotide exchange factor H OS=*Dictyostelium discoideum* OX=44689 GN=gefH PE=1 SV=1
P19198	3,972731849	0,1244	NSC	cAMP-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=capA-1 PE=2 SV=2
Q54K47	3,96618369	0,0344	C	Proliferating cell nuclear antigen OS=*Dictyostelium discoideum* OX=44689 GN=pcna PE=3 SV=1
P27685	3,907692921	0,0018	SC	40S ribosomal protein S2 OS=*Dictyostelium discoideum* OX=44689 GN=rps2 PE=1 SV=1
Q54VQ0	3,681848527	0,0332	C	Uncharacterized protein DDB_G0280205 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0280205 PE=4 SV=2
Q55BZ5	3,677459549	0,0028	C	Protein dcd1A OS=*Dictyostelium discoideum* OX=44689 GN=dcd1A PE=2 SV=1
O60952	3,534510749	0,0752	NSC	LIM domain-containing protein E OS=*Dictyostelium discoideum* OX=44689 GN=limE PE=1 SV=1
Q54F07	3,432791255	0,0722	NSC	S-adenosylmethionine synthase OS=*Dictyostelium discoideum* OX=44689 GN=metK PE=1 SV=1
Q7KWQ2	3,393374187	0,0842	NSC	Serine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=serS PE=1 SV=1
Q54YD2	3,360556073	0,0175	SC	Putative phosphatidylglycerol/phosphatidylinositol transfer protein DDB_G0278295 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0278295 PE=2 SV=1
Q55ED1	3,348288415	0,0698	NSC	Probable nucleosome assembly protein OS=*Dictyostelium discoideum* OX=44689 GN=nap1 PE=2 SV=1
Q1ZXQ8	3,281890613	0,0030	C	Centrosomal protein 224 OS=*Dictyostelium discoideum* OX=44689 GN=mtaA PE=1 SV=1
Q558Z9	3,09223241	0,0115	C	Exocyst complex component 7 OS=*Dictyostelium discoideum* OX=44689 GN=exoc7 PE=3 SV=1
P46794	3,060366794	0,1123	NSC	Cystathionine beta-synthase OS=*Dictyostelium discoideum* OX=44689 GN=cysB PE=2 SV=2
Q54JP5	2,981098523	0,0070	C	Probable ornithine aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=oatA PE=3 SV=1

Q553R3	2,967351727	0,0006	C	Eukaryotic translation initiation factor 4 gamma OS=*Dictyostelium discoideum* OX=44689 GN=eif4g PE=3 SV=1
Q6TMK3	2,945577496	0,0735	NSC	Heat shock protein 88 OS=*Dictyostelium discoideum* OX=44689 GN=hspH PE=1 SV=1
P13466	2,876695211	0,0819	NSC	Gelation factor OS=*Dictyostelium discoideum* OX=44689 GN=abpC PE=1 SV=1
Q54EW3	2,862059332	0,0147	C	Probable importin-5 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0291650 PE=3 SV=1
Q54LP8	2,851322803	0,0159	SC	Histone H2B.v3 OS=*Dictyostelium discoideum* OX=44689 GN=H2Bv3 PE=3 SV=1
P54640	2,809742594	0,0312	C	Cysteine proteinase 5 OS=*Dictyostelium discoideum* OX=44689 GN=cprE PE=2 SV=2
Q54ZI6	2,794674848	0,0479	NSC	Phospholipase B-like protein E OS=*Dictyostelium discoideum* OX=44689 GN=plbE PE=3 SV=1
Q54NZ5	2,786503874	0,0979	NSC	Cullin-3 OS=*Dictyostelium discoideum* OX=44689 GN=culC PE=3 SV=1
Q54LN4	2,756902037	0,0056	C	Gamma-glutamyl hydrolase A OS=*Dictyostelium discoideum* OX=44689 GN=gghA PE=3 SV=1
Q54MZ5	2,75429735	0,0019	SC	40S ribosomal protein S28 OS=*Dictyostelium discoideum* OX=44689 GN=rps28 PE=3 SV=1
Q552L5	2,745471026	0,0357	C	THO complex subunit 7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=thoc7 PE=3 SV=1
Q54TR1	2,729084599	0,0009	C	Counting factor associated protein D OS=*Dictyostelium discoideum* OX=44689 GN=cfaD PE=1 SV=1
P10733	2,686563231	0,1016	NSC	Severin OS=*Dictyostelium discoideum* OX=44689 GN=sevA PE=1 SV=1
Q54R45	2,64899556	0,0095	SC	Translocon-associated protein subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=ssr1 PE=3 SV=1
Q54HI5	2,63344212	0,0048	SC	Lamin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=lmnB PE=1 SV=1
Q554D9	2,605329622	0,1406	NSC	Asparagine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=asnS1 PE=1 SV=1
Q9GPM4	2,587728279	0,1383	NSC	Phosphoglycerate kinase OS=*Dictyostelium discoideum* OX=44689 GN=pgkA PE=1 SV=2
O15819	2,552528972	0,0141	SC	Histone H3.3 type a OS=*Dictyostelium discoideum* OX=44689 GN=H3a PE=1 SV=1
P46800	2,548901779	0,0026	SC	Guanine nucleotide-binding protein subunit beta-like protein OS=*Dictyostelium discoideum* OX=44689 GN=gpbB PE=1 SV=2
Q54BC2	2,548325026	0,0276	C	Histone H2B.v1 OS=*Dictyostelium discoideum* OX=44689 GN=H2Bv1 PE=3 SV=1
Q54Q48	2,523804097	0,0007	SC	Putative uncharacterized protein DDB_G0284097 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284097 PE=1 SV=1
Q54SM3	2,478074869	0,1353	NSC	Peptidyl-prolyl cis-trans isomerase A OS=*Dictyostelium discoideum* OX=44689 GN=ppiA PE=1 SV=1
Q55FE0	2,463705324	0,0870	NSC	Eukaryotic translation initiation factor 4E OS=*Dictyostelium discoideum* OX=44689 GN=eif4e PE=3 SV=1
Q54NB6	2,395201671	0,0400	NSC	FK506-binding protein 4 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp4 PE=1 SV=1

Q54XB5	2,394465441	0,0003	SC	60S ribosomal protein L31 OS=*Dictyostelium discoideum* OX=44689 GN=rpl31 PE=3 SV=1
Q94464	2,367374041	0,0035	SC	Dynamin-A OS=*Dictyostelium discoideum* OX=44689 GN=dymA PE=1 SV=2
P05095	2,36152399	0,0551	NSC	Alpha-actinin A OS=*Dictyostelium discoideum* OX=44689 GN=abpA PE=1 SV=2
Q54JY7	2,34435531	0,0001	SC	Syntaxin-7A OS=*Dictyostelium discoideum* OX=44689 GN=syn7A PE=1 SV=1
P14132	2,317792072	0,0025	SC	40S ribosomal protein S9 OS=*Dictyostelium discoideum* OX=44689 GN=rps9 PE=1 SV=1
Q23915	2,296495245	0,0042	SC	Probable serine/threonine-protein kinase kinX OS=*Dictyostelium discoideum* OX=44689 GN=kinX PE=3 SV=2
Q54DU9	2,288386717	0,0068	SC	Probable protein tyrosine phosphatase type IVA A OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292024 PE=3 SV=1
Q54CL0	2,282077878	0,0064	C	Apoptosis inhibitor 5 homolog OS=*Dictyostelium discoideum* OX=44689 GN=api5 PE=3 SV=1
Q55F94	2,270636708	0,0002	SC	Dynamin-like protein A OS=*Dictyostelium discoideum* OX=44689 GN=dlpA PE=2 SV=1
Q76P23	2,25039604	0,0826	NSC	Mitochondrial substrate carrier family protein Q OS=*Dictyostelium discoideum* OX=44689 GN=mcfQ PE=2 SV=1
P54638	2,235131184	0,1560	NSC	Acetylornithine deacetylase OS=*Dictyostelium discoideum* OX=44689 GN=argE PE=1 SV=2
P32255	2,234898966	0,1303	NSC	Tubulin alpha chain OS=*Dictyostelium discoideum* OX=44689 GN=tubA PE=1 SV=1
Q54GT6	2,23264237	0,0354	C	Serine--pyruvate aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=agxt PE=3 SV=1
Q54N17	2,228768698	0,0111	SC	40S ribosomal protein S15 OS=*Dictyostelium discoideum* OX=44689 GN=rps15 PE=3 SV=1
Q54U07	2,198728008	0,0072	SC	Nascent polypeptide-associated complex subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=nacA PE=3 SV=1
Q54CK6	2,195725076	0,0009	C	Vesicle transport through interaction with t-SNAREs homolog 1A OS=*Dictyostelium discoideum* OX=44689 GN=vti1A PE=1 SV=1
Q55FR8	2,194248384	0,0186	C	Probable carboxypeptidase S-like 2 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267984 PE=3 SV=1
Q8IS15	2,190973262	0,0542	NSC	Ras guanine nucleotide exchange factor I OS=*Dictyostelium discoideum* OX=44689 GN=gefI PE=2 SV=1
Q5XM24	2,188309337	0,0422	NSC	Autocrine proliferation repressor protein A OS=*Dictyostelium discoideum* OX=44689 GN=aprA PE=1 SV=1
Q86H60	2,187993328	0,0794	NSC	Small heat shock protein hspK OS=*Dictyostelium discoideum* OX=44689 GN=hspK PE=3 SV=1
Q54M70	2,164403786	0,0191	C	Aspartyl aminopeptidase OS=*Dictyostelium discoideum* OX=44689 GN=dnpep PE=1 SV=1
Q54UJ0	2,160980325	0,0064	C	26S proteasome non-ATPase regulatory subunit 12 OS=*Dictyostelium discoideum* OX=44689 GN=psmD12 PE=2 SV=1
Q557J6	2,160962479	0,0955	NSC	Drebrin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=abpE-1 PE=2 SV=1
Q54UH8	2,137129463	0,0257	C	D-3-phosphoglycerate dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=serA PE=1 SV=1

O77082	2,10482462	0,0008	SC	40S ribosomal protein S10 OS=*Dictyostelium discoideum* OX=44689 GN=rps10 PE=1 SV=3
Q54HM2	2,090638605	0,0380	NSC	Uncharacterized protein DDB_G0289357 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289357 PE=4 SV=1
Q54WR9	2,069802229	0,1256	NSC	Type-3 glutamine synthetase OS=*Dictyostelium discoideum* OX=44689 GN=glnA3 PE=1 SV=1
P22684	2,053401743	0,0346	SC	60S acidic ribosomal protein P1 OS=*Dictyostelium discoideum* OX=44689 GN=rplp1 PE=3 SV=1
P02889	2,048235267	0,0860	NSC	Probable 26S proteasome non-ATPase regulatory subunit 8 OS=*Dictyostelium discoideum* OX=44689 GN=psmD8-1 PE=2 SV=2
P22683	2,046080017	0,0160	SC	60S acidic ribosomal protein P2 OS=*Dictyostelium discoideum* OX=44689 GN=rplp2 PE=1 SV=3
Q54Z26	2,0318049	0,1575	NSC	Serine hydroxymethyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=shmt1 PE=1 SV=1
Q54M21	2,030328841	0,0798	NSC	DnaJ homolog subfamily C member 3 homolog OS=*Dictyostelium discoideum* OX=44689 GN=dnajc3 PE=3 SV=1
Q55DV9	2,02771713	0,0493	NSC	Cystathionine gamma-lyase OS=*Dictyostelium discoideum* OX=44689 GN=cysA PE=1 SV=1
Q54RK5	2,024429737	0,1307	NSC	Enolase A OS=*Dictyostelium discoideum* OX=44689 GN=enoA PE=3 SV=1
Q55DR6	2,020767508	0,0058	SC	Fatty acyl-CoA synthetase A OS=*Dictyostelium discoideum* OX=44689 GN=fcsA PE=1 SV=1
Q54JD4	2,020458918	0,0019	SC	Uncharacterized protein DDB_G0288133 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288133 PE=4 SV=1
Q54UB5	2,008062932	0,0038	C	26S proteasome non-ATPase regulatory subunit 11 OS=*Dictyostelium discoideum* OX=44689 GN=psmD11 PE=2 SV=1
P22887	1,998705574	0,0569	NSC	Nucleoside diphosphate kinase, cytosolic OS=*Dictyostelium discoideum* OX=44689 GN=ndkC-1 PE=1 SV=1
Q94504	1,985550608	0,0086	C	Cysteine proteinase 7 OS=*Dictyostelium discoideum* OX=44689 GN=cprG PE=1 SV=1
P14326	1,983556098	0,1384	NSC	Vegetative-specific protein H5 OS=*Dictyostelium discoideum* OX=44689 GN=cinB PE=2 SV=2
Q557E0	1,982450077	0,0448	NSC	Heat shock cognate 70 kDa protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=hspE-1 PE=1 SV=1
P52922	1,982244481	0,0358	SC	Leukotriene A-4 hydrolase homolog OS=*Dictyostelium discoideum* OX=44689 GN=lkhA PE=2 SV=2
Q27562	1,975787744	0,1228	NSC	Proteasome subunit alpha type-1 OS=*Dictyostelium discoideum* OX=44689 GN=psmA1 PE=3 SV=1
Q54MA6	1,956912389	0,0166	SC	40S ribosomal protein S5 OS=*Dictyostelium discoideum* OX=44689 GN=rps5 PE=1 SV=1
P36415	1,953076028	0,0320	SC	Heat shock cognate 70 kDa protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=hspB PE=1 SV=2
P29447	1,940892126	0,0879	NSC	Thioredoxin-3 OS=*Dictyostelium discoideum* OX=44689 GN=trxC PE=3 SV=2
Q556J0	1,937546678	0,0706	NSC	Transketolase OS=*Dictyostelium discoideum* OX=44689 GN=tkt-1 PE=1 SV=1
Q55G04	1,929288216	0,0711	NSC	Proteasome subunit alpha type-5 OS=*Dictyostelium discoideum* OX=44689 GN=psmA5 PE=3 SV=1

Q86IV5	1,925931674	0,0235	C	Countin-1 OS=*Dictyostelium discoideum* OX=44689 GN=ctnA PE=1 SV=1
P13021	1,915359247	0,0027	SC	F-actin-capping protein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=acpA PE=1 SV=1
O61122	1,913439911	0,0306	C	Serine/threonine-protein kinase svkA OS=*Dictyostelium discoideum* OX=44689 GN=svkA PE=1 SV=1
Q550R2	1,913125363	0,0165	SC	Cortexillin-2 OS=*Dictyostelium discoideum* OX=44689 GN=ctxB PE=1 SV=1
Q54J34	1,909154051	0,0040	C	Adenylosuccinate lyase OS=*Dictyostelium discoideum* OX=44689 GN=purB PE=3 SV=1
P46793	1,90464358	0,0010	SC	40S ribosomal protein S15a OS=*Dictyostelium discoideum* OX=44689 GN=rps15a PE=2 SV=3
P24639	1,894389724	0,0436	NSC	Annexin A7 OS=*Dictyostelium discoideum* OX=44689 GN=nxnA PE=1 SV=1
Q54HG2	1,879336531	0,0121	SC	Cortexillin-1 OS=*Dictyostelium discoideum* OX=44689 GN=ctxA PE=1 SV=1
P28178	1,866509507	0,0184	C	Protein kinase 2 OS=*Dictyostelium discoideum* OX=44689 GN=pkgB PE=1 SV=2
P13651	1,859574863	0,0517	NSC	Eukaryotic translation initiation factor 5A OS=*Dictyostelium discoideum* OX=44689 GN=eif5a PE=1 SV=2
Q55E35	1,858409399	0,0223	C	Signal peptidase complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=spcs2 PE=3 SV=2
Q54DS3	1,846905456	0,0163	C	Transmembrane protein DDB_G0292058 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292058 PE=2 SV=1
Q23921	1,841362988	0,0706	NSC	Protein pkiA OS=*Dictyostelium discoideum* OX=44689 GN=pkiA PE=1 SV=2
Q54TW3	1,839243727	0,0587	NSC	60S ribosomal protein L29 OS=*Dictyostelium discoideum* OX=44689 GN=rpl29 PE=3 SV=1
Q54QR9	1,837903034	0,0416	NSC	Protein phosphatase 2A scaffold subunit OS=*Dictyostelium discoideum* OX=44689 GN=pppA PE=1 SV=1
P54632	1,837659481	0,1344	NSC	14-3-3-like protein OS=*Dictyostelium discoideum* OX=44689 GN=fttB PE=1 SV=2
Q8MYF0	1,826650197	0,0205	C	Mitochondrial genome maintenance protein mgm101 homolog OS=*Dictyostelium discoideum* OX=44689 GN=mgm101 PE=3 SV=1
P09402	1,826182391	0,0017	SC	Myosin, essential light chain OS=*Dictyostelium discoideum* OX=44689 GN=mlcE PE=2 SV=2
Q54G42	1,820815873	0,0218	C	Chitinase domain-containing protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=chid1 PE=3 SV=1
Q76P36	1,819184697	0,0125	SC	40S ribosomal protein S29 OS=*Dictyostelium discoideum* OX=44689 GN=rps29 PE=3 SV=1
O76856	1,810052197	0,0092	SC	Cathepsin D OS=*Dictyostelium discoideum* OX=44689 GN=ctsD PE=1 SV=1
Q54IX6	1,802324472	0,0670	NSC	Probable syntaxin-8B OS=*Dictyostelium discoideum* OX=44689 GN=syn8B PE=3 SV=1
O77257	1,801324937	0,0330	SC	Protein gp17 OS=*Dictyostelium discoideum* OX=44689 GN=p17 PE=2 SV=1
Q555L8	1,795905144	0,0091	C	SH3 and F-BAR domain-containing protein DDB_G0274695 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274695 PE=4 SV=1
Q54Y41	1,795415377	0,0008	SC	40S ribosomal protein S20 OS=*Dictyostelium discoideum* OX=44689 GN=rps20 PE=3 SV=1

Q54BM2	1,79373552	0,0002	SC	Polyadenylate-binding protein 1-A OS=*Dictyostelium discoideum* OX=44689 GN=pabpc1A PE=1 SV=1
Q54NG2	1,79071366	0,0005	SC	60S ribosomal protein L17 OS=*Dictyostelium discoideum* OX=44689 GN=rpl17 PE=3 SV=1
Q86HV4	1,78936711	0,0341	C	Oxysterol-binding protein 6 OS=*Dictyostelium discoideum* OX=44689 GN=osbF PE=3 SV=1
P54657	1,782160269	0,1205	NSC	Calcium-dependent cell adhesion molecule 1 OS=*Dictyostelium discoideum* OX=44689 GN=cadA PE=1 SV=1
Q54DR1	1,781620146	0,1897	NSC	Squalene synthase OS=*Dictyostelium discoideum* OX=44689 GN=fdfT PE=3 SV=1
Q54ZW5	1,779233184	0,0009	SC	40S ribosomal protein S3a OS=*Dictyostelium discoideum* OX=44689 GN=rps3a PE=3 SV=1
Q86L05	1,774078073	0,0173	SC	60S ribosomal protein L10a OS=*Dictyostelium discoideum* OX=44689 GN=rpl10a PE=1 SV=1
Q55EQ3	1,76729469	0,0144	SC	Uncharacterized abhydrolase domain-containing protein DDB_G0269086 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0269086 PE=1 SV=2
Q1ZXP3	1,765745131	0,0125	SC	Probable cytochrome b-c1 complex subunit 6 OS=*Dictyostelium discoideum* OX=44689 GN=uqcrh PE=3 SV=1
Q1ZXF5	1,763754813	0,0688	NSC	Probable cytochrome P450 508A4 OS=*Dictyostelium discoideum* OX=44689 GN=cyp508A4 PE=3 SV=1
Q54N00	1,762084775	0,0749	NSC	Formin-H OS=*Dictyostelium discoideum* OX=44689 GN=forH PE=1 SV=1
P34112	1,757544799	0,0928	NSC	Cyclin-dependent kinase 1 OS=*Dictyostelium discoideum* OX=44689 GN=cdk1 PE=2 SV=1
Q54WH2	1,750767587	0,0775	NSC	Formin-A OS=*Dictyostelium discoideum* OX=44689 GN=forA PE=1 SV=1
Q54PX9	1,748741646	0,0105	SC	40S ribosomal protein S12 OS=*Dictyostelium discoideum* OX=44689 GN=rps12 PE=1 SV=1
Q54X86	1,743824195	0,0811	NSC	Probable syntaxin-7B OS=*Dictyostelium discoideum* OX=44689 GN=syn7B PE=3 SV=1
Q54Q94	1,743715093	0,0391	NSC	Probable ATP-dependent RNA helicase ddx10 OS=*Dictyostelium discoideum* OX=44689 GN=ddx10 PE=3 SV=1
Q54YG5	1,736445078	0,0398	NSC	Trafficking protein particle complex subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=trappc5 PE=3 SV=1
Q55BY1	1,724756391	0,0000	SC	40S ribosomal protein SA OS=*Dictyostelium discoideum* OX=44689 GN=rpsA PE=1 SV=1
P42520	1,722005949	0,0022	SC	40S ribosomal protein S17 OS=*Dictyostelium discoideum* OX=44689 GN=rps17 PE=3 SV=2
Q23892	1,712717334	0,0713	NSC	Lysosomal beta glucosidase OS=*Dictyostelium discoideum* OX=44689 GN=gluA PE=1 SV=2
Q556U6	1,702496301	0,0364	SC	Luminal-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=bip1-1 PE=3 SV=1
P54648	1,698512208	0,0248	SC	V-type proton ATPase subunit C OS=*Dictyostelium discoideum* OX=44689 GN=vatC PE=2 SV=1
Q869U7	1,69075743	0,0184	SC	40S ribosomal protein S18 OS=*Dictyostelium discoideum* OX=44689 GN=rps18 PE=3 SV=1
Q54WR2	1,690180617	0,1014	NSC	eIF-2-alpha kinase activator GCN1 OS=*Dictyostelium discoideum* OX=44689 GN=gcn1 PE=3 SV=1

Q869Q8	1,686630089	0,0835	NSC	Probable serine carboxypeptidase CPVL OS=*Dictyostelium discoideum* OX=44689 GN=cpvl PE=3 SV=1
Q54PH8	1,680273604	0,0006	SC	40S ribosomal protein S13 OS=*Dictyostelium discoideum* OX=44689 GN=rps13 PE=3 SV=1
Q869Z0	1,677066016	0,0007	SC	Putative protein disulfide-isomerase DDB_G0275025 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275025 PE=1 SV=1
Q8MML6	1,673683939	0,0006	SC	V-type proton ATPase subunit H OS=*Dictyostelium discoideum* OX=44689 GN=vatH PE=1 SV=1
Q54C24	1,673058429	0,0036	SC	Vacuolar protein sorting-associated protein 35 OS=*Dictyostelium discoideum* OX=44689 GN=vps35 PE=3 SV=1
Q54N80	1,672147947	0,0354	C	FK506-binding protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp3 PE=2 SV=1
Q54MB5	1,660941565	0,2510	NSC	Adenosine kinase OS=*Dictyostelium discoideum* OX=44689 GN=adk PE=3 SV=2
Q54ST6	1,659941167	0,0986	NSC	ER membrane protein complex subunit 7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282229 PE=3 SV=2
Q75JD4	1,656757012	0,0456	NSC	SH3 and F-BAR domain-containing protein DDB_G0271676 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271676 PE=4 SV=1
P34121	1,651755453	0,2141	NSC	Coactosin OS=*Dictyostelium discoideum* OX=44689 GN=coaA PE=1 SV=1
Q554H5	1,64432487	0,0618	NSC	Phospholipase B-like protein F OS=*Dictyostelium discoideum* OX=44689 GN=plbF PE=3 SV=1
Q54HL0	1,642154817	0,1747	NSC	Coatomer subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=copG PE=1 SV=1
P34116	1,638884687	0,0355	C	Cell surface glycoprotein gp138B OS=*Dictyostelium discoideum* OX=44689 GN=GP138B PE=1 SV=1
P34149	1,637112541	0,0020	SC	Rho-related protein racC OS=*Dictyostelium discoideum* OX=44689 GN=racC PE=1 SV=1
P22685	1,636006216	0,0056	SC	60S acidic ribosomal protein P0 OS=*Dictyostelium discoideum* OX=44689 GN=rplp0 PE=1 SV=2
O96624	1,63439169	0,0442	NSC	Actin-related protein 2/3 complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=arcC PE=1 SV=1
Q54BQ3	1,633831846	0,0065	SC	60S ribosomal protein L23a OS=*Dictyostelium discoideum* OX=44689 GN=rpl23a PE=1 SV=1
Q559R0	1,615058378	0,0335	SC	GTP-binding protein Sar1A OS=*Dictyostelium discoideum* OX=44689 GN=sarA PE=1 SV=1
Q54RQ1	1,612954876	0,0034	SC	Extracellular superoxide dismutase [Cu-Zn] 3 OS=*Dictyostelium discoideum* OX=44689 GN=sodC PE=2 SV=1
Q76NV5	1,609742685	0,2278	NSC	4-hydroxyphenylpyruvate dioxygenase OS=*Dictyostelium discoideum* OX=44689 GN=hpd PE=1 SV=1
Q54S60	1,60440558	0,0826	NSC	Translation machinery-associated protein 16 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282655 PE=3 SV=1
Q55AH5	1,599393937	0,0524	NSC	V-type proton ATPase subunit F OS=*Dictyostelium discoideum* OX=44689 GN=vatF PE=3 SV=1
Q54HP3	1,596083924	0,0789	NSC	Developmentally-regulated GTP-binding protein 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=drg1 PE=3 SV=1
Q54PR9	1,582825711	0,0318	C	Counting factor 60 OS=*Dictyostelium discoideum* OX=44689 GN=cf60 PE=1 SV=1

Q54UP4	1,578307419	0,2289	NSC	Probable transaldolase OS=*Dictyostelium discoideum* OX=44689 GN=tal PE=3 SV=1
O15757	1,569699721	0,0052	SC	Serine/threonine-protein phosphatase PP1 OS=*Dictyostelium discoideum* OX=44689 GN=pppB PE=1 SV=1
Q55GQ6	1,568943312	0,1449	NSC	Uracil phosphoribosyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=uprt PE=3 SV=1
P16168	1,563239851	0,0392	NSC	60S ribosomal protein L11 OS=*Dictyostelium discoideum* OX=44689 GN=rpl11 PE=1 SV=2
P90526	1,562716088	0,0020	SC	40S ribosomal protein S3 OS=*Dictyostelium discoideum* OX=44689 GN=rps3 PE=1 SV=1
Q03409	1,559328749	0,0228	SC	40S ribosomal protein S25 OS=*Dictyostelium discoideum* OX=44689 GN=rps25 PE=3 SV=1
Q75K27	1,557694103	0,0035	SC	40S ribosomal protein S24 OS=*Dictyostelium discoideum* OX=44689 GN=rps24 PE=3 SV=1
Q54PQ4	1,555526865	0,1739	NSC	Ras guanine nucleotide exchange factor A OS=*Dictyostelium discoideum* OX=44689 GN=gefA PE=1 SV=1
Q54VI6	1,547419499	0,0396	NSC	Translocon-associated protein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=ssr2 PE=2 SV=2
Q23862	1,547379574	0,0047	SC	Rho-related protein racE OS=*Dictyostelium discoideum* OX=44689 GN=racE PE=1 SV=1
O00780	1,546467914	0,0207	SC	V-type proton ATPase subunit E OS=*Dictyostelium discoideum* OX=44689 GN=vatE PE=1 SV=1
Q76NW2	1,545175171	0,0445	NSC	Histone H4 OS=*Dictyostelium discoideum* OX=44689 GN=H4a PE=1 SV=1
O96626	1,542374814	0,0031	SC	Actin-related protein 2/3 complex subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=arcE PE=1 SV=1
Q869R8	1,540140758	0,1247	NSC	Triosephosphate isomerase OS=*Dictyostelium discoideum* OX=44689 GN=tpiA PE=3 SV=1
Q54YW1	1,535445693	0,1253	NSC	ELMO domain-containing protein A OS=*Dictyostelium discoideum* OX=44689 GN=elmoA PE=1 SV=1
P27133	1,529405044	0,0097	SC	Coronin-A OS=*Dictyostelium discoideum* OX=44689 GN=corA PE=1 SV=2
Q54TR8	1,520284015	0,0329	SC	Nascent polypeptide-associated complex subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=nacB PE=3 SV=1
P13723	1,520184163	0,1101	NSC	Beta-hexosaminidase subunit A1 OS=*Dictyostelium discoideum* OX=44689 GN=hexa1 PE=1 SV=1
P34115	1,512756703	0,1120	NSC	Cell surface glycoprotein gp138A OS=*Dictyostelium discoideum* OX=44689 GN=GP138A PE=1 SV=1
Q9NKX1	1,512684931	0,0080	SC	Endoplasmin homolog OS=*Dictyostelium discoideum* OX=44689 GN=grp94 PE=2 SV=2
Q54PX7	1,510253818	0,1586	NSC	PCI domain-containing protein 2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=pcid2 PE=3 SV=1
P21900	1,508709192	0,0044	SC	Adenylosuccinate synthetase OS=*Dictyostelium discoideum* OX=44689 GN=purA PE=1 SV=1
Q54J47	1,504295472	0,1729	NSC	Probable pyridoxal 5'-phosphate synthase subunit pdx1 OS=*Dictyostelium discoideum* OX=44689 GN=pdx1 PE=1 SV=1
Q556Y1	1,498808962	0,1204	NSC	40S ribosomal protein S30 OS=*Dictyostelium discoideum* OX=44689 GN=rps30-1 PE=3 SV=1

Q54J23	1,496341938	0,0359	SC	60S ribosomal protein L35 OS=*Dictyostelium discoideum* OX=44689 GN=rpl35 PE=3 SV=1
Q6IMN8	1,490739222	0,2265	NSC	Aldose reductase A OS=*Dictyostelium discoideum* OX=44689 GN=alrA PE=2 SV=1
Q556Y4	1,489498706	0,0764	NSC	Casein kinase I OS=*Dictyostelium discoideum* OX=44689 GN=cak1-1 PE=1 SV=1
Q8TA03	1,48944123	0,0088	SC	6-phosphogluconate dehydrogenase, decarboxylating OS=*Dictyostelium discoideum* OX=44689 GN=gnd PE=1 SV=1
Q555L5	1,487348348	0,1276	NSC	Peroxiredoxin-4 OS=*Dictyostelium discoideum* OX=44689 GN=prdx4 PE=1 SV=2
Q5TJ65	1,485868007	0,0111	SC	Protein VASP homolog OS=*Dictyostelium discoideum* OX=44689 GN=vasp PE=1 SV=1
Q54XX1	1,482145106	0,0196	C	Signal recognition particle receptor subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=srprb PE=3 SV=1
Q55CW5	1,476596237	0,0054	SC	60S ribosomal protein L36a OS=*Dictyostelium discoideum* OX=44689 GN=rpl36a PE=3 SV=2
Q8T869	1,4699542	0,0273	SC	Luminal-binding protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=bip2 PE=1 SV=1
Q86H98	1,466346061	0,1011	NSC	Charged multivesicular body protein 4 OS=*Dictyostelium discoideum* OX=44689 GN=chmp4 PE=3 SV=1
Q8T191	1,463955139	0,0387	NSC	Probable UDP-glucose:glycoprotein glucosyltransferase A OS=*Dictyostelium discoideum* OX=44689 GN=ggtA PE=1 SV=2
Q54MK8	1,461251057	0,0020	SC	60S ribosomal protein L18a OS=*Dictyostelium discoideum* OX=44689 GN=rpl18a PE=3 SV=2
Q54RD6	1,45627202	0,2917	NSC	Protein phosphatase 2A catalytic subunit B OS=*Dictyostelium discoideum* OX=44689 GN=pho2B PE=1 SV=1
P13022	1,454718074	0,0046	SC	F-actin-capping protein subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=acpB PE=1 SV=1
Q54I41	1,443932097	0,0022	SC	40S ribosomal protein S7 OS=*Dictyostelium discoideum* OX=44689 GN=rps7 PE=1 SV=1
P52285	1,443223629	0,1756	NSC	SCF ubiquitin ligase complex protein SKP1a OS=*Dictyostelium discoideum* OX=44689 GN=fpaA PE=1 SV=1
Q9GRF8	1,442151693	0,2583	NSC	Elongation factor 1-beta OS=*Dictyostelium discoideum* OX=44689 GN=efa1B PE=1 SV=1
Q54NX0	1,440933503	0,1590	NSC	Putative rRNA methyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=fsjC PE=3 SV=1
Q23911	1,43892889	0,0873	NSC	Protein 29C OS=*Dictyostelium discoideum* OX=44689 GN=29C PE=3 SV=2
P54639	1,437361124	0,0736	NSC	Cysteine proteinase 4 OS=*Dictyostelium discoideum* OX=44689 GN=cprD PE=2 SV=2
Q54X53	1,432274718	0,0005	SC	60S ribosomal protein L21 OS=*Dictyostelium discoideum* OX=44689 GN=rpl21 PE=3 SV=1
P18613	1,425970495	0,0085	SC	Ras-related protein rapA OS=*Dictyostelium discoideum* OX=44689 GN=rapA PE=1 SV=1
P51405	1,424021657	0,0071	SC	40S ribosomal protein S4 OS=*Dictyostelium discoideum* OX=44689 GN=rps4 PE=1 SV=3
Q54FD6	1,420442854	0,1083	NSC	Transcription initiation factor IIB OS=*Dictyostelium discoideum* OX=44689 GN=gtf2b PE=3 SV=1

Q54FG5	1,41891275	0,0987	NSC	Rho GTPase-activating protein gacJJ OS=*Dictyostelium discoideum* OX=44689 GN=gacJJ PE=3 SV=1
Q54RP6	1,413299097	0,1717	NSC	Hybrid signal transduction histidine kinase L OS=*Dictyostelium discoideum* OX=44689 GN=dhkL PE=3 SV=1
Q9NH03	1,410523919	0,2679	NSC	Farnesyl diphosphate synthase OS=*Dictyostelium discoideum* OX=44689 GN=fps PE=2 SV=1
Q9TW32	1,410222801	0,1362	NSC	Peptidyl-prolyl cis-trans isomerase B OS=*Dictyostelium discoideum* OX=44689 GN=cypB PE=1 SV=1
Q86K94	1,400337181	0,0771	NSC	Trafficking protein particle complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=trappc3 PE=3 SV=2
P15064	1,398873052	0,1126	NSC	Ras-like protein rasG OS=*Dictyostelium discoideum* OX=44689 GN=rasG PE=1 SV=1
Q55D66	1,395923245	0,0852	NSC	Proteasome subunit beta type-3 OS=*Dictyostelium discoideum* OX=44689 GN=psmB3 PE=3 SV=1
Q558Z0	1,394224412	0,2008	NSC	Probable arginine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=argS1 PE=3 SV=1
P34123	1,391215146	0,0867	NSC	26S proteasome regulatory subunit 6B homolog OS=*Dictyostelium discoideum* OX=44689 GN=psmC4 PE=1 SV=1
Q54S90	1,391154393	0,0174	SC	40S ribosomal protein S11 OS=*Dictyostelium discoideum* OX=44689 GN=rps11 PE=1 SV=1
Q55AQ9	1,390462918	0,0222	SC	60S ribosomal protein L36 OS=*Dictyostelium discoideum* OX=44689 GN=rpl36 PE=3 SV=1
Q54SG3	1,388686061	0,0895	NSC	Uncharacterized transmembrane protein DDB_G0282483 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282483 PE=4 SV=1
Q86JD4	1,388353113	0,2049	NSC	Signal peptidase complex catalytic subunit sec11 OS=*Dictyostelium discoideum* OX=44689 GN=sec11 PE=3 SV=1
Q54VN6	1,387985776	0,0002	SC	60S ribosomal protein L24 OS=*Dictyostelium discoideum* OX=44689 GN=rpl24 PE=1 SV=1
Q54CC5	1,387207804	0,0746	NSC	Eukaryotic translation initiation factor 3 subunit E OS=*Dictyostelium discoideum* OX=44689 GN=eif3E PE=3 SV=1
Q54F42	1,38707983	0,0294	C	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=*Dictyostelium discoideum* OX=44689 GN=ndufa6 PE=3 SV=1
Q869W6	1,387013376	0,1300	NSC	Probable myosin light chain kinase DDB_G0275057 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275057 PE=3 SV=1
P10819	1,383210055	0,2960	NSC	Adenosylhomocysteinase OS=*Dictyostelium discoideum* OX=44689 GN=sahA PE=1 SV=2
Q55DJ3	1,382054863	0,1093	NSC	Protein MAK16 homolog OS=*Dictyostelium discoideum* OX=44689 GN=mak16l PE=3 SV=1
Q54EG3	1,380542209	0,0012	SC	40S ribosomal protein S14 OS=*Dictyostelium discoideum* OX=44689 GN=rps14 PE=3 SV=1
Q94490	1,380252818	0,2908	NSC	Ubiquitin conjugating enzyme E2 B OS=*Dictyostelium discoideum* OX=44689 GN=ubcB PE=1 SV=1
Q54G21	1,376751257	0,3373	NSC	FK506-binding protein 5 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp5 PE=1 SV=1
Q54DS8	1,376318585	0,1429	NSC	Protein SEC13 homolog OS=*Dictyostelium discoideum* OX=44689 GN=sec13 PE=3 SV=1
Q551M2	1,371883332	0,1373	NSC	Eukaryotic translation initiation factor 6 OS=*Dictyostelium discoideum* OX=44689 GN=eif6 PE=1 SV=1

Q54BK2	1,370101066	0,1210	NSC	Neutral ceramidase A OS=*Dictyostelium discoideum* OX=44689 GN=dcd2A PE=1 SV=1
Q54F10	1,369319482	0,0769	NSC	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufv2 PE=3 SV=1
Q54UU6	1,36767705	0,0643	NSC	KRR1 small subunit processome component homolog OS=*Dictyostelium discoideum* OX=44689 GN=krr1 PE=3 SV=1
P54651	1,36430945	0,2227	NSC	Heat shock cognate 90 kDa protein OS=*Dictyostelium discoideum* OX=44689 GN=hspD PE=1 SV=2
C7G046	1,362345278	0,1164	NSC	von Willebrand factor A domain-containing protein DDB_G0286969 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286969 PE=4 SV=1
O96623	1,358083453	0,0275	SC	Actin-related protein 2/3 complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=arcB PE=1 SV=1
Q1ZXA8	1,356869756	0,1276	NSC	Uncharacterized protein DDB_G0292160 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292160 PE=3 SV=1
Q54GK6	1,349795701	0,0038	SC	60S ribosomal protein L22 2 OS=*Dictyostelium discoideum* OX=44689 GN=rpl22a PE=3 SV=1
Q54Q51	1,344941248	0,0014	SC	40S ribosomal protein S16 OS=*Dictyostelium discoideum* OX=44689 GN=rps16 PE=3 SV=1
Q86K01	1,342067649	0,1315	NSC	60S ribosomal protein L15 OS=*Dictyostelium discoideum* OX=44689 GN=rpl15-1 PE=1 SV=1
Q54J50	1,338419439	0,0109	SC	60S ribosomal protein L12 OS=*Dictyostelium discoideum* OX=44689 GN=rpl12 PE=1 SV=1
Q54BC6	1,338006015	0,2532	NC	26S proteasome non-ATPase regulatory subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=psmD2 PE=1 SV=1
P26310	1,337915806	0,2464	NC	Cytochrome c oxidase polypeptide 6, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cxfA PE=1 SV=2
Q55BP5	1,337786398	0,3179	NC	Probable DNA topoisomerase 2 OS=*Dictyostelium discoideum* OX=44689 GN=top2 PE=3 SV=1
Q86A77	1,332294279	0,0184	SC	V-type proton ATPase subunit D OS=*Dictyostelium discoideum* OX=44689 GN=atp6v1d PE=1 SV=1
Q65YR7	1,328382177	0,2577	NC	Cystatin-A2 OS=*Dictyostelium discoideum* OX=44689 GN=cpiB PE=2 SV=1
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P42528	1,324416149	0,0138	SC	Actin-related protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=arpC PE=1 SV=1
Q7Z2B8	1,324400124	0,1502	NC	Myosin-ID light chain OS=*Dictyostelium discoideum* OX=44689 GN=mlcD PE=1 SV=1
Q54W90	1,319916681	0,0961	NSC	Protein SEY1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_0206311 PE=3 SV=1
Q54K32	1,319217134	0,1268	NC	Ras GTPase-activating-like protein rgaA OS=*Dictyostelium discoideum* OX=44689 GN=rgaA PE=1 SV=1
Q54NC1	1,318175053	0,0587	NSC	NADH-cytochrome b5 reductase 1 OS=*Dictyostelium discoideum* OX=44689 GN=cyb5r1 PE=3 SV=1
Q9U9A3	1,314413961	0,0517	NSC	Serine/threonine-protein phosphatase 6 catalytic subunit OS=*Dictyostelium discoideum* OX=44689 GN=ppp6c PE=2 SV=2
Q54DF1	1,31433457	0,0317	SC	ATP synthase subunit gamma, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5C1 PE=1 SV=1

P36410	1,314001818	0,0162	SC	Ras-related protein Rab-14 OS=*Dictyostelium discoideum* OX=44689 GN=rab14 PE=1 SV=2
Q54WN8	1,312257844	0,0276	C	Uncharacterized protein DDB_G0279527 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0279527 PE=1 SV=1
Q55BN7	1,310571968	0,0015	SC	60S ribosomal protein L35a OS=*Dictyostelium discoideum* OX=44689 GN=rpl35a PE=3 SV=1
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Q54X51	1,308017937	0,0505	NSC	40S ribosomal protein S19 OS=*Dictyostelium discoideum* OX=44689 GN=rps19 PE=3 SV=1
Q553P5	1,305411739	0,1971	NC	Syntaxin-8A OS=*Dictyostelium discoideum* OX=44689 GN=syn8A PE=1 SV=1
Q54EN4	1,3052478	0,0172	SC	Protein disulfide-isomerase 2 OS=*Dictyostelium discoideum* OX=44689 GN=pdi2 PE=3 SV=1
Q86KC1	1,304263364	0,2871	NC	Probable GH family 25 lysozyme 2 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274181 PE=3 SV=1
Q54VZ4	1,303094299	0,0023	SC	60S ribosomal protein L18 OS=*Dictyostelium discoideum* OX=44689 GN=rpl18 PE=1 SV=1
Q54MR6	1,300855684	0,2371	NC	Heat shock 70-related protein 5 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0285709 PE=3 SV=1
Q54CT8	1,297970816	0,1777	NC	Probable adenylate kinase B OS=*Dictyostelium discoideum* OX=44689 GN=adkB PE=3 SV=1
Q54YA0	1,294537226	0,1539	NC	Probable ATP-citrate synthase OS=*Dictyostelium discoideum* OX=44689 GN=acly PE=1 SV=1
Q55BJ9	1,291340559	0,1640	NC	Superoxide dismutase [Mn], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sod2 PE=3 SV=1
Q54UU3	1,289815506	0,1751	NC	40S ribosomal protein S6 OS=*Dictyostelium discoideum* OX=44689 GN=rps6 PE=1 SV=1
Q54NQ0	1,289143888	0,3006	NC	26S proteasome non-ATPase regulatory subunit 13 OS=*Dictyostelium discoideum* OX=44689 GN=psmD13 PE=2 SV=1
Q54SR7	1,285982455	0,1746	NC	FK506-binding protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp2 PE=3 SV=1
B0G104	1,280950402	0,2099	NC	60S ribosome subunit biogenesis protein NIP7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=nip7 PE=3 SV=1
Q54WU3	1,280700604	0,2318	NC	Methionine aminopeptidase 1 OS=*Dictyostelium discoideum* OX=44689 GN=metap1 PE=3 SV=1
Q54WG0	1,272170368	0,3309	NC	Density-regulated protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=denr PE=3 SV=1
Q54R04	1,271505604	0,3451	NC	ADP-ribosylation factor-like protein 8 OS=*Dictyostelium discoideum* OX=44689 GN=arl8 PE=3 SV=1
Q54VG1	1,268462926	0,2736	NC	Guanine nucleotide-binding protein alpha-12 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaL PE=1 SV=1
Q8I8U2	1,263489794	0,2175	NC	AP-1 complex subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=ap1g1 PE=1 SV=1
O96625	1,262758447	0,0795	NC	Actin-related protein 2/3 complex subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=arcD PE=1 SV=1
Q54QN4	1,260734923	0,2428	NC	Uncharacterized transmembrane protein DDB_G0283731 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283731 PE=4 SV=1

O77229	1,259260372	0,0568	NC	Catalase-A OS=*Dictyostelium discoideum* OX=44689 GN=catA PE=2 SV=2
Q75JI3	1,256833681	0,1852	NC	Vesicle-fusing ATPase OS=*Dictyostelium discoideum* OX=44689 GN=nsfA PE=1 SV=1
O00899	1,255602817	0,2159	NC	Ras GTPase-activating-like protein gapA OS=*Dictyostelium discoideum* OX=44689 GN=gapA PE=1 SV=1
Q54YJ6	1,252413141	0,2820	NC	Eukaryotic translation initiation factor 1A OS=*Dictyostelium discoideum* OX=44689 GN=eif1a PE=3 SV=1
Q54RX9	1,249656131	0,0972	NC	Putative ras-related protein Rab-5B OS=*Dictyostelium discoideum* OX=44689 GN=rab5B PE=5 SV=1
Q54PJ1	1,249123331	0,1954	NC	26S proteasome regulatory subunit 10B OS=*Dictyostelium discoideum* OX=44689 GN=psmC6 PE=1 SV=1
Q554S6	1,24807574	0,0676	NC	Actin-17 OS=*Dictyostelium discoideum* OX=44689 GN=act17 PE=3 SV=1
Q54TL8	1,243657428	0,1401	NC	40S ribosomal protein S26 OS=*Dictyostelium discoideum* OX=44689 GN=rps26 PE=3 SV=1
Q55BV5	1,241222497	0,0615	NC	26S proteasome regulatory subunit 4 homolog OS=*Dictyostelium discoideum* OX=44689 GN=psmC1 PE=1 SV=1
O00897	1,241168984	0,1126	NC	Calmodulin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=calB PE=2 SV=1
P34124	1,233397916	0,2927	NC	26S proteasome regulatory subunit 8 OS=*Dictyostelium discoideum* OX=44689 GN=psmC5 PE=1 SV=2
Q23858	1,233248779	0,0613	NC	Calreticulin OS=*Dictyostelium discoideum* OX=44689 GN=crtA PE=1 SV=3
Q54K74	1,231582879	0,1990	NC	Endoplasmic reticulum transmembrane protein YET-like OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0287543 PE=3 SV=2
Q54JN0	1,219913992	0,1386	NC	Ribosome biogenesis protein BRX1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=bxdc2 PE=3 SV=1
Q8MY12	1,219690036	0,1996	NC	Myosin heavy chain kinase C OS=*Dictyostelium discoideum* OX=44689 GN=mhkC PE=1 SV=1
Q55EK2	1,218557343	0,2416	NC	Probable cytochrome P450 524A1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp524A1 PE=3 SV=1
Q54NP6	1,211463928	0,0710	NC	Alpha-soluble NSF attachment protein OS=*Dictyostelium discoideum* OX=44689 GN=snpA PE=1 SV=1
Q54RN1	1,210455722	0,1555	NC	Extracellular superoxide dismutase [Cu-Zn] 2 OS=*Dictyostelium discoideum* OX=44689 GN=sodB PE=2 SV=1
Q55CW0	1,209514681	0,0933	NC	rRNA 2'-O-methyltransferase fibrillarin OS=*Dictyostelium discoideum* OX=44689 GN=fbl PE=3 SV=1
P83401	1,207059247	0,3740	NC	Putative aldehyde dehydrogenase family 7 member A1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0276821 PE=3 SV=2
P34142	1,205162543	0,2074	NC	Ras-related protein Rab-21 OS=*Dictyostelium discoideum* OX=44689 GN=rab21 PE=1 SV=2
Q869Q2	1,203632233	0,2629	NC	Ribosome biogenesis regulatory protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=rrs1 PE=3 SV=1
O15706	1,201984159	0,2376	NC	Vacuolin-A OS=*Dictyostelium discoideum* OX=44689 GN=vacA PE=1 SV=1
Q557D2	1,201752318	0,2312	NC	Glucose-6-phosphate 1-dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=g6pd-1 PE=3 SV=1

P42530	1,200271833	0,3298	NC	Discoidin-2 OS=*Dictyostelium discoideum* OX=44689 GN=dscE PE=1 SV=1
Q54UF3	1,195309714	0,1849	NC	Probable ornithine decarboxylase OS=*Dictyostelium discoideum* OX=44689 GN=odc PE=3 SV=1
P11874	1,192909969	0,0010	SC	60S ribosomal protein L7 OS=*Dictyostelium discoideum* OX=44689 GN=rpl7 PE=1 SV=3
P54647	1,18890206	0,0655	NC	V-type proton ATPase catalytic subunit A OS=*Dictyostelium discoideum* OX=44689 GN=vatA PE=1 SV=2
Q54ZD1	1,188802866	0,0367	NC	60S ribosomal protein L7a OS=*Dictyostelium discoideum* OX=44689 GN=rpl7a PE=1 SV=1
P15808	1,187440167	0,3290	NC	Flavin-dependent thymidylate synthase OS=*Dictyostelium discoideum* OX=44689 GN=thyA PE=3 SV=2
Q54XE6	1,186418312	0,1877	NC	Probable H/ACA ribonucleoprotein complex subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=gar1 PE=3 SV=1
Q54JE3	1,185824966	0,0058	NC	60S ribosomal protein L22 1 OS=*Dictyostelium discoideum* OX=44689 GN=rpl22 PE=3 SV=1
Q54E21	1,179799067	0,3364	NC	Probable replication factor C subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=rfc2 PE=3 SV=1
Q54Q99	1,177352198	0,2770	NC	Serine/threonine-protein phosphatase 2A regulatory subunit phr2AB OS=*Dictyostelium discoideum* OX=44689 GN=phr2aB PE=3 SV=1
Q54FD7	1,173579558	0,2064	NC	Electron transfer flavoprotein subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=etfa PE=3 SV=1
P36412	1,173262596	0,1907	NC	Ras-related protein Rab-11A OS=*Dictyostelium discoideum* OX=44689 GN=rab11A PE=1 SV=1
Q54HB4	1,171475651	0,2683	NC	Transcription and mRNA export factor ENY2 OS=*Dictyostelium discoideum* OX=44689 GN=eny2 PE=3 SV=1
Q54PA9	1,171435192	0,2851	NC	Ribose-phosphate pyrophosphokinase A OS=*Dictyostelium discoideum* OX=44689 GN=prsA PE=1 SV=1
P02599	1,168933006	0,2040	NC	Calmodulin OS=*Dictyostelium discoideum* OX=44689 GN=calA PE=1 SV=3
Q54PV8	1,168218202	0,4092	NC	Inorganic pyrophosphatase OS=*Dictyostelium discoideum* OX=44689 GN=ppa1 PE=1 SV=1
Q95YL5	1,167500896	0,1359	NC	Penta-EF hand domain-containing protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=pefA PE=1 SV=1
Q54VA2	1,166435069	0,1505	NC	Fumarate hydratase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=fumH PE=3 SV=1
P54642	1,166002824	0,3821	NC	V-type proton ATPase proteolipid subunit OS=*Dictyostelium discoideum* OX=44689 GN=vatP PE=2 SV=1
Q54HF1	1,163984789	0,1246	NC	Putative actin-24 OS=*Dictyostelium discoideum* OX=44689 GN=act24 PE=3 SV=1
Q55FB8	1,16188193	0,3648	NC	Presporeless protein A OS=*Dictyostelium discoideum* OX=44689 GN=pslA PE=1 SV=1
P33519	1,16081832	0,2477	NC	GTP-binding nuclear protein Ran OS=*Dictyostelium discoideum* OX=44689 GN=ranA PE=1 SV=1
O00909	1,159591096	0,3109	NC	ADP-ribosylation factor 1 OS=*Dictyostelium discoideum* OX=44689 GN=arfA PE=1 SV=3
P07829	1,155309623	0,1140	NC	Actin-3 OS=*Dictyostelium discoideum* OX=44689 GN=act3 PE=3 SV=3

Q54E24	1,155228736	0,1124	NC	40S ribosomal protein S8 OS=*Dictyostelium discoideum* OX=44689 GN=rps8 PE=1 SV=1
P14329	1,154669769	0,0115	NC	60S ribosomal protein L19 OS=*Dictyostelium discoideum* OX=44689 GN=rpl19 PE=1 SV=1
Q54Y20	1,154150064	0,2083	NC	Alanine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=alaS PE=2 SV=1
Q76P29	1,153938702	0,1303	NC	Importin subunit alpha-B OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272318 PE=3 SV=1
P32252	1,153443093	0,1070	NC	Ras-like protein rasB OS=*Dictyostelium discoideum* OX=44689 GN=rasB PE=1 SV=1
P36411	1,144713884	0,0734	NC	Ras-related protein Rab-7A OS=*Dictyostelium discoideum* OX=44689 GN=rab7A PE=1 SV=1
P34098	1,144005889	0,1321	NC	Lysosomal alpha-mannosidase OS=*Dictyostelium discoideum* OX=44689 GN=manA PE=1 SV=2
O96621	1,142089123	0,1781	NC	Actin-related protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=arpB PE=1 SV=1
P34144	1,141179082	0,0916	NC	Rho-related protein rac1A OS=*Dictyostelium discoideum* OX=44689 GN=rac1A PE=1 SV=2
Q54I98	1,138257489	0,1834	NC	Probable cycloartenol-C-24-methyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=smt1 PE=1 SV=1
Q55C21	1,136989927	0,2893	NC	Methionine aminopeptidase 2 OS=*Dictyostelium discoideum* OX=44689 GN=metap2 PE=3 SV=3
Q54XC4	1,128360394	0,3744	NC	Myeloid-derived growth factor homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0279047 PE=3 SV=2
P54872	1,124447911	0,3123	NC	Hydroxymethylglutaryl-CoA synthase A OS=*Dictyostelium discoideum* OX=44689 GN=hgsA PE=1 SV=2
Q55AB5	1,124235143	0,1278	NC	60S ribosomal protein L32 OS=*Dictyostelium discoideum* OX=44689 GN=rpl32 PE=3 SV=1
P32254	1,121748218	0,2914	NC	Ras-like protein rasS OS=*Dictyostelium discoideum* OX=44689 GN=rasS PE=2 SV=1
Q54MT2	1,119996468	0,4115	NC	Nucleolar protein 56 OS=*Dictyostelium discoideum* OX=44689 GN=nop56 PE=3 SV=1
Q76NU1	1,119831707	0,1125	NC	V-type proton ATPase subunit B OS=*Dictyostelium discoideum* OX=44689 GN=vatB PE=1 SV=1
Q54Z69	1,116326135	0,1194	NC	60S ribosomal protein L4 OS=*Dictyostelium discoideum* OX=44689 GN=rpl4 PE=1 SV=1
Q54JT7	1,114804844	0,4085	NC	Nicastrin OS=*Dictyostelium discoideum* OX=44689 GN=ncstn PE=3 SV=2
P11872	1,114277897	0,3705	NC	cAMP-regulated M3R protein OS=*Dictyostelium discoideum* OX=44689 GN=prtB PE=2 SV=4
P26199	1,11343068	0,4014	NC	Profilin-1 OS=*Dictyostelium discoideum* OX=44689 GN=proA PE=2 SV=1
Q54QW5	1,111658715	0,3897	NC	Ragulator complex protein LAMTOR5 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283567 PE=3 SV=1
Q964D8	1,110551823	0,3654	NC	Beta-ureidopropionase OS=*Dictyostelium discoideum* OX=44689 GN=pyd3 PE=1 SV=1
Q54U31	1,110311365	0,4079	NC	Dual specificity protein kinase shkD OS=*Dictyostelium discoideum* OX=44689 GN=shkD PE=3 SV=1
Q86L14	1,110138493	0,3212	NC	Bifunctional purine biosynthesis protein purH OS=*Dictyostelium discoideum* OX=44689 GN=purH PE=1 SV=1

Q86KZ5	1,108099564	0,3388	NC	Ribosome maturation protein SBDS OS=*Dictyostelium discoideum* OX=44689 GN=sbds PE=3 SV=2
Q8T1V6	1,107190248	0,3651	NC	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufs4 PE=3 SV=2
Q54M82	1,106523594	0,2463	NC	Probable cytochrome b-c1 complex subunit 7 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286171 PE=3 SV=1
P13833	1,104274689	0,2395	NC	Myosin regulatory light chain OS=*Dictyostelium discoideum* OX=44689 GN=mlcR PE=2 SV=1
Q02720	1,103926367	0,4183	NC	Casein kinase II subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=casK PE=2 SV=1
Q54C49	1,099816268	0,2310	NC	Eukaryotic translation initiation factor 3 subunit F OS=*Dictyostelium discoideum* OX=44689 GN=eif3f PE=3 SV=1
Q54KA7	1,098459133	0,3862	NC	Ankyrin repeat, PH and SEC7 domain containing protein secG OS=*Dictyostelium discoideum* OX=44689 GN=secG PE=2 SV=1
Q1ZXD3	1,097225627	0,3092	NC	26S proteasome non-ATPase regulatory subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=psmD3 PE=1 SV=1
Q54GW3	1,097036372	0,3852	NC	Coiled-coil domain-containing protein 124 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289893 PE=3 SV=1
Q556M4	1,096212077	0,3759	NC	Probable cytochrome P450 508A2 OS=*Dictyostelium discoideum* OX=44689 GN=cyp508A2-1 PE=3 SV=1
Q54TU8	1,093389645	0,3031	NC	Calcium load-activated calcium channel homolog OS=*Dictyostelium discoideum* OX=44689 GN=tmco1 PE=2 SV=1
Q01501	1,092763056	0,3049	NC	Mitochondrial outer membrane protein porin OS=*Dictyostelium discoideum* OX=44689 GN=porA PE=1 SV=1
P13023	1,092661299	0,0410	NC	60S ribosomal protein L8 OS=*Dictyostelium discoideum* OX=44689 GN=rpl8 PE=1 SV=2
Q65YR8	1,085962363	0,4253	NC	Cystatin-A1 OS=*Dictyostelium discoideum* OX=44689 GN=cpiA PE=2 SV=1
Q86JA1	1,083414624	0,4135	NC	26S proteasome regulatory subunit 7 OS=*Dictyostelium discoideum* OX=44689 GN=psmC2 PE=1 SV=1
Q54D99	1,08337964	0,3968	NC	Probable 39S ribosomal protein L53, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl53 PE=3 SV=1
Q86A67	1,080705995	0,0817	NC	Fructose-bisphosphate aldolase OS=*Dictyostelium discoideum* OX=44689 GN=fba PE=3 SV=1
Q95VZ3	1,076978371	0,4343	NC	Protein CARMIL OS=*Dictyostelium discoideum* OX=44689 GN=carmil PE=1 SV=1
Q54KZ8	1,0755429	0,3168	NC	Eukaryotic translation initiation factor 3 subunit M OS=*Dictyostelium discoideum* OX=44689 GN=eif3m PE=1 SV=1
Q9GS21	1,070284056	0,2321	NC	60S ribosomal protein L28 OS=*Dictyostelium discoideum* OX=44689 GN=rpl28 PE=2 SV=1
Q54SF7	1,069800946	0,3237	NC	Aspartate aminotransferase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=aatB PE=3 SV=1
Q55EX9	1,066812866	0,4457	NC	Putative methyltransferase DDB_G0268948 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268948 PE=1 SV=2
Q54J69	1,065062129	0,1224	NC	60S ribosomal protein L10 OS=*Dictyostelium discoideum* OX=44689 GN=rpl10 PE=1 SV=2

Q54MD4	1,064021027	0,4182	NC	Probable replication factor C subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=rfc4 PE=3 SV=1
Q86IA3	1,061253564	0,2994	NC	Protein disulfide-isomerase 1 OS=*Dictyostelium discoideum* OX=44689 GN=pdi1 PE=1 SV=2
Q54UD0	1,060288709	0,4303	NC	Eukaryotic translation initiation factor 3 subunit H OS=*Dictyostelium discoideum* OX=44689 GN=eif3H PE=3 SV=1
Q554J3	1,054272114	0,4281	NC	FK506-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp1 PE=3 SV=1
Q86AV6	1,049416352	0,2464	NC	Citrate synthase OS=*Dictyostelium discoideum* OX=44689 GN=gltA PE=3 SV=1
Q86A92	1,042710206	0,4175	NC	Enhancer of rudimentary homolog OS=*Dictyostelium discoideum* OX=44689 GN=erh PE=3 SV=1
Q54G86	1,041462441	0,3588	NC	60S ribosomal protein L23 OS=*Dictyostelium discoideum* OX=44689 GN=rpl23 PE=1 SV=1
Q54QQ0	1,039364152	0,4188	NC	Inosine-5'-monophosphate dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=impdh PE=1 SV=1
Q54K91	1,03913591	0,3836	NC	Acetyl-CoA hydrolase OS=*Dictyostelium discoideum* OX=44689 GN=ach1 PE=3 SV=1
Q55EX6	1,035474025	0,4593	NC	Trafficking protein particle complex subunit 13 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0269062 PE=3 SV=2
P32256	1,033528279	0,4694	NC	Tubulin beta chain OS=*Dictyostelium discoideum* OX=44689 GN=tubB PE=1 SV=2
Q54Z13	1,032307688	0,4166	NC	V-type proton ATPase subunit G OS=*Dictyostelium discoideum* OX=44689 GN=atp6v1g PE=1 SV=2
P54660	1,031696675	0,3880	NC	Ponticulin OS=*Dictyostelium discoideum* OX=44689 GN=ponA PE=1 SV=1
Q54X82	1,029030804	0,4623	NC	AP-1 complex subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=ap1b1 PE=3 SV=1
Q54WZ2	1,028370715	0,4726	NC	Vacuolin-B OS=*Dictyostelium discoideum* OX=44689 GN=vacB PE=1 SV=1
P26200	1,02262232	0,4761	NC	Profilin-2 OS=*Dictyostelium discoideum* OX=44689 GN=proB PE=1 SV=1
Q8T2H0	1,021363288	0,4716	NC	Protein FAM49 homolog OS=*Dictyostelium discoideum* OX=44689 GN=fam49 PE=3 SV=2
Q54KD9	1,021238429	0,4859	NC	Ran-specific GTPase-activating protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=ranbp1 PE=1 SV=1
P54644	1,020482821	0,4771	NC	RAC family serine/threonine-protein kinase homolog OS=*Dictyostelium discoideum* OX=44689 GN=pkbA PE=1 SV=1
Q54Z09	1,01988144	0,4413	NC	60S ribosomal protein L14 OS=*Dictyostelium discoideum* OX=44689 GN=rpl14 PE=3 SV=1
Q54XI5	1,018904379	0,4672	NC	60S ribosomal protein L9 OS=*Dictyostelium discoideum* OX=44689 GN=rpl9 PE=1 SV=2
Q54S03	1,018669459	0,4685	NC	Probable ATP-dependent RNA helicase ddx18 OS=*Dictyostelium discoideum* OX=44689 GN=ddx18 PE=3 SV=1
Q54Y72	1,017498287	0,4818	NC	Rho GTPase-activating protein gacA OS=*Dictyostelium discoideum* OX=44689 GN=gacA PE=3 SV=1
Q75JR3	1,016876983	0,4541	NC	Isocitrate dehydrogenase [NADP] cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=idhC PE=1 SV=1

Q54C94	1,010807679	0,4894	NC	Ras guanine nucleotide exchange factor F OS=*Dictyostelium discoideum* OX=44689 GN=gefF PE=2 SV=1
Q54QS3	1,009721225	0,4882	NC	Probable ATP-dependent RNA helicase ddx3 OS=*Dictyostelium discoideum* OX=44689 GN=ddx3 PE=3 SV=1
Q54T27	1,002670298	0,4934	NC	Eukaryotic translation initiation factor 2 subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=eif2s2 PE=3 SV=1
Q54DD2	-1,006089395	0,4960	NC	Thimet-like oligopeptidase OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292362 PE=3 SV=1
Q75JD5	-1,006567623	0,4846	NC	Phosphoenolpyruvate carboxykinase (ATP) OS=*Dictyostelium discoideum* OX=44689 GN=pckA PE=1 SV=1
Q54MG6	-1,008560641	0,4727	NC	60S ribosomal protein L37 OS=*Dictyostelium discoideum* OX=44689 GN=rpl37 PE=3 SV=1
Q55BE6	-1,011739955	0,4460	NC	60S ribosomal protein L27 OS=*Dictyostelium discoideum* OX=44689 GN=rpl27 PE=3 SV=1
Q54YR4	-1,019302318	0,4766	NC	Protein transport protein Sec61 subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=sec61b PE=3 SV=1
Q54SV6	-1,019302318	0,4766	NC	Mitochondrial import inner membrane translocase subunit tim16 OS=*Dictyostelium discoideum* OX=44689 GN=timm16 PE=3 SV=1
Q556Q3	-1,019920478	0,4600	NC	Probable serine/threonine-protein kinase irlF OS=*Dictyostelium discoideum* OX=44689 GN=irlF-1 PE=3 SV=1
Q94469	-1,021736132	0,4734	NC	Glyceraldehyde-3-phosphate dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=gpdA PE=1 SV=2
Q54RA8	-1,023438179	0,4468	NC	ATP synthase subunit O, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5O PE=3 SV=1
Q54U94	-1,02405354	0,4795	NC	RNA exonuclease 4 OS=*Dictyostelium discoideum* OX=44689 GN=rexo4 PE=3 SV=1
Q54SE2	-1,024554029	0,4553	NC	1-Cys peroxiredoxin OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282517 PE=3 SV=1
P30815	-1,025616817	0,4296	NC	Cytochrome c oxidase subunit 4, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cxdA PE=2 SV=2
P25323	-1,027408905	0,4815	NC	Myosin light chain kinase A OS=*Dictyostelium discoideum* OX=44689 GN=mlkA PE=1 SV=2
Q550H6	-1,027420264	0,4514	NC	Ras-related protein Rab-11C OS=*Dictyostelium discoideum* OX=44689 GN=rab11C PE=1 SV=1
Q54QF9	-1,0279537	0,4573	NC	GrpE protein homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=grpE PE=3 SV=1
Q54ST4	-1,030938004	0,4572	NC	Probable replication factor C subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=rfc5 PE=3 SV=1
Q54NI6	-1,031531826	0,4542	NC	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufs7 PE=3 SV=1
Q58A42	-1,034235314	0,3906	NC	Protein DD3-3 OS=*Dictyostelium discoideum* OX=44689 GN=DD3-3 PE=2 SV=1
Q54P71	-1,036319762	0,4438	NC	Probable acid phosphatase DDB_G0284755 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284755 PE=3 SV=2
Q54KS4	-1,03747021	0,4524	NC	Guanine nucleotide-binding protein-like 3 homolog OS=*Dictyostelium discoideum* OX=44689 GN=gnl3 PE=3 SV=1
P54654	-1,037652529	0,4711	NC	Adenylyl cyclase-associated protein OS=*Dictyostelium discoideum* OX=44689 GN=cap PE=1 SV=1

Q54UI0	-1,038635373	0,4501	NC	Uncharacterized transmembrane protein DDB_G0281067 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0281067 PE=1 SV=1
Q54HW8	-1,0480347	0,4629	NC	Uncharacterized protein DDB_G0289171 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289171 PE=2 SV=1
Q54QM8	-1,051273892	0,1379	NC	60S ribosomal protein L26 OS=*Dictyostelium discoideum* OX=44689 GN=rpl26 PE=3 SV=1
Q54EQ1	-1,051487338	0,4033	NC	Eukaryotic translation initiation factor 3 subunit K OS=*Dictyostelium discoideum* OX=44689 GN=eif3K PE=3 SV=2
P34093	-1,05258045	0,3454	NC	Nucleoside diphosphate kinase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndkM PE=1 SV=2
Q557H1	-1,052686087	0,4359	NC	Dipeptidyl peptidase 3 OS=*Dictyostelium discoideum* OX=44689 GN=dpp3-1 PE=3 SV=1
A0A0F6B980	-1,056211522	0,4357	NC	Thioredoxin OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=trxA PE=3 SV=1
Q54JV6	-1,056230488	0,4376	NC	Protein transport protein Sec61 subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=sec61g PE=3 SV=1
O96552	-1,060074174	0,3894	NC	Charged multivesicular body protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=chmp1 PE=3 SV=1
Q54E20	-1,060179864	0,1214	NC	60S ribosomal protein L13 OS=*Dictyostelium discoideum* OX=44689 GN=rpl13 PE=1 SV=1
Q54BN3	-1,072622449	0,4213	NC	Probable replication factor C subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=rfc3 PE=3 SV=1
Q8T1V4	-1,075874708	0,4150	NC	40S ribosomal protein S27 OS=*Dictyostelium discoideum* OX=44689 GN=rps27 PE=3 SV=2
Q9NGQ2	-1,08137539	0,4207	NC	Kinesin-related protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=kif1 PE=1 SV=1
Q86I43	-1,082431125	0,4060	NC	Uncharacterized protein DDB_G0275161 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275161 PE=2 SV=1
Q55BX3	-1,086693611	0,3757	NC	NDRG-like protein OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0270324 PE=3 SV=1
Q54XZ0	-1,091403368	0,3666	NC	Probable enoyl-CoA hydratase 2 OS=*Dictyostelium discoideum* OX=44689 GN=mfeB PE=2 SV=1
Q54GB3	-1,09192865	0,3985	NC	Synaptobrevin-B OS=*Dictyostelium discoideum* OX=44689 GN=sybB PE=3 SV=1
Q86AD5	-1,099783466	0,3060	NC	Pyruvate dehydrogenase complex subunit homolog DDB_G0271564, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhX PE=3 SV=1
Q54I58	-1,100721579	0,3130	NC	Protein NipSnap homolog OS=*Dictyostelium discoideum* OX=44689 GN=nipsnap PE=3 SV=1
P36416	-1,100855064	0,3823	NC	N-terminal acetyltransferase complex ARD1 subunit homolog OS=*Dictyostelium discoideum* OX=44689 GN=natA PE=2 SV=1
Q9BKJ9	-1,102131965	0,0369	NC	Lysosome membrane protein 2-B OS=*Dictyostelium discoideum* OX=44689 GN=lmpB PE=1 SV=1
Q54LV8	-1,104428233	0,3486	NC	60S ribosomal protein L34 OS=*Dictyostelium discoideum* OX=44689 GN=rpl34 PE=3 SV=1
O77203	-1,105791661	0,4223	NC	Protein pianissimo A OS=*Dictyostelium discoideum* OX=44689 GN=piaA PE=1 SV=1
Q6UK63	-1,108051684	0,3743	NC	Protein pirA OS=*Dictyostelium discoideum* OX=44689 GN=pirA PE=1 SV=1

Q553M7	-1,108606594	0,2009	NC	60S ribosomal protein L13a OS=*Dictyostelium discoideum* OX=44689 GN=rpl13a PE=1 SV=1
Q7KWL3	-1,108878812	0,3859	NC	DDB1- and CUL4-associated factor 13 OS=*Dictyostelium discoideum* OX=44689 GN=wdsof1 PE=3 SV=1
Q54PN7	-1,111378278	0,4158	NC	26S proteasome regulatory subunit 6A homolog OS=*Dictyostelium discoideum* OX=44689 GN=psmC3 PE=1 SV=1
P32253	-1,112648216	0,2644	NC	Ras-like protein rasC OS=*Dictyostelium discoideum* OX=44689 GN=rasC PE=2 SV=1
Q54E22	-1,113606291	0,3259	NC	Acyl carrier protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufab1 PE=3 SV=1
Q54QB1	-1,115118597	0,3349	NC	Extracellular signal-regulated kinase 2 OS=*Dictyostelium discoideum* OX=44689 GN=erkB PE=1 SV=1
P36408	-1,116489392	0,2971	NC	Guanine nucleotide-binding protein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=gpbA PE=1 SV=1
P29505	-1,117491816	0,1743	NC	Cytochrome c oxidase subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=cxeA PE=1 SV=3
P02887	-1,12673864	0,2236	NC	Discoidin-1 subunit B/C OS=*Dictyostelium discoideum* OX=44689 GN=dscC-1 PE=1 SV=1
Q54UG4	-1,127482292	0,3330	NC	60S ribosomal protein L37a OS=*Dictyostelium discoideum* OX=44689 GN=rpl37A PE=3 SV=1
P48160	-1,130702945	0,1416	NC	60S ribosomal protein L27a OS=*Dictyostelium discoideum* OX=44689 GN=rpl27a PE=3 SV=1
Q54QG4	-1,139791036	0,3092	NC	Uncharacterized protein DDB_G0283843 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283843 PE=4 SV=1
Q54QR3	-1,140960396	0,2677	NC	Ras-related protein Rab-32A OS=*Dictyostelium discoideum* OX=44689 GN=rab32A PE=1 SV=1
Q54D04	-1,142031216	0,2065	NC	Probable malate dehydrogenase 2, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mdhB PE=1 SV=1
Q1ZXG4	-1,143134436	0,2218	NC	Proliferation-associated protein A OS=*Dictyostelium discoideum* OX=44689 GN=prlA PE=2 SV=1
Q54B68	-1,143968823	0,1799	NC	Isocitrate dehydrogenase [NAD] regulatory subunit B, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=idhB PE=3 SV=1
Q54P23	-1,144834347	0,2703	NC	Stromal cell-derived factor 2-like protein OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284847 PE=3 SV=1
Q55C75	-1,152266892	0,2460	NC	26S proteasome non-ATPase regulatory subunit 6 OS=*Dictyostelium discoideum* OX=44689 GN=psmD6 PE=1 SV=1
O96759	-1,153258372	0,3515	NC	Alkyldihydroxyacetonephosphate synthase OS=*Dictyostelium discoideum* OX=44689 GN=eapA PE=1 SV=1
Q54YT4	-1,154896626	0,1258	NC	Enoyl-[acyl-carrier-protein] reductase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mecr PE=3 SV=1
P24005	-1,158166918	0,3580	NC	Calcium-regulated actin-bundling protein OS=*Dictyostelium discoideum* OX=44689 GN=abpB PE=1 SV=1
Q54NU0	-1,158661143	0,3936	NC	Flap endonuclease 1 OS=*Dictyostelium discoideum* OX=44689 GN=repG PE=3 SV=1
Q54BN0	-1,160570878	0,2207	NC	Transmembrane emp24 domain-containing protein B OS=*Dictyostelium discoideum* OX=44689 GN=empB PE=3 SV=1
Q553V1	-1,161009402	0,0084	NC	Citrate synthase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cs PE=3 SV=1

Q54NS7	-1,161225891	0,2729	NC	PRA1 family protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=prafB PE=3 SV=2
Q55G10	-1,162152056	0,2887	NC	Nicotinate phosphoribosyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=naprt PE=2 SV=1
Q54KN7	-1,169120541	0,3092	NC	Putative thioredoxin-5 OS=*Dictyostelium discoideum* OX=44689 GN=trxE PE=3 SV=1
P02886	-1,178562794	0,1661	NC	Discoidin-1 subunit A OS=*Dictyostelium discoideum* OX=44689 GN=dscA-1 PE=1 SV=3
Q86IC8	-1,178699781	0,2332	NC	Probable caffeoyl-CoA O-methyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=omt6 PE=1 SV=1
Q54IT3	-1,179949734	0,3040	NC	Probable flavin-containing monoamine oxidase A OS=*Dictyostelium discoideum* OX=44689 GN=maoA PE=3 SV=1
Q54XK0	-1,181986316	0,0742	NC	Probable 39S ribosomal protein L27, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl27 PE=3 SV=1
Q55GJ6	-1,18211225	0,3096	NC	Proteasome subunit beta type-6 OS=*Dictyostelium discoideum* OX=44689 GN=psmB6 PE=1 SV=1
Q54ME1	-1,183514934	0,2922	NC	Gamete and mating-type specific protein A OS=*Dictyostelium discoideum* OX=44689 GN=gmsA PE=2 SV=1
O96042	-1,184912149	0,3369	NC	Differentiation-associated protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=dia2 PE=2 SV=1
Q54Y55	-1,186259864	0,1157	NC	Dual specificity protein kinase shkC OS=*Dictyostelium discoideum* OX=44689 GN=shkC PE=3 SV=1
P0C7B6	-1,202239587	0,2367	NC	Type-1 glutamine synthetase 2 OS=*Dictyostelium discoideum* OX=44689 GN=glnA2 PE=1 SV=1
Q86J23	-1,204603286	0,2404	NC	Ragulator complex protein LAMTOR3 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274833 PE=3 SV=1
Q869S7	-1,207851332	0,1555	NC	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=scsB PE=3 SV=1
Q553V2	-1,211336467	0,1388	NC	Methylmalonyl-CoA epimerase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mcee PE=3 SV=1
Q54CE0	-1,216621342	0,3216	NC	Probable ATP-dependent RNA helicase ddx17 OS=*Dictyostelium discoideum* OX=44689 GN=ddx17 PE=3 SV=1
Q55GU3	-1,217879843	0,2480	NC	Probable mitochondrial pyruvate carrier 2 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268478 PE=3 SV=1
Q86HD3	-1,218431745	0,1944	NC	Ribosome assembly factor mrt4 OS=*Dictyostelium discoideum* OX=44689 GN=mrt4 PE=3 SV=1
Q55GE2	-1,220571568	0,1889	NC	Probable mitochondrial 2-oxodicarboxylate carrier OS=*Dictyostelium discoideum* OX=44689 GN=mcfT PE=3 SV=1
Q54GN8	-1,222493052	0,3636	NC	Ribosome biogenesis protein NSA2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=nsa2 PE=3 SV=1
Q4W6B5	-1,225298884	0,1798	NC	Mitochondrial-processing peptidase subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=mppB PE=1 SV=1
Q55F42	-1,227581796	0,2719	NC	ATP synthase subunit delta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5D PE=3 SV=1
Q54E49	-1,227755293	0,3090	NC	Probable ATP-dependent RNA helicase ddx6 OS=*Dictyostelium discoideum* OX=44689 GN=ddx6 PE=3 SV=1

Q54EW1	-1,229826579	0,0404	NC	Serine hydroxymethyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=shmt2 PE=3 SV=1
Q54FL2	-1,230217093	0,2163	NC	Ras-related protein RabG2 OS=*Dictyostelium discoideum* OX=44689 GN=rabG2 PE=3 SV=2
Q54FW9	-1,230848518	0,2863	NC	WD repeat-containing protein DDB_G0290555 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0290555 PE=4 SV=1
Q54NS3	-1,238626344	0,3233	NC	TPR repeat-containing protein DDB_G0285095 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0285095 PE=4 SV=1
Q54XS2	-1,242065555	0,0333	NC	Probable aconitate hydratase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aco2 PE=3 SV=1
P34118	-1,247537378	0,1453	NC	Major vault protein alpha OS=*Dictyostelium discoideum* OX=44689 GN=mvpA PE=1 SV=1
Q54YZ4	-1,259065109	0,0823	NC	Electron transfer flavoprotein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=etfb PE=3 SV=1
P34139	-1,262644759	0,0750	NC	Ras-related protein Rab-1A OS=*Dictyostelium discoideum* OX=44689 GN=rab1A PE=2 SV=2
Q54VI3	-1,26362679	0,1783	NC	Glutamate dehydrogenase 2 OS=*Dictyostelium discoideum* OX=44689 GN=glud2 PE=1 SV=2
Q75JR2	-1,264003176	0,0846	NC	Isocitrate dehydrogenase [NADP], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=idhM PE=3 SV=1
Q54GE3	-1,26426951	0,1819	NC	Vacuolar protein sorting-associated protein 45 OS=*Dictyostelium discoideum* OX=44689 GN=vps45 PE=1 SV=1
Q550U9	-1,267526329	0,2513	NC	Phospholipase B-like protein A OS=*Dictyostelium discoideum* OX=44689 GN=plbA PE=1 SV=1
Q54VN2	-1,268598583	0,1516	NC	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=coq5 PE=3 SV=1
P54659	-1,271721131	0,0890	NC	Major vault protein beta OS=*Dictyostelium discoideum* OX=44689 GN=mvpB PE=1 SV=1
Q54DD3	-1,27229954	0,0381	NC	Aminomethyltransferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcvT PE=3 SV=1
Q54WM4	-1,273280705	0,2379	NC	Eukaryotic translation initiation factor 3 subunit G OS=*Dictyostelium discoideum* OX=44689 GN=eif3G PE=3 SV=1
Q54JD2	-1,274394577	0,0094	SC	Putative uncharacterized protein DDB_G0288137 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288137 PE=4 SV=1
Q9NKW1	-1,275791087	0,1436	NC	Peroxisomal multifunctional enzyme A OS=*Dictyostelium discoideum* OX=44689 GN=mfeA PE=2 SV=1
Q54G58	-1,278459897	0,0457	NC	Uncharacterized protein DDB_G0290387 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0290387 PE=3 SV=1
Q1ZXL7	-1,278862161	0,1899	NC	Probable cytochrome P450 508A3 OS=*Dictyostelium discoideum* OX=44689 GN=cyp508A3-1 PE=3 SV=1
Q86CR8	-1,28177244	0,2018	NC	Autophagy-related protein 8 OS=*Dictyostelium discoideum* OX=44689 GN=atg8 PE=2 SV=1
Q869Z4	-1,286009595	0,1276	NC	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pck2 PE=3 SV=1
Q54C27	-1,286932816	0,2399	NC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=ost1 PE=2 SV=1

P54671	-1,290046241	0,0980	NC	Histone H1 OS=*Dictyostelium discoideum* OX=44689 GN=H1 PE=1 SV=3
Q54HG9	-1,294828237	0,2031	NC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit swp1 OS=*Dictyostelium discoideum* OX=44689 GN=swp1 PE=3 SV=1
Q54M18	-1,295927669	0,0166	SC	Bifunctional protein argC, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=argC PE=1 SV=1
Q54UC0	-1,296981353	0,2296	NC	DNA-dependent protein kinase catalytic subunit OS=*Dictyostelium discoideum* OX=44689 GN=dnapkcs PE=3 SV=2
Q86B05	-1,297048823	0,2747	NC	Probable ribosome biogenesis protein RLP24 OS=*Dictyostelium discoideum* OX=44689 GN=rlp24 PE=2 SV=1
Q55FI1	-1,297965678	0,0980	NC	4-aminobutyrate aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=gabT PE=3 SV=1
Q54CX6	-1,302173571	0,1681	NC	Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=hibA PE=3 SV=1
Q54GY8	-1,302239239	0,2329	NC	Ras-related protein Rab-18 OS=*Dictyostelium discoideum* OX=44689 GN=rab18 PE=3 SV=1
Q55BU8	-1,303221596	0,1481	NC	Protein erg2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=erg2 PE=3 SV=1
Q7KWM5	-1,306339739	0,2721	NC	Alpha-1,3/1,6-mannosyltransferase ALG2 OS=*Dictyostelium discoideum* OX=44689 GN=alg2 PE=3 SV=1
Q23889	-1,309273644	0,2367	NC	Ribosomal protein S19, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps19 PE=3 SV=1
P14797	-1,309876288	0,0457	NSC	Ubiquitin-40S ribosomal protein S27a OS=*Dictyostelium discoideum* OX=44689 GN=ubqC PE=1 SV=2
Q75JL2	-1,318285431	0,2974	NC	Mitochondrial DNA repair protein recA homolog OS=*Dictyostelium discoideum* OX=44689 GN=recA PE=3 SV=1
P54641	-1,320294299	0,0131	SC	V-type proton ATPase subunit d OS=*Dictyostelium discoideum* OX=44689 GN=vatD-1 PE=1 SV=2
Q54XF7	-1,320489936	0,2287	NC	Cullin-5 OS=*Dictyostelium discoideum* OX=44689 GN=culE PE=3 SV=1
Q55CS9	-1,321718645	0,0063	SC	ATP synthase subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5b PE=1 SV=1
Q559X6	-1,32519286	0,0367	SC	Ras-related protein Rab-2B OS=*Dictyostelium discoideum* OX=44689 GN=rab2B PE=3 SV=1
Q54WP3	-1,326087138	0,0999	NSC	Probable 39S ribosomal protein L22, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl22 PE=3 SV=1
Q9UA41	-1,328066897	0,1169	NSC	Peptidyl-prolyl cis-trans isomerase D, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cypD PE=1 SV=1
Q54LP3	-1,331789015	0,1153	NSC	Dolichol-phosphate mannosyltransferase subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=dpm1 PE=3 SV=1
O15736	-1,334444634	0,1312	NSC	Protein tipD OS=*Dictyostelium discoideum* OX=44689 GN=tipD PE=3 SV=1
Q54JC2	-1,336146981	0,1137	NSC	Uncharacterized protein DDB_G0288155 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288155 PE=1 SV=1
Q54I10	-1,345212274	0,1111	NSC	Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mmsdh PE=3 SV=1

Q54F47	-1,347798065	0,1574	NSC	Probable cytochrome P450 513C1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp513C1 PE=3 SV=1
Q55BF2	-1,358236604	0,2317	NSC	60S ribosomal export protein NMD3 OS=*Dictyostelium discoideum* OX=44689 GN=nmd3 PE=3 SV=1
Q55C70	-1,363366996	0,1551	NSC	Mitochondrial import inner membrane translocase subunit tim50 OS=*Dictyostelium discoideum* OX=44689 GN=timm50 PE=3 SV=1
Q86AQ7	-1,369366995	0,0355	SC	Vesicle-associated membrane protein 7B OS=*Dictyostelium discoideum* OX=44689 GN=vamp7B PE=3 SV=1
P34046	-1,375459214	0,1009	NSC	Guanine nucleotide-binding protein alpha-8 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaH PE=2 SV=2
Q86I22	-1,375560123	0,0380	NSC	Acylpyruvase FAHD1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=fahd1 PE=3 SV=1
Q54WD9	-1,37583629	0,3213	NSC	Probable tyrosine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mtyrS PE=3 SV=1
Q54NU2	-1,377845313	0,1973	NSC	Ras-related protein Rab-1D OS=*Dictyostelium discoideum* OX=44689 GN=rab1D PE=1 SV=1
Q54TY5	-1,38042387	0,2184	NSC	Probable 39S ribosomal protein L17, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl17 PE=3 SV=1
P08800	-1,39097353	0,1996	NSC	UTP--glucose-1-phosphate uridylyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=uppA PE=2 SV=2
Q869L3	-1,395291295	0,2806	NSC	Midasin OS=*Dictyostelium discoideum* OX=44689 GN=mdn1 PE=3 SV=2
Q54K93	-1,398636933	0,1508	NSC	Putative uncharacterized protein DDB_G0287517 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0287517 PE=4 SV=1
Q559Z0	-1,403107317	0,0114	SC	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufa9 PE=3 SV=1
Q54LZ8	-1,404153806	0,2232	NSC	Putative uncharacterized protein DDB_G0286285 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286285 PE=4 SV=1
Q554U9	-1,408567922	0,0388	NSC	Eukaryotic translation initiation factor 3 subunit D OS=*Dictyostelium discoideum* OX=44689 GN=eif3d PE=3 SV=1
Q55CC2	-1,418436384	0,0575	NSC	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sdhB PE=3 SV=1
Q556J2	-1,41858263	0,1888	NSC	3-ketodihydrosphingosine reductase OS=*Dictyostelium discoideum* OX=44689 GN=ksrA-1 PE=3 SV=1
Q54JV8	-1,419636502	0,1078	NSC	Probable glycine cleavage system H protein 1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcvH1 PE=3 SV=1
Q55BI2	-1,421573703	0,0213	SC	Isocitrate dehydrogenase [NAD] regulatory subunit A, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=idhA PE=3 SV=1
P34092	-1,423960321	0,1598	NSC	Myosin IB heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=myoB PE=1 SV=2
Q86IV4	-1,429853735	0,0941	NSC	PH domain-containing protein DDB_G0274775 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274775 PE=4 SV=1
P09556	-1,434929994	0,1421	NSC	Uridine 5'-monophosphate synthase OS=*Dictyostelium discoideum* OX=44689 GN=pyr56 PE=1 SV=2
Q54QJ9	-1,436776141	0,1333	NSC	Adenylate kinase OS=*Dictyostelium discoideum* OX=44689 GN=adkA PE=3 SV=1

Q54D07	-1,439043613	0,0792	NSC	Cytochrome c1, heme protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cyc1 PE=3 SV=1
Q554Z5	-1,443833909	0,1286	NSC	Acyl-CoA synthetase short-chain family member B, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aslB PE=3 SV=1
Q54J68	-1,44681287	0,0360	SC	10 kDa heat shock protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=hspe1 PE=3 SV=1
Q54CL2	-1,446930849	0,1538	NSC	T-complex protein 1 subunit delta OS=*Dictyostelium discoideum* OX=44689 GN=cct4 PE=3 SV=1
Q75JK6	-1,454301509	0,0157	C	ATP synthase subunit epsilon, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5e PE=3 SV=1
Q54ZM4	-1,457823932	0,2163	NSC	Probable cytochrome P450 518A1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp518A1 PE=3 SV=1
Q54LV3	-1,460175175	0,1396	NSC	Elongation factor Ts, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=tsfm PE=3 SV=1
P34113	-1,464675925	0,0699	NSC	60S ribosomal protein L3 OS=*Dictyostelium discoideum* OX=44689 GN=rpl3 PE=1 SV=2
Q55CV5	-1,469258282	0,1211	NSC	Probable tetraspanin tspA OS=*Dictyostelium discoideum* OX=44689 GN=tspA PE=2 SV=1
Q55F21	-1,48001782	0,0292	SC	Aspartate aminotransferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aatA PE=3 SV=1
Q54C70	-1,482230505	0,0039	SC	Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhA PE=1 SV=1
Q76NU3	-1,483230235	0,1753	NSC	T-complex protein 1 subunit zeta OS=*Dictyostelium discoideum* OX=44689 GN=cct6 PE=1 SV=1
Q8T2K9	-1,489951783	0,0666	NSC	Malate synthase OS=*Dictyostelium discoideum* OX=44689 GN=masA PE=2 SV=2
Q54DG1	-1,492977157	0,1150	NSC	Aldehyde dehydrogenase family 3 comG OS=*Dictyostelium discoideum* OX=44689 GN=comG PE=3 SV=1
Q86KI1	-1,493969331	0,1242	NSC	AP-2 complex subunit alpha-2 OS=*Dictyostelium discoideum* OX=44689 GN=ap2a1-1 PE=3 SV=1
Q869Y7	-1,495208871	0,0023	SC	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=odhB PE=1 SV=1
Q86AD9	-1,4958709	0,1023	NSC	Probable acetyl-CoA acetyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271544 PE=2 SV=1
Q54R41	-1,505359687	0,1185	NSC	Guanine nucleotide-binding protein alpha-9 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaI PE=2 SV=1
Q54V77	-1,512071209	0,0359	C	CTP synthase OS=*Dictyostelium discoideum* OX=44689 GN=ctps PE=3 SV=1
Q8I0H7	-1,516853051	0,0280	SC	Heat shock 70 kDa protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mhsp70 PE=1 SV=1
Q54DJ0	-1,51733698	0,1552	NSC	Ribosome production factor 2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=bxdc1 PE=3 SV=1
Q54YZ0	-1,51767646	0,1386	NSC	UTP--glucose-1-phosphate uridylyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=ugpB PE=2 SV=1
Q54Q31	-1,520487587	0,0701	NSC	Prohibitin-2 OS=*Dictyostelium discoideum* OX=44689 GN=phbB PE=3 SV=1

Q86HX0	-1,52164481	0,0213	SC	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhB PE=1 SV=1
Q55E60	-1,53420424	0,2263	NSC	Xaa-Pro dipeptidase OS=*Dictyostelium discoideum* OX=44689 GN=pepd PE=1 SV=1
Q54BF6	-1,54353586	0,0668	NSC	Mitochondrial substrate carrier family protein N OS=*Dictyostelium discoideum* OX=44689 GN=mcfN PE=1 SV=2
Q23883	-1,549916731	0,1133	NSC	NADH-ubiquinone oxidoreductase 49 kDa subunit OS=*Dictyostelium discoideum* OX=44689 GN=nad7 PE=1 SV=1
Q552P9	-1,554038128	0,1007	NSC	Uncharacterized protein DDB_G0275933 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275933 PE=3 SV=1
Q54XX3	-1,555886944	0,0061	SC	60S ribosomal protein L5 OS=*Dictyostelium discoideum* OX=44689 GN=rpl5 PE=1 SV=1
Q54LT2	-1,558167213	0,0669	NSC	Uricase OS=*Dictyostelium discoideum* OX=44689 GN=uox PE=3 SV=1
Q55G75	-1,560555698	0,1000	NSC	PH domain-containing protein DDB_G0267786 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267786 PE=4 SV=1
Q55GH8	-1,564265089	0,0621	NSC	Small heat shock protein hspL OS=*Dictyostelium discoideum* OX=44689 GN=hspL PE=3 SV=1
Q553B6	-1,569698698	0,0816	NSC	Glycylpeptide N-tetradecanoyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=nmt PE=3 SV=2
Q55D12	-1,573777119	0,1273	NSC	Probable histidine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mhisS PE=3 SV=1
Q54K35	-1,577243938	0,1162	NSC	Mitochondrial import inner membrane translocase subunit tim17 OS=*Dictyostelium discoideum* OX=44689 GN=timm17 PE=3 SV=1
Q37315	-1,582413291	0,0028	SC	ATP synthase subunit 9, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp9 PE=3 SV=1
Q54GI9	-1,582647253	0,0657	NSC	Prohibitin-1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=phbA PE=3 SV=1
Q54KB7	-1,582888071	0,0136	SC	Glutamate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gluD PE=1 SV=1
Q54B67	-1,588346158	0,0216	SC	Mitochondrial substrate carrier family protein Z OS=*Dictyostelium discoideum* OX=44689 GN=mcfZ PE=2 SV=1
Q54TH8	-1,603727968	0,2112	NSC	T-complex protein 1 subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=cct3 PE=1 SV=1
Q55E31	-1,604391027	0,1475	NSC	Ras-related protein Rab-32B OS=*Dictyostelium discoideum* OX=44689 GN=rab32B PE=3 SV=1
Q869N6	-1,619604245	0,0073	C	3-hydroxybutyryl-CoA dehydratase-like protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271866 PE=3 SV=1
Q54JE4	-1,622660164	0,0242	SC	2-oxoglutarate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ogdh PE=3 SV=1
Q54IP4	-1,629713691	0,0488	NSC	Dual specificity protein kinase shkB OS=*Dictyostelium discoideum* OX=44689 GN=shkB PE=3 SV=1
Q55FL5	-1,62984694	0,1230	NSC	Serine palmitoyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=sptA PE=3 SV=1
P08799	-1,63690313	0,0005	SC	Myosin-2 heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=mhcA PE=1 SV=3
Q54R47	-1,646051338	0,1480	NSC	Glutaryl-CoA dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcdh PE=3 SV=1

P36413	-1,660780193	0,0090	SC	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhC PE=1 SV=2
O96622	-1,662409985	0,0104	SC	Actin-related protein 2/3 complex subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=arcA PE=1 SV=1
Q54DK1	-1,663127112	0,0916	NSC	Sulfide:quinone oxidoreductase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sqor PE=3 SV=1
Q54IF7	-1,671401105	0,0316	C	Vacuolar protein sorting-associated protein 29 OS=*Dictyostelium discoideum* OX=44689 GN=vps29 PE=3 SV=1
Q7KWK5	-1,687483178	0,0387	NSC	Pre-mRNA-processing factor 19 OS=*Dictyostelium discoideum* OX=44689 GN=prp19 PE=3 SV=1
Q9GRX6	-1,687751529	0,0526	NSC	Apoptosis-inducing factor 1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aif PE=2 SV=1
B0G180	-1,689415642	0,0270	C	Signal peptidase complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=spcs3 PE=3 SV=1
Q54YN3	-1,691189992	0,0801	NSC	ER membrane protein complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=emc3 PE=3 SV=1
O15818	-1,708726711	0,0393	NSC	Clustered mitochondria protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=clua PE=1 SV=2
Q54X04	-1,717847366	0,0554	NSC	Probable cysteine desulfurase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=nfs1 PE=1 SV=1
Q55EL3	-1,728651821	0,0121	C	Uridine-cytidine kinase A OS=*Dictyostelium discoideum* OX=44689 GN=udkA PE=3 SV=1
Q55AI5	-1,734554548	0,0098	SC	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=scsC PE=3 SV=1
Q54RA2	-1,743196979	0,0047	SC	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283293 PE=3 SV=1
Q54DW2	-1,755365904	0,0426	NSC	Probable endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=ergic3 PE=3 SV=1
Q556S2	-1,756443608	0,2652	NSC	Serine/threonine-protein kinase pakH OS=*Dictyostelium discoideum* OX=44689 GN=pakH-1 PE=3 SV=1
Q55C16	-1,761504418	0,1411	NSC	Ubiquitin-like modifier-activating enzyme 1 OS=*Dictyostelium discoideum* OX=44689 GN=uba1 PE=3 SV=1
Q86AV5	-1,762315806	0,0448	NSC	Mitochondrial substrate carrier family protein X OS=*Dictyostelium discoideum* OX=44689 GN=mcfX PE=3 SV=1
Q54VF1	-1,768180584	0,0512	NSC	Probable ATP-dependent RNA helicase ddx56 OS=*Dictyostelium discoideum* OX=44689 GN=ddx56 PE=3 SV=1
Q54NW7	-1,780163176	0,0290	C	Vesicle-associated membrane protein 7A OS=*Dictyostelium discoideum* OX=44689 GN=vamp7A PE=1 SV=1
Q54G18	-1,794830173	0,0775	NSC	Rho GTPase-activating protein gacW OS=*Dictyostelium discoideum* OX=44689 GN=gacW PE=3 SV=1
Q54N47	-1,810459235	0,0151	SC	Branched-chain-amino-acid aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=bcaA PE=3 SV=1
P34136	-1,812367398	0,0201	C	3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 OS=*Dictyostelium discoideum* OX=44689 GN=hmgB PE=2 SV=2
Q54GE6	-1,812612958	0,0554	NSC	Probable malate dehydrogenase 1 OS=*Dictyostelium discoideum* OX=44689 GN=mdhA PE=1 SV=1

Q54H86	-1,822243339	0,1142	NSC	Peroxisomal membrane protein 11 homolog OS=*Dictyostelium discoideum* OX=44689 GN=pex11 PE=3 SV=1
Q55A19	-1,827484677	0,0004	SC	40S ribosomal protein S23 OS=*Dictyostelium discoideum* OX=44689 GN=rps23 PE=3 SV=1
Q03380	-1,828177545	0,0160	SC	Comitin OS=*Dictyostelium discoideum* OX=44689 GN=comA PE=1 SV=1
P20790	-1,834401521	0,0089	SC	Ras-related protein Rab-8A OS=*Dictyostelium discoideum* OX=44689 GN=rab8A PE=3 SV=1
Q5V9F0	-1,85045389	0,0069	C	Cytosol aminopeptidase OS=*Dictyostelium discoideum* OX=44689 GN=lap PE=1 SV=1
P21837	-1,851159114	0,0336	SC	Crystal protein OS=*Dictyostelium discoideum* OX=44689 GN=cryS PE=1 SV=1
Q54P26	-1,865531737	0,0908	NSC	Probable serine/threonine-protein kinase samkB OS=*Dictyostelium discoideum* OX=44689 GN=samkB PE=3 SV=1
Q869N1	-1,872734591	0,1513	NSC	Cytochrome c OS=*Dictyostelium discoideum* OX=44689 GN=cytC PE=3 SV=1
Q54WN5	-1,878407918	0,0280	C	U3 small nucleolar RNA-associated protein 6 homolog OS=*Dictyostelium discoideum* OX=44689 GN=utp6 PE=1 SV=1
Q8T2J9	-1,879056801	0,0029	C	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mccb PE=3 SV=2
O15743	-1,88263279	0,0452	NSC	Protein spalten OS=*Dictyostelium discoideum* OX=44689 GN=spnA PE=1 SV=1
Q54RB9	-1,888316911	0,0200	C	Calcium-binding mitochondrial carrier protein OS=*Dictyostelium discoideum* OX=44689 GN=mcfO PE=3 SV=1
Q54N72	-1,889331754	0,0513	NSC	Probable nucleolar GTP-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=nog1 PE=1 SV=1
Q54JD9	-1,897416034	0,0012	SC	Probable succinyl-CoA:3-ketoacid coenzyme A transferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=oxct1 PE=3 SV=1
Q54VG0	-1,898844299	0,0072	C	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1 homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=odhA PE=3 SV=1
Q86C65	-1,915552869	0,2297	NSC	Serine/threonine-protein kinase tor OS=*Dictyostelium discoideum* OX=44689 GN=tor PE=1 SV=1
Q54T81	-1,924753608	0,0846	NSC	Probable H/ACA ribonucleoprotein complex subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=nola4 PE=1 SV=1
Q86L04	-1,936158416	0,0105	C	TNF receptor-associated protein 1 homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=trap1 PE=2 SV=1
Q54E62	-1,937506438	0,0228	SC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=*Dictyostelium discoideum* OX=44689 GN=ddost PE=3 SV=1
Q1ZXF1	-1,958002112	0,0199	C	Probable enoyl-CoA hydratase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=echs1 PE=3 SV=1
Q54D63	-1,960462812	0,0015	SC	60S ribosomal protein L6 OS=*Dictyostelium discoideum* OX=44689 GN=rpl6 PE=1 SV=1
Q23887	-1,962963111	0,0717	NSC	Ribosomal protein S7, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps7 PE=3 SV=1
Q8T2T5	-1,965770297	0,0377	NSC	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sdhC PE=3 SV=1

Q54F93	-1,969432944	0,0142	SC	Mitochondrial-processing peptidase subunit alpha-2 OS=*Dictyostelium discoideum* OX=44689 GN=mppA2 PE=1 SV=1
Q54NZ8	-1,999319273	0,0377	NSC	Isochorismatase family protein 1B OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284901 PE=3 SV=1
P36967	-2,001213345	0,0210	SC	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=scsA PE=1 SV=3
Q6S001	-2,00481091	0,0187	C	Kinesin-related protein 11 OS=*Dictyostelium discoideum* OX=44689 GN=kif11 PE=3 SV=1
Q9U3X4	-2,020480198	0,0037	SC	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sdhA PE=3 SV=1
Q86LA2	-2,025230532	0,0141	C	Eukaryotic translation initiation factor 3 subunit L OS=*Dictyostelium discoideum* OX=44689 GN=eif3L PE=3 SV=1
P0CE94	-2,033823406	0,0868	NSC	Talin-A OS=*Dictyostelium discoideum* OX=44689 GN=talA PE=3 SV=1
Q54XM6	-2,041127572	0,0872	NSC	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=etfdh PE=3 SV=1
Q54IN6	-2,042270412	0,0270	SC	Uncharacterized protein DDB_G0288629 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288629 PE=4 SV=1
Q54HB2	-2,063934279	0,0047	SC	Elongation factor Tu, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=tufm PE=1 SV=2
Q54TS4	-2,093458623	0,0131	C	Protein YIPF1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=yipf1 PE=3 SV=1
Q94502	-2,103671641	0,0335	C	Neutral alpha-glucosidase AB OS=*Dictyostelium discoideum* OX=44689 GN=modA PE=3 SV=1
Q54NS1	-2,109422758	0,0385	NSC	Putative transferase caf17 homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=caf17 PE=3 SV=1
Q54ET0	-2,129776039	0,0914	NSC	Metabotropic glutamate receptor-like protein E OS=*Dictyostelium discoideum* OX=44689 GN=grlE PE=2 SV=2
Q54E04	-2,172515925	0,0013	SC	Vacuolar proton translocating ATPase 100 kDa subunit OS=*Dictyostelium discoideum* OX=44689 GN=vatM PE=1 SV=2
Q54BM3	-2,178145783	0,0492	NSC	Mitochondrial substrate carrier family protein G OS=*Dictyostelium discoideum* OX=44689 GN=mcfG PE=2 SV=1
Q54QK7	-2,185210248	0,0089	C	Probable dimethyladenosine transferase OS=*Dictyostelium discoideum* OX=44689 GN=dimt1 PE=3 SV=1
P53766	-2,2013875	0,0414	NSC	Uracil-DNA glycosylase OS=*Dictyostelium discoideum* OX=44689 GN=uglA PE=2 SV=2
Q54B10	-2,211765629	0,1052	NSC	NADPH oxidoreductase A OS=*Dictyostelium discoideum* OX=44689 GN=redA PE=2 SV=1
P15112	-2,22001013	0,0042	SC	Elongation factor 2 OS=*Dictyostelium discoideum* OX=44689 GN=efbA PE=1 SV=2
Q54X97	-2,223263842	0,0260	C	Eukaryotic translation initiation factor 3 subunit C OS=*Dictyostelium discoideum* OX=44689 GN=eif3C PE=3 SV=1
Q76P24	-2,24888875	0,0770	NSC	HD protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=htt PE=3 SV=1
P54661	-2,261812626	0,0899	NSC	Small aggregate formation protein OS=*Dictyostelium discoideum* OX=44689 GN=smlA PE=2 SV=2

Q54J42	-2,279470445	0,0528	NSC	Dolichyl-phosphate beta-glucosyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=alg5 PE=2 SV=1
Q9U641	-2,292260176	0,0006	SC	Conditioned medium factor receptor 1 OS=*Dictyostelium discoideum* OX=44689 GN=cmfB PE=1 SV=1
Q555C8	-2,300128393	0,0517	NSC	Monothiol glutaredoxin-5, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=grx5 PE=3 SV=1
Q54DF7	-2,314126697	0,0081	C	Probable serine/threonine-protein kinase DDB_G0292354 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292354 PE=3 SV=1
Q54I92	-2,327482111	0,0182	C	Protein psiI OS=*Dictyostelium discoideum* OX=44689 GN=psiI PE=3 SV=1
Q55GW4	-2,328489191	0,0476	NSC	Putative uncharacterized protein DDB_G0267482 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267482 PE=4 SV=1
Q9U9R7	-2,332111395	0,0246	C	Gamma-soluble NSF attachment protein OS=*Dictyostelium discoideum* OX=44689 GN=snpC PE=1 SV=1
Q54I90	-2,353268587	0,0073	C	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufv1 PE=2 SV=1
P34045	-2,362386854	0,0089	C	Guanine nucleotide-binding protein alpha-7 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaG PE=2 SV=3
P34140	-2,375326341	0,0008	SC	Ras-related protein Rab-1B OS=*Dictyostelium discoideum* OX=44689 GN=rab1B PE=2 SV=2
P0C7W5	-2,383110996	0,0258	C	Uncharacterized protein DDB_G0281707 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0281707 PE=4 SV=1
Q54XD8	-2,387099556	0,0067	SC	Eukaryotic translation initiation factor 2 subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=eif2s3 PE=2 SV=1
Q54KM7	-2,394449613	0,0331	C	Glycine dehydrogenase (decarboxylating), mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcvP PE=3 SV=1
P08796	-2,4008131	0,0195	C	Contact site A protein OS=*Dictyostelium discoideum* OX=44689 GN=csaA PE=1 SV=3
Q1ZXH9	-2,407016035	0,0276	SC	Probable lanosterol 14-alpha demethylase OS=*Dictyostelium discoideum* OX=44689 GN=cyp51 PE=3 SV=1
Q55FK2	-2,419937187	0,0085	SC	Ras-related protein Rab-6 OS=*Dictyostelium discoideum* OX=44689 GN=rab6 PE=3 SV=1
Q54QE4	-2,445442845	0,0024	SC	Bifunctional purine synthesis protein purC/E OS=*Dictyostelium discoideum* OX=44689 GN=purC/E PE=1 SV=1
Q9BMX0	-2,458510563	0,0877	NSC	Eukaryotic peptide chain release factor subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=erf1 PE=2 SV=2
O21049	-2,52472055	0,0201	C	Cytochrome c oxidase subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=cox3 PE=3 SV=1
Q9U1M8	-2,534916642	0,0582	NSC	Myosin-I heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=myoI PE=1 SV=1
P16894	-2,561760293	0,0023	SC	Guanine nucleotide-binding protein alpha-1 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaA PE=2 SV=1
Q54I48	-2,609376845	0,0204	C	Choline transporter-like protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=slc44a2 PE=3 SV=1
Q55GM5	-2,724268381	0,0003	C	rRNA-processing protein FCF1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=fcf1 PE=3 SV=1

Q559Z4	-2,737450903	0,0301	SC	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=ndufa5 PE=3 SV=1
Q54EX7	-2,748455348	0,0113	C	Glutaredoxin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=grxB PE=3 SV=1
Q55CT1	-2,758454583	0,0422	NSC	NADPH--cytochrome P450 reductase OS=*Dictyostelium discoideum* OX=44689 GN=redB PE=2 SV=1
Q54EW8	-2,877979571	0,0010	SC	Dihydrolipoyl dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=lpd PE=3 SV=1
Q54JH4	-2,925059356	0,0077	C	P2X receptor E OS=*Dictyostelium discoideum* OX=44689 GN=p2xE PE=3 SV=2
Q54KE6	-2,949742125	0,0011	SC	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mccA PE=3 SV=1
P36409	-2,975736144	0,0002	SC	Ras-related protein Rab-2A OS=*Dictyostelium discoideum* OX=44689 GN=rab2A PE=2 SV=2
Q54PV7	-2,981596706	0,0026	C	Eukaryotic translation initiation factor 2A OS=*Dictyostelium discoideum* OX=44689 GN=eif2a PE=3 SV=1
Q55FI4	-3,011654112	0,0024	SC	Nucleolar protein 58 OS=*Dictyostelium discoideum* OX=44689 GN=nop58 PE=3 SV=1
Q54WA4	-3,03161703	0,0061	C	Probable 28S ribosomal protein S10, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps10 PE=3 SV=1
Q54KB8	-3,050080138	0,1106	NSC	Probable glutamate--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=gluS PE=2 SV=1
Q54UU8	-3,050246157	0,0223	C	Thioredoxin reductase OS=*Dictyostelium discoideum* OX=44689 GN=trrA PE=3 SV=1
Q86JP3	-3,058451767	0,0012	SC	Ras-related protein Rab-5A OS=*Dictyostelium discoideum* OX=44689 GN=rab5A PE=3 SV=1
Q55GT5	-3,101515172	0,0036	C	Translocon-associated protein subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=ssr3 PE=3 SV=1
Q54HS9	-3,122984219	0,0046	C	AP-1 complex subunit mu OS=*Dictyostelium discoideum* OX=44689 GN=apm1 PE=1 SV=1
Q54H97	-3,146175319	0,0059	C	CBS domain-containing protein DDB_G0289609 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289609 PE=2 SV=1
Q86B20	-3,188270858	0,0123	C	Eukaryotic translation initiation factor 3 subunit A OS=*Dictyostelium discoideum* OX=44689 GN=eif3A PE=1 SV=1
P34036	-3,195275839	0,0019	SC	Dynein heavy chain, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=dhcA PE=1 SV=2
Q54J97	-3,206592575	0,0011	SC	60 kDa heat shock protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=hspA PE=2 SV=1
Q54BU4	-3,247012552	0,0447	NSC	ABC transporter B family member 1 OS=*Dictyostelium discoideum* OX=44689 GN=abcB1 PE=3 SV=1
Q555H8	-3,260364775	0,0076	C	E3 ubiquitin-protein ligase listerin OS=*Dictyostelium discoideum* OX=44689 GN=rnf160 PE=3 SV=1
Q55FN7	-3,265532139	0,0082	C	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=bkdB PE=3 SV=1
Q54HJ2	-3,27661052	0,0156	C	Pescadillo homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289415 PE=3 SV=1
Q54T02	-3,298158023	0,0019	C	ABC transporter G family member 24 OS=*Dictyostelium discoideum* OX=44689 GN=abcG24 PE=3 SV=1

O97470	-3,30624032	0,0009	SC	Mitochondrial substrate carrier family protein ancA OS=*Dictyostelium discoideum* OX=44689 GN=ancA PE=1 SV=1
Q54LT7	-3,312909255	0,0664	NSC	Probable cytochrome P450 519E1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp519E1 PE=3 SV=1
Q54ML4	-3,426523184	0,0048	C	HEAT repeat-containing protein 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=heatr1 PE=3 SV=1
Q55CE0	-3,502488676	0,0336	C	Probable serine/threonine-protein kinase mkcF OS=*Dictyostelium discoideum* OX=44689 GN=mkcF PE=3 SV=1
Q769F9	-3,518960673	0,0037	SC	Transmembrane emp24 domain-containing protein A OS=*Dictyostelium discoideum* OX=44689 GN=empA PE=3 SV=1
P18142	-3,588180437	0,0028	SC	cAMP-regulated D2 protein OS=*Dictyostelium discoideum* OX=44689 GN=D2 PE=2 SV=3
Q7YXD4	-3,648654404	0,0118	C	Protein P80 OS=*Dictyostelium discoideum* OX=44689 GN=p80 PE=2 SV=1
Q55FP0	-3,656192171	0,0002	SC	Putative phagocytic receptor 1a OS=*Dictyostelium discoideum* OX=44689 GN=phg1a PE=2 SV=1
Q54PP1	-3,690619514	0,0004	SC	Delta(14)-sterol reductase OS=*Dictyostelium discoideum* OX=44689 GN=erg24 PE=3 SV=1
Q54XK2	-3,781922095	0,0008	SC	Protein transport protein Sec61 subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=sec61a PE=3 SV=1
Q55EJ3	-3,792556307	0,0002	C	RNA cytidine acetyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=nat10 PE=3 SV=1
P32073	-3,995074643	0,0022	C	GMP synthase [glutamine-hydrolyzing] OS=*Dictyostelium discoideum* OX=44689 GN=guaA PE=1 SV=2
Q1ZXD6	-4,010792447	0,0363	C	Probable serine/threonine-protein kinase roco5 OS=*Dictyostelium discoideum* OX=44689 GN=roco5 PE=3 SV=1
Q54EX5	-4,086432757	0,0422	NSC	Serine palmitoyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=sptB PE=1 SV=1
Q869Q3	-4,097251827	0,0423	NSC	Nck-associated protein 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=napA PE=1 SV=1
O21042	-4,169176882	0,0027	C	Cytochrome c oxidase subunit 1+2 OS=*Dictyostelium discoideum* OX=44689 GN=cox1/2 PE=2 SV=1
Q86JM5	-4,176819407	0,0004	C	Putative elongation of fatty acids protein DDB_G0272012 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272012 PE=3 SV=1
A0A0F6AYZ4	-4,2311936	0,0795	NSC	Outer membrane protein X OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=ompX PE=4 SV=1
Q54EW2	-4,402672609	0,0032	SC	Putative bifunctional amine oxidase DDB_G0291301 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0291301 PE=1 SV=1
B0G159	-4,477067023	0,0442	NSC	Mitochondrial substrate carrier family protein C OS=*Dictyostelium discoideum* OX=44689 GN=mcfC PE=2 SV=1
Q54RR5	-4,54447498	0,0011	C	Probable short/branched chain specific acyl-CoA dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=acadsb PE=3 SV=1
Q55DW4	-4,585726608	0,0045	C	ABC transporter G family member 1 OS=*Dictyostelium discoideum* OX=44689 GN=abcG1 PE=3 SV=1
P54679	-4,803059671	0,0004	C	Probable plasma membrane ATPase OS=*Dictyostelium discoideum* OX=44689 GN=patB PE=2 SV=2
O76173	-4,830591906	0,0002	C	Ras-related protein Rab-1C OS=*Dictyostelium discoideum* OX=44689 GN=Rab1C PE=2 SV=1

Q54VT4	-4,986670446	0,0307	C	Probable ATP-dependent RNA helicase ddx47 OS=*Dictyostelium discoideum* OX=44689 GN=ddx47 PE=3 SV=1
Q54P13	-4,991222827	0,0017	C	ABC transporter C family member 8 OS=*Dictyostelium discoideum* OX=44689 GN=abcC8 PE=3 SV=1
Q54NM9	-4,993731591	0,0056	SC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 OS=*Dictyostelium discoideum* OX=44689 GN=stt3 PE=3 SV=1
Q9XYS3	-5,052926757	0,0179	C	Superoxide-generating NADPH oxidase heavy chain subunit A OS=*Dictyostelium discoideum* OX=44689 GN=noxA PE=2 SV=1
P54678	-5,147342989	0,0002	SC	Calcium-transporting ATPase PAT1 OS=*Dictyostelium discoideum* OX=44689 GN=patA PE=2 SV=2
Q7YTA6	-5,147906905	0,0015	C	Putative phagocytic receptor 1c OS=*Dictyostelium discoideum* OX=44689 GN=phg1c PE=2 SV=1
Q9NGP5	-5,180260353	0,0053	C	ABC transporter G family member 2 OS=*Dictyostelium discoideum* OX=44689 GN=abcG2 PE=1 SV=2
Q54CE4	-5,557684086	0,0460	NSC	Probable isoleucine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mileS PE=3 SV=1
Q54RV9	-5,618671607	0,0051	C	Sphingosine-1-phosphate lyase OS=*Dictyostelium discoideum* OX=44689 GN=sglA PE=2 SV=1
P34042	-5,692104954	0,0016	SC	Guanine nucleotide-binding protein alpha-4 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaD PE=1 SV=1
Q54KD0	-5,716589178	0,0113	C	TPR repeat-containing protein DDB_G0287407 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0287407 PE=4 SV=1
P25870	-5,732618045	0,0004	C	Clathrin heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=chcA PE=1 SV=1
Q55AW9	-6,026789427	0,0138	SC	Phosphatidylinositide phosphatase SAC1 OS=*Dictyostelium discoideum* OX=44689 GN=sac1 PE=3 SV=1
Q54QW1	-6,130036011	0,0001	SC	Eukaryotic translation initiation factor 3 subunit B OS=*Dictyostelium discoideum* OX=44689 GN=eif3B PE=3 SV=2
Q55DA0	-6,155015745	0,0007	C	ABC transporter G family member 22 OS=*Dictyostelium discoideum* OX=44689 GN=abcG22 PE=2 SV=1
P34109	-6,185778837	0,0057	C	Myosin ID heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=myoD PE=1 SV=2
Q03479	-6,34465177	0,0017	C	Myosin IE heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=myoE PE=1 SV=2
Q34312	-6,417482917	0,0004	C	NADH-ubiquinone oxidoreductase 75 kDa subunit OS=*Dictyostelium discoideum* OX=44689 GN=nad11 PE=3 SV=1
P20054	-6,861523612	0,0001	SC	Protein PYR1-3 OS=*Dictyostelium discoideum* OX=44689 GN=pyr1-3 PE=1 SV=3
A0A0F6B3Z7	-7,034795233	0,0025	C	Outer membrane porin protein C OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=ompC PE=3 SV=1
Q9XPJ9	-7,18937353	0,0000	SC	ATP synthase subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp1 PE=1 SV=1
Q55CA0	-7,221890676	0,0000	SC	Vacuolar protein sorting-associated protein 26 OS=*Dictyostelium discoideum* OX=44689 GN=vps26 PE=2 SV=1
Q54BT3	-7,984933347	0,0005	C	ABC transporter B family member 2 OS=*Dictyostelium discoideum* OX=44689 GN=abcB2 PE=3 SV=1
Q8T690	-8,293658272	0,0084	C	ABC transporter G family member 3 OS=*Dictyostelium discoideum* OX=44689 GN=abcG3 PE=3 SV=1

P16051	-8,505975577	0,0029	SC	Guanine nucleotide-binding protein alpha-2 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaB PE=1 SV=3
Q54ET6	-8,587627851	0,0551	NSC	Actin-binding protein F OS=*Dictyostelium discoideum* OX=44689 GN=abpF PE=1 SV=1
Q869N9	-10,53911162	0,0008	C	Eukaryotic translation initiation factor 2 subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=eif2s1 PE=1 SV=1
Q54VJ0	-19,18920781	0,0003	C	ABC transporter C family member 2 OS=*Dictyostelium discoideum* OX=44689 GN=abcC2 PE=3 SV=1

Supplementary Table 5 – Proteins present only in Δ*sifA*-infected samples

Locus ID	Description
Q55EU6	Putative actin-23 OS=*Dictyostelium discoideum* OX=44689 GN=act23 PE=1 SV=1
P42526	Hisactophilin-2 OS=*Dictyostelium discoideum* OX=44689 GN=hatB PE=1 SV=2
Q6TMJ9	Synaptobrevin-A OS=*Dictyostelium discoideum* OX=44689 GN=sybA PE=2 SV=1
P07828	Actin-18 OS=*Dictyostelium discoideum* OX=44689 GN=act18 PE=3 SV=3
Q54BN4	40S ribosomal protein S21 OS=*Dictyostelium discoideum* OX=44689 GN=rps21 PE=3 SV=1
Q54LW6	Uncharacterized protein DDB_G0286463 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286463 PE=4 SV=1
A0A0F6BB72	Putative cytoplasmic protein OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=yjiX PE=4 SV=1
Q95ZG8	Guanine nucleotide-binding protein subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=gpgA PE=1 SV=1
Q55DU1	Actobindin-B/C OS=*Dictyostelium discoideum* OX=44689 GN=abnB PE=3 SV=1
Q54HE9	Putative actin-27 OS=*Dictyostelium discoideum* OX=44689 GN=act27 PE=3 SV=2
Q54D06	Probable ubiquitin-conjugating enzyme E2 variant OS=*Dictyostelium discoideum* OX=44689 GN=ube2v PE=3 SV=1
Q54WY5	Ribosomal RNA processing protein 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=rrp1 PE=3 SV=1
Q86HB8	Counting factor-associated protein C OS=*Dictyostelium discoideum* OX=44689 GN=cfaC PE=3 SV=1
Q54LX0	Calcium-binding protein M OS=*Dictyostelium discoideum* OX=44689 GN=cbpM PE=1 SV=1
Q1ZXQ1	Fumarylacetoacetase OS=*Dictyostelium discoideum* OX=44689 GN=fah PE=3 SV=1
P54658	32 kDa heat shock protein OS=*Dictyostelium discoideum* OX=44689 GN=hspC PE=2 SV=1
Q54JM3	NEDD8-activating enzyme E1 regulatory subunit OS=*Dictyostelium discoideum* OX=44689 GN=nae1 PE=3 SV=1
Q558Y7	Protein costars OS=*Dictyostelium discoideum* OX=44689 GN=cosA PE=2 SV=1
Q54B20	Succinate dehydrogenase assembly factor 2, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0293946 PE=3 SV=1
Q54K33	RING-box protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=rbx1 PE=3 SV=1
Q54YX3	CRAL-TRIO domain-containing protein DDB_G0278031 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0278031 PE=4 SV=2
Q553W9	Ceroid-lipofuscinosis neuronal protein 5 homolog OS=*Dictyostelium discoideum* OX=44689 GN=cln5 PE=3 SV=1
Q54I79	Centractin OS=*Dictyostelium discoideum* OX=44689 GN=arpA PE=1 SV=1
Q54VI4	Putative glutathione S-transferase alpha-3 OS=*Dictyostelium discoideum* OX=44689 GN=gsta3 PE=1 SV=1
Q553E8	RNA transcription, translation and transport factor protein OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275847 PE=2 SV=1
Q54TF6	Probable U6 snRNA-associated Sm-like protein LSm2 OS=*Dictyostelium discoideum* OX=44689 GN=lsm2 PE=3 SV=1
Q54PB8	Putative uncharacterized protein DDB_G0284711 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284711 PE=4 SV=1
Q54U86	Peroxisome biogenesis factor 3 OS=*Dictyostelium discoideum* OX=44689 GN=pex3 PE=3 SV=1
Q54GP8	Glutaredoxin OS=*Dictyostelium discoideum* OX=44689 GN=grxA PE=2 SV=1
Q54XP2	Small nuclear ribonucleoprotein F OS=*Dictyostelium discoideum* OX=44689 GN=snrpf PE=3 SV=1
Q86HT3	BolA-like protein DDB_G0274439 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274439 PE=3 SV=1
Q86IZ3	Ubiquitin-conjugating enzyme E2 pex4 OS=*Dictyostelium discoideum* OX=44689 GN=pex4 PE=3 SV=1
Q54QX0	Calcium-binding protein B OS=*Dictyostelium discoideum* OX=44689 GN=cbpB PE=4 SV=1

Q54HF6	Probable U6 snRNA-associated Sm-like protein LSm7 OS=*Dictyostelium discoideum* OX=44689 GN=lsm7 PE=3 SV=1
Q55E83	NIF3-like protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=nif3 PE=2 SV=1
Q556L1	Signal recognition particle 14 kDa protein OS=*Dictyostelium discoideum* OX=44689 GN=srp14-1 PE=3 SV=1
Q55AB6	DNA-directed RNA polymerases I, II, and III subunit rpabc5 OS=*Dictyostelium discoideum* OX=44689 GN=polr2l PE=3 SV=1
Q54RX0	Probable small nuclear ribonucleoprotein G OS=*Dictyostelium discoideum* OX=44689 GN=snrpG PE=3 SV=1
Q55DP8	Aminoacylase-1 OS=*Dictyostelium discoideum* OX=44689 GN=acy1 PE=2 SV=1
Q55FM0	ER membrane protein complex subunit 8/9 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268048 PE=3 SV=1
Q550G0	Peroxisome biogenesis factor 16 OS=*Dictyostelium discoideum* OX=44689 GN=pex16 PE=3 SV=1
Q54KI0	Eukaryotic translation initiation factor 3 subunit J OS=*Dictyostelium discoideum* OX=44689 GN=eif3J PE=3 SV=1
Q54DF9	Uroporphyrinogen decarboxylase OS=*Dictyostelium discoideum* OX=44689 GN=hemE PE=1 SV=1
Q557G3	Trafficking protein particle complex subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=trappc1-1 PE=3 SV=1
Q54P14	COMM domain-containing protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=commd2 PE=4 SV=1
Q55F34	3'(2'),5'-bisphosphate nucleotidase OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268652 PE=3 SV=1
Q86CR6	Ubiquitin-like protein atg12 OS=*Dictyostelium discoideum* OX=44689 GN=atg12 PE=3 SV=1
Q86KL1	Probable E3 ubiquitin-protein ligase bre1 OS=*Dictyostelium discoideum* OX=44689 GN=bre1 PE=3 SV=1
Q54GK9	Charged multivesicular body protein 2a homolog 1 OS=*Dictyostelium discoideum* OX=44689 GN=chmp2a1 PE=3 SV=2
Q556Z0	SWI/SNF complex component SNF12 homolog OS=*Dictyostelium discoideum* OX=44689 GN=snf12-1 PE=3 SV=1
Q54BC8	Proteasome subunit beta type-5 OS=*Dictyostelium discoideum* OX=44689 GN=psmB5 PE=1 SV=1
Q55C77	GDP-L-fucose synthase OS=*Dictyostelium discoideum* OX=44689 GN=ger PE=3 SV=1
Q55GN3	Probable prefoldin subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=pfdn2 PE=3 SV=1
Q54GT9	Autophagy protein 5 OS=*Dictyostelium discoideum* OX=44689 GN=atg5 PE=3 SV=1
Q86HS0	Probable ubiquinone biosynthesis protein coq9, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=coq9 PE=3 SV=2
Q54DQ8	Uncharacterized transmembrane protein DDB_G0292078 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292078 PE=4 SV=1
Q54N50	Dynactin subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=dynB PE=3 SV=1
Q54NZ7	Aldose reductase B OS=*Dictyostelium discoideum* OX=44689 GN=alrB PE=3 SV=2
Q8T293	Probable di-N-acetylchitobiase 2 OS=*Dictyostelium discoideum* OX=44689 GN=ctbs2 PE=3 SV=1
Q55BD5	COP9 signalosome complex subunit 7 OS=*Dictyostelium discoideum* OX=44689 GN=csn7 PE=1 SV=1
Q55CK2	Mental retardation GTPase activating protein homolog 2 OS=*Dictyostelium discoideum* OX=44689 GN=mgp2 PE=3 SV=1
Q54MR1	Hydroxyacylglutathione hydrolase OS=*Dictyostelium discoideum* OX=44689 GN=hagh PE=3 SV=1
Q54D73	Flavohemoprotein B OS=*Dictyostelium discoideum* OX=44689 GN=fhbB PE=1 SV=1
Q54TH4	Golgi to ER traffic protein 4 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0281815 PE=3 SV=1
Q550A8	Autophagy-related protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=atg3 PE=3 SV=3
Q54I82	Probable cytidine deaminase OS=*Dictyostelium discoideum* OX=44689 GN=cda PE=3 SV=1
Q54VB3	5-demethoxyubiquinone hydroxylase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=coq7 PE=2 SV=1
Q9NGP4	Sumo-conjugating enzyme ubc9 OS=*Dictyostelium discoideum* OX=44689 GN=ubc9 PE=3 SV=1

Q55FK4	Acyl-protein thioesterase 1 homolog 2 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268064 PE=1 SV=1
Q556N5	Proteasomal ubiquitin receptor ADRM1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=adrm1-1 PE=1 SV=1
Q55GU4	Probable mitochondrial pyruvate carrier 1 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267508 PE=3 SV=2
Q54RS2	Uncharacterized protein DDB_G0282957 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282957 PE=4 SV=1
Q54DA8	Protein STIP1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=sti1 PE=3 SV=1
Q54E53	COP9 signalosome complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=csn3 PE=1 SV=1
Q23919	Phosphoglucomutase-1 OS=*Dictyostelium discoideum* OX=44689 GN=pgmA PE=2 SV=1
Q55GN6	Probable phosphatidylinositol phosphate kinase DDB_G0267588 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267588 PE=1 SV=1
Q6RZZ9	Kinesin-related protein 13 OS=*Dictyostelium discoideum* OX=44689 GN=kif13 PE=1 SV=1
Q54X03	Phosphomannomutase 1 OS=*Dictyostelium discoideum* OX=44689 GN=pmmA PE=3 SV=1
Q967U1	Proteasome activator 28 OS=*Dictyostelium discoideum* OX=44689 GN=psmE3 PE=1 SV=1
Q55CQ7	Transportin OS=*Dictyostelium discoideum* OX=44689 GN=tnpo PE=3 SV=1
Q54Q05	Elongin-C OS=*Dictyostelium discoideum* OX=44689 GN=tceb1 PE=3 SV=1
Q54HL6	COP9 signalosome complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=csn2 PE=1 SV=1
Q54ZB3	Conserved oligomeric Golgi complex subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=cog1 PE=3 SV=1
Q54XJ0	MOB kinase activator-like 1 homolog A OS=*Dictyostelium discoideum* OX=44689 GN=mobA PE=3 SV=1
Q8T662	ATPase ASNA1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=arsA PE=1 SV=1
Q86G47	Ras guanine nucleotide exchange factor Q OS=*Dictyostelium discoideum* OX=44689 GN=gefQ PE=2 SV=1
Q54KR1	Cysteine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=cysS PE=3 SV=1
Q54D10	Protein RER1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=rer1 PE=3 SV=1
Q55E13	Zinc finger protein ZPR1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=zpr1 PE=3 SV=1
Q54EH2	DNA-directed RNA polymerases I, II, and III subunit rpabc1 OS=*Dictyostelium discoideum* OX=44689 GN=polr2e PE=3 SV=2
Q54QK4	COMM domain-containing protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=commd3 PE=4 SV=1
Q54ES8	Putative synaptobrevin homolog YKT6 OS=*Dictyostelium discoideum* OX=44689 GN=ykt6 PE=1 SV=1
Q552E2	WASH complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=washc2 PE=1 SV=1
Q75JP5	Calponin homology domain-containing protein DDB_G0272472 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272472 PE=4 SV=1
Q54RE8	Kynurenine 3-monooxygenase OS=*Dictyostelium discoideum* OX=44689 GN=kmo PE=3 SV=1
Q54KT7	General transcription factor IIF subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=gtf2f2 PE=3 SV=2
Q54XD0	Ubiquinone biosynthesis O-methyltransferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=coq3 PE=3 SV=1
Q55GC7	Sphingomyelinase phosphodiesterase D OS=*Dictyostelium discoideum* OX=44689 GN=sgmD PE=3 SV=1
Q54T40	Uncharacterized protein DDB_G0282021 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282021 PE=4 SV=1
Q54NV1	Exocyst complex component 1 OS=*Dictyostelium discoideum* OX=44689 GN=exoc1 PE=3 SV=1
Q76NT6	Dolichol-phosphate mannosyltransferase subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=dpm3 PE=3 SV=1
Q556G4	Deoxyhypusine hydroxylase OS=*Dictyostelium discoideum* OX=44689 GN=dohh-1 PE=3 SV=1
Q54C92	COP9 signalosome complex subunit 6 OS=*Dictyostelium discoideum* OX=44689 GN=csn6 PE=1 SV=1

P34122	cAMP-binding protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=capB PE=1 SV=2
Q54P93	Porphobilinogen deaminase OS=*Dictyostelium discoideum* OX=44689 GN=hemC PE=3 SV=1
Q55BF5	Splicing factor 3B subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=sf3b5 PE=3 SV=1
Q54CS6	Protein dcd1B OS=*Dictyostelium discoideum* OX=44689 GN=dcd1B PE=2 SV=1
Q54N41	Pre-mRNA-splicing factor ISY1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=isy1 PE=3 SV=1
Q54CV3	Coiled-coil domain-containing protein 93 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292680 PE=3 SV=1
Q7M438	Ribonuclease DdI OS=*Dictyostelium discoideum* OX=44689 GN=ddiA PE=1 SV=3
Q55FE3	Protein FAM45 homolog OS=*Dictyostelium discoideum* OX=44689 GN=fam45 PE=3 SV=1
Q55FT5	Conserved oligomeric Golgi complex subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=cog4 PE=3 SV=1
Q54LV0	Structural maintenance of chromosomes protein 4 OS=*Dictyostelium discoideum* OX=44689 GN=smc4 PE=3 SV=1
Q556I2	Probable 2-aminoethanethiol dioxygenase OS=*Dictyostelium discoideum* OX=44689 GN=ado-1 PE=4 SV=2
P20425	UMP-CMP kinase OS=*Dictyostelium discoideum* OX=44689 GN=pyrK PE=1 SV=2
Q54TD7	ATP-dependent RNA helicase ddx24 OS=*Dictyostelium discoideum* OX=44689 GN=ddx24 PE=3 SV=1
Q86IL5	Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=ppp4r2 PE=3 SV=2
Q54T58	LYR motif-containing protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=lyrm1 PE=3 SV=1
Q54QS0	E3 UFM1-protein ligase 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283667 PE=3 SV=1
Q54YQ9	Diphosphomevalonate decarboxylase OS=*Dictyostelium discoideum* OX=44689 GN=mvd PE=3 SV=1
Q54V55	Probable prefoldin subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=pfdn5 PE=3 SV=1
Q54C55	Peroxisomal membrane protein PEX14 OS=*Dictyostelium discoideum* OX=44689 GN=pex14 PE=3 SV=1
Q86JM3	DNA-directed RNA polymerase III subunit rpc6 OS=*Dictyostelium discoideum* OX=44689 GN=polr3f PE=3 SV=1
Q54JK4	Charged multivesicular body protein 5 OS=*Dictyostelium discoideum* OX=44689 GN=chmp5 PE=3 SV=1
Q86JE1	Recoverin family protein DDB_G0272130 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272130 PE=1 SV=1
Q54HX6	Myb-like protein I OS=*Dictyostelium discoideum* OX=44689 GN=mybI PE=3 SV=1
Q54EH1	Epsin OS=*Dictyostelium discoideum* OX=44689 GN=epnA PE=3 SV=1
Q552R1	DDB1- and CUL4-associated factor 7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=wdr68 PE=3 SV=2
Q54NA0	Nuclear pore complex protein nup85 OS=*Dictyostelium discoideum* OX=44689 GN=nup85 PE=3 SV=1
Q54K78	Putative uncharacterized protein DDB_G0287573 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0287573 PE=4 SV=2
Q54BM5	Branchpoint-bridging protein OS=*Dictyostelium discoideum* OX=44689 GN=sf1 PE=3 SV=1
Q54CK9	WAS protein family homolog DDB_G0292878 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292878 PE=1 SV=1
Q7KWX2	Probable CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=pgs1 PE=3 SV=1
Q54XC1	Cytosolic purine 5'-nucleotidase OS=*Dictyostelium discoideum* OX=44689 GN=nt5c2 PE=3 SV=1
Q9U7C9	Nucleomorphin OS=*Dictyostelium discoideum* OX=44689 GN=numA PE=1 SV=2
Q550D2	Phenylalanine--tRNA ligase beta subunit OS=*Dictyostelium discoideum* OX=44689 GN=phesB PE=3 SV=2
Q75K24	COP9 signalosome complex subunit 8 OS=*Dictyostelium discoideum* OX=44689 GN=csn8 PE=1 SV=1
Q54LA1	Eukaryotic translation initiation factor 5 OS=*Dictyostelium discoideum* OX=44689 GN=eif5 PE=3 SV=1

Q54LT4	Uncharacterized protein DDB_G0286423 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286423 PE=4 SV=1
Q54XS1	Phenylalanine-4-hydroxylase OS=*Dictyostelium discoideum* OX=44689 GN=pah PE=1 SV=1
Q9XPI8	Ribosomal protein S4, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps4 PE=3 SV=1
Q55D99	Serine/threonine-protein kinase pakA OS=*Dictyostelium discoideum* OX=44689 GN=pakA PE=1 SV=1
Q54IA7	Oxygen-dependent coproporphyrinogen-III oxidase OS=*Dictyostelium discoideum* OX=44689 GN=cpox PE=3 SV=1
Q54YY1	Protein SCAI homolog OS=*Dictyostelium discoideum* OX=44689 GN=scai PE=3 SV=1
Q553X3	Rho GTPase-activating protein gacI OS=*Dictyostelium discoideum* OX=44689 GN=gacI PE=3 SV=1
B0G0Y8	cGMP-specific 3',5'-cGMP phosphodiesterase 3 OS=*Dictyostelium discoideum* OX=44689 GN=pde3 PE=1 SV=1
Q8T197	Dehydrogenase/reductase SDR family protein 7-like OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274201 PE=3 SV=1
Q8IS18	Ras guanine nucleotide exchange factor E OS=*Dictyostelium discoideum* OX=44689 GN=gefE PE=2 SV=1
Q54BA2	Ankyrin repeat, bromo and BTB domain-containing protein DDB_G0293800 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0293800 PE=4 SV=1
Q54N83	Leucine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=leuS PE=3 SV=1
Q8T2I8	Serine/threonine-protein kinase sepA OS=*Dictyostelium discoideum* OX=44689 GN=sepA PE=2 SV=1
O77033	General transcriptional corepressor trfA OS=*Dictyostelium discoideum* OX=44689 GN=trfA PE=2 SV=1
Q54K96	Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66 OS=*Dictyostelium discoideum* OX=44689 GN=jcdg PE=3 SV=1
Q54IK9	Protein hook homolog OS=*Dictyostelium discoideum* OX=44689 GN=hook PE=3 SV=1
Q7KWN2	Probable cytochrome P450 525A1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp525A1 PE=3 SV=1
O60950	Golvesin OS=*Dictyostelium discoideum* OX=44689 GN=gol PE=1 SV=1
Q55CV0	NAD(P)H-hydrate epimerase OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0269890 PE=3 SV=1
Q54WZ0	Cell division cycle 5-like protein OS=*Dictyostelium discoideum* OX=44689 GN=cdc5l PE=3 SV=1
Q54QD9	Cathepsin B OS=*Dictyostelium discoideum* OX=44689 GN=ctsB PE=3 SV=1
Q54RJ4	Probable serine/threonine-protein kinase iksA OS=*Dictyostelium discoideum* OX=44689 GN=iksA PE=3 SV=1
Q55BM5	DNA primase large subunit OS=*Dictyostelium discoideum* OX=44689 GN=prim2 PE=3 SV=1
Q54CD6	Probable ATP-dependent RNA helicase ddx5 OS=*Dictyostelium discoideum* OX=44689 GN=ddx5 PE=3 SV=1
Q54RV3	Serine/threonine-protein kinase pakG OS=*Dictyostelium discoideum* OX=44689 GN=pakG PE=3 SV=1
Q54J86	Dictomallein-1 OS=*Dictyostelium discoideum* OX=44689 GN=dtmlA PE=3 SV=1
Q54GZ0	O-methyltransferase 9 OS=*Dictyostelium discoideum* OX=44689 GN=omt9 PE=3 SV=1
Q54B82	COP9 signalosome complex subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=csn4 PE=2 SV=1
Q55AR8	U5 small nuclear ribonucleoprotein 40 kDa protein OS=*Dictyostelium discoideum* OX=44689 GN=snrnp40 PE=3 SV=1
Q55G31	Expansin-like protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=expl1 PE=2 SV=1
B0G163	Exocyst complex component 5 OS=*Dictyostelium discoideum* OX=44689 GN=exoc5 PE=3 SV=1
P14325	Probable glutamine--tRNA ligase OS=*Dictyostelium discoideum* OX=44689 GN=glnS PE=2 SV=2
Q54J37	Striatin homolog OS=*Dictyostelium discoideum* OX=44689 GN=strn PE=3 SV=1
Q54P76	Exocyst complex component 4 OS=*Dictyostelium discoideum* OX=44689 GN=exoc4 PE=3 SV=1
Q54DY7	Serine carboxypeptidase S10 family member 1 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0291912 PE=3 SV=1

Q54K00	Aromatic amino acid aminotransferase DDB_G0287711 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0287711 PE=3 SV=1
Q86JE5	ER lumen protein-retaining receptor OS=*Dictyostelium discoideum* OX=44689 GN=kdelr PE=3 SV=1
Q54Z23	Integrator complex subunit 6 homolog OS=*Dictyostelium discoideum* OX=44689 GN=ints6 PE=3 SV=2
Q55GI5	L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=l2hgdh PE=3 SV=1
P42525	Extracellular signal-regulated kinase 1 OS=*Dictyostelium discoideum* OX=44689 GN=erkA PE=2 SV=2
Q555I8	Kinesin-related protein 9 OS=*Dictyostelium discoideum* OX=44689 GN=kif9 PE=2 SV=1
Q54TC3	Probable inactive serine/threonine-protein kinase slob1 OS=*Dictyostelium discoideum* OX=44689 GN=slob1 PE=3 SV=1
Q1ZXD9	Sphingomyelinase DDB_G0288017 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288017 PE=3 SV=1
Q54N40	Putative peroxisome assembly protein 12 OS=*Dictyostelium discoideum* OX=44689 GN=pex12 PE=3 SV=1
Q8T133	Protein tortoise OS=*Dictyostelium discoideum* OX=44689 GN=torA PE=2 SV=1
Q54G05	Putative leucine-rich repeat-containing protein DDB_G0290503 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0290503 PE=4 SV=1
Q54MV3	Rho GTPase-activating protein gacJ OS=*Dictyostelium discoideum* OX=44689 GN=gacJ PE=3 SV=1
Q54C64	Probable N-acetylglucosaminyl-phosphatidylinositol de-N-acetylase OS=*Dictyostelium discoideum* OX=44689 GN=pigl PE=3 SV=1
Q54IL2	Striatin-interacting protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=fam40 PE=3 SV=1
Q1ZXI2	CCR4-NOT transcription complex subunit 11 OS=*Dictyostelium discoideum* OX=44689 GN=cnot11 PE=3 SV=1
Q75JQ3	Peroxisome biogenesis factor 2 OS=*Dictyostelium discoideum* OX=44689 GN=pex2 PE=3 SV=1
Q9GPT6	Elongator complex protein 6 OS=*Dictyostelium discoideum* OX=44689 GN=elp6 PE=3 SV=1
Q54WH7	Putative uncharacterized protein DDB_G0279653 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0279653 PE=4 SV=1
Q55DV8	Vacuolar protein sorting-associated protein 37 OS=*Dictyostelium discoideum* OX=44689 GN=vps37 PE=3 SV=1
Q54CM0	Palmitoyl-protein thioesterase 3 OS=*Dictyostelium discoideum* OX=44689 GN=ppt3 PE=3 SV=1
Q86AD7	Probable myosin light chain kinase DDB_G0271550 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271550 PE=3 SV=1
Q54IT1	Putative uncharacterized protein DDB_G0288537 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288537 PE=4 SV=1
Q8MML5	Paxillin-B OS=*Dictyostelium discoideum* OX=44689 GN=paxB PE=2 SV=1
Q54NL0	Rho GTPase-activating protein gacT OS=*Dictyostelium discoideum* OX=44689 GN=gacT PE=3 SV=1
Q23917	3',5'-cyclic-nucleotide phosphodiesterase regA OS=*Dictyostelium discoideum* OX=44689 GN=regA PE=1 SV=1
Q54VX5	Exocyst complex component 2 OS=*Dictyostelium discoideum* OX=44689 GN=exoc2 PE=3 SV=1
Q54GC1	Diacylglycerol O-acyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=dgat2 PE=3 SV=1
Q86A12	Probable serine/threonine-protein kinase sky1 OS=*Dictyostelium discoideum* OX=44689 GN=sky1 PE=3 SV=1
Q54M35	Putative lysozyme-like protein OS=*Dictyostelium discoideum* OX=44689 GN=alyL PE=3 SV=2
Q54QB9	Rho GTPase-activating protein gacG OS=*Dictyostelium discoideum* OX=44689 GN=gacG PE=3 SV=1
Q54U61	Protein transport protein SEC24 OS=*Dictyostelium discoideum* OX=44689 GN=sec24 PE=3 SV=1
Q54ER9	Basic-leucine zipper transcription factor B OS=*Dictyostelium discoideum* OX=44689 GN=dimB PE=1 SV=1
Q54PL2	Integrator complex subunit 7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=ints7 PE=3 SV=1
P54201	Ubiquitin carboxyl-terminal hydrolase A OS=*Dictyostelium discoideum* OX=44689 GN=ubpA PE=2 SV=2
Q23924	Coatomer subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=copb PE=2 SV=2

Q55BA2	UPF0522 protein C OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271242 PE=3 SV=1
Q86H43	Alanine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=malaS PE=3 SV=1
Q555L9	Transcription initiation factor TFIID subunit 12 OS=*Dictyostelium discoideum* OX=44689 GN=TAF12 PE=3 SV=2
Q9NIF3	Ubiquilin OS=*Dictyostelium discoideum* OX=44689 GN=ubqln PE=1 SV=1
Q54Y09	tRNA-splicing ligase RtcB homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0278481 PE=3 SV=1
Q54DD0	AMP deaminase OS=*Dictyostelium discoideum* OX=44689 GN=amdA PE=1 SV=1
Q55BR7	Protein raptor homolog OS=*Dictyostelium discoideum* OX=44689 GN=raptor PE=1 SV=1
Q54G43	Dual specificity protein kinase shkE OS=*Dictyostelium discoideum* OX=44689 GN=shkE PE=3 SV=1
Q55BN0	Putative mediator of RNA polymerase II transcription subunit 23 OS=*Dictyostelium discoideum* OX=44689 GN=med23 PE=3 SV=1
Q1ZXE2	PH domain-containing protein DDB_G0287875 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0287875 PE=2 SV=1
Q95ZG4	Spindle pole body component 98 OS=*Dictyostelium discoideum* OX=44689 GN=spc98 PE=1 SV=2
Q54WH5	ELMO domain-containing protein E OS=*Dictyostelium discoideum* OX=44689 GN=elmoE PE=4 SV=1
Q55E98	Probable zinc transporter protein DDB_G0269332 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0269332 PE=3 SV=1
Q54UC9	Kinesin-related protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=kif3 PE=1 SV=1
Q54KG3	Vacuolar protein sorting-associated protein 51 homolog OS=*Dictyostelium discoideum* OX=44689 GN=vps51 PE=3 SV=1
Q54S40	Cyclic GMP-binding protein D OS=*Dictyostelium discoideum* OX=44689 GN=gbpD PE=2 SV=1
Q6S003	Kinesin-related protein 8 OS=*Dictyostelium discoideum* OX=44689 GN=kif8 PE=2 SV=1
Q54MI3	SUN domain-containing protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=sun2 PE=3 SV=1
Q75J96	RapA guanosine triphosphatase-activating protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=rapgap1 PE=2 SV=1
Q54VQ7	Type-2 histone deacetylase 2 OS=*Dictyostelium discoideum* OX=44689 GN=hdaC PE=2 SV=1
Q54XI9	Probable inactive serine/threonine-protein kinase DDB_G0278909 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0278909 PE=4 SV=1

Supplementary Table 6 – Proteins differentially expressed in Δ*sifA*-infected and control samples. Proteins are ordered in descending order according to their Fold change value. Classification is as follows: **SC**: Identifications satisfied both, the automatic fold and statistical criteria. **NSC**: These identifications satisfied the fold criteria but, most likely, this happened by chance. **NC**: These identifications did not meet the fold and P-value criteria. **C**: These identifications were filtered out by the L-stringency and so deserve further experimentation to verify if they are indeed differentially expressed.

Locus ID	Fold Change	P-value	Classification	Description
P54680	4,988785639	0,0020	C	Fimbrin OS=*Dictyostelium discoideum* OX=44689 GN=fimA PE=2 SV=2
Q54K47	4,591217959	0,0364	C	Proliferating cell nuclear antigen OS=*Dictyostelium discoideum* OX=44689 GN=pcna PE=3 SV=1
Q54JP5	4,297947	0,0617	NSC	Probable ornithine aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=oatA PE=3 SV=1
Q54VQ0	3,774825065	0,0034	C	Uncharacterized protein DDB_G0280205 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0280205 PE=4 SV=2
Q6TMK3	3,709794604	0,0249	C	Heat shock protein 88 OS=*Dictyostelium discoideum* OX=44689 GN=hspH PE=1 SV=1
Q54LV1	3,653441696	0,0508	NSC	UV excision repair protein RAD23 homolog OS=*Dictyostelium discoideum* OX=44689 GN=rcbA PE=1 SV=1
Q55B10	3,498841212	0,0088	C	Probable alpha-galactosidase OS=*Dictyostelium discoideum* OX=44689 GN=melA PE=3 SV=1
P27685	3,393181154	0,0001	SC	40S ribosomal protein S2 OS=*Dictyostelium discoideum* OX=44689 GN=rps2 PE=1 SV=1
P19198	3,337615345	0,0160	C	cAMP-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=capA-1 PE=2 SV=2
Q54YD2	3,300501275	0,0037	SC	Putative phosphatidylglycerol/phosphatidylinositol transfer protein DDB_G0278295 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0278295 PE=2 SV=1
Q54LN4	3,18512312	0,0023	C	Gamma-glutamyl hydrolase A OS=*Dictyostelium discoideum* OX=44689 GN=gghA PE=3 SV=1
Q54F07	3,103729861	0,0254	C	S-adenosylmethionine synthase OS=*Dictyostelium discoideum* OX=44689 GN=metK PE=1 SV=1
Q1ZXQ8	3,054834993	0,0023	C	Centrosomal protein 224 OS=*Dictyostelium discoideum* OX=44689 GN=mtaA PE=1 SV=1
Q54LP8	3,0535926	0,0369	SC	Histone H2B.v3 OS=*Dictyostelium discoideum* OX=44689 GN=H2Bv3 PE=3 SV=1
Q54MZ5	2,948710667	0,0066	SC	40S ribosomal protein S28 OS=*Dictyostelium discoideum* OX=44689 GN=rps28 PE=3 SV=1
Q8IS16	2,936243337	0,0294	C	Ras guanine nucleotide exchange factor H OS=*Dictyostelium discoideum* OX=44689 GN=gefH PE=1 SV=1
Q7KWQ2	2,934845027	0,0179	C	Serine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=serS PE=1 SV=1
Q54DR1	2,843866879	0,0042	C	Squalene synthase OS=*Dictyostelium discoideum* OX=44689 GN=fdfT PE=3 SV=1
Q76P23	2,835951775	0,0518	NSC	Mitochondrial substrate carrier family protein Q OS=*Dictyostelium discoideum* OX=44689 GN=mcfQ PE=2 SV=1

P46794	2,815924784	0,0017	C	Cystathionine beta-synthase OS=*Dictyostelium discoideum* OX=44689 GN=cysB PE=2 SV=2
Q55ED1	2,79455335	0,0044	C	Probable nucleosome assembly protein OS=*Dictyostelium discoideum* OX=44689 GN=nap1 PE=2 SV=1
Q558Z9	2,780154086	0,0267	C	Exocyst complex component 7 OS=*Dictyostelium discoideum* OX=44689 GN=exoc7 PE=3 SV=1
Q553R3	2,730807225	0,0050	C	Eukaryotic translation initiation factor 4 gamma OS=*Dictyostelium discoideum* OX=44689 GN=eif4g PE=3 SV=1
Q54HI5	2,725020218	0,0048	SC	Lamin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=lmnB PE=1 SV=1
Q55BZ5	2,724700388	0,0299	C	Protein dcd1A OS=*Dictyostelium discoideum* OX=44689 GN=dcd1A PE=2 SV=1
Q54R45	2,679914235	0,0402	SC	Translocon-associated protein subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=ssr1 PE=3 SV=1
Q552L5	2,640764363	0,0059	C	THO complex subunit 7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=thoc7 PE=3 SV=1
Q54TW3	2,63589339	0,0160	SC	60S ribosomal protein L29 OS=*Dictyostelium discoideum* OX=44689 GN=rpl29 PE=3 SV=1
O60952	2,590358153	0,0532	NSC	LIM domain-containing protein E OS=*Dictyostelium discoideum* OX=44689 GN=limE PE=1 SV=1
Q554D9	2,544546512	0,0288	C	Asparagine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=asnS1 PE=1 SV=1
P13466	2,48685397	0,0103	SC	Gelation factor OS=*Dictyostelium discoideum* OX=44689 GN=abpC PE=1 SV=1
Q5XM24	2,486250348	0,0532	NSC	Autocrine proliferation repressor protein A OS=*Dictyostelium discoideum* OX=44689 GN=aprA PE=1 SV=1
Q54RK5	2,446221902	0,0456	NSC	Enolase A OS=*Dictyostelium discoideum* OX=44689 GN=enoA PE=3 SV=1
Q54Q48	2,446175664	0,0101	SC	Putative uncharacterized protein DDB_G0284097 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284097 PE=1 SV=1
Q54N80	2,442906779	0,1846	NSC	FK506-binding protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp3 PE=2 SV=1
Q54XB5	2,430796151	0,0000	SC	60S ribosomal protein L31 OS=*Dictyostelium discoideum* OX=44689 GN=rpl31 PE=3 SV=1
Q54SM3	2,397563787	0,0076	C	Peptidyl-prolyl cis-trans isomerase A OS=*Dictyostelium discoideum* OX=44689 GN=ppiA PE=1 SV=1
Q54Z26	2,342822983	0,0302	C	Serine hydroxymethyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=shmt1 PE=1 SV=1
Q27562	2,339061205	0,0514	NSC	Proteasome subunit alpha type-1 OS=*Dictyostelium discoideum* OX=44689 GN=psmA1 PE=3 SV=1
Q54MB5	2,298932766	0,0965	NSC	Adenosine kinase OS=*Dictyostelium discoideum* OX=44689 GN=adk PE=3 SV=2
Q54ZI6	2,297935886	0,0102	C	Phospholipase B-like protein E OS=*Dictyostelium discoideum* OX=44689 GN=plbE PE=3 SV=1
Q54FD7	2,295612341	0,0057	SC	Electron transfer flavoprotein subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=etfa PE=3 SV=1
Q54QR9	2,291504979	0,0116	C	Protein phosphatase 2A scaffold subunit OS=*Dictyostelium discoideum* OX=44689 GN=pppA PE=1 SV=1
Q556Y1	2,287502394	0,0766	NSC	40S ribosomal protein S30 OS=*Dictyostelium discoideum* OX=44689 GN=rps30-1 PE=3 SV=1

Q54TR1	2,267355366	0,0086	C	Counting factor associated protein D OS=*Dictyostelium discoideum* OX=44689 GN=cfaD PE=1 SV=1
Q55F94	2,236039587	0,0007	SC	Dynamin-like protein A OS=*Dictyostelium discoideum* OX=44689 GN=dlpA PE=2 SV=1
P54640	2,232365017	0,0122	C	Cysteine proteinase 5 OS=*Dictyostelium discoideum* OX=44689 GN=cprE PE=2 SV=2
Q54GT6	2,228618118	0,0336	C	Serine--pyruvate aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=agxt PE=3 SV=1
Q55FE0	2,223151364	0,0203	C	Eukaryotic translation initiation factor 4E OS=*Dictyostelium discoideum* OX=44689 GN=eif4e PE=3 SV=1
Q94504	2,205107433	0,0303	C	Cysteine proteinase 7 OS=*Dictyostelium discoideum* OX=44689 GN=cprG PE=1 SV=1
P22887	2,203360061	0,0146	SC	Nucleoside diphosphate kinase, cytosolic OS=*Dictyostelium discoideum* OX=44689 GN=ndkC-1 PE=1 SV=1
Q54JY7	2,190817704	0,0212	SC	Syntaxin-7A OS=*Dictyostelium discoideum* OX=44689 GN=syn7A PE=1 SV=1
Q54ST6	2,190817141	0,0766	NSC	ER membrane protein complex subunit 7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282229 PE=3 SV=2
P14132	2,183010198	0,0049	SC	40S ribosomal protein S9 OS=*Dictyostelium discoideum* OX=44689 GN=rps9 PE=1 SV=1
P10733	2,171635282	0,0557	NSC	Severin OS=*Dictyostelium discoideum* OX=44689 GN=sevA PE=1 SV=1
P32255	2,170438873	0,0068	C	Tubulin alpha chain OS=*Dictyostelium discoideum* OX=44689 GN=tubA PE=1 SV=1
Q555L8	2,163972449	0,0041	C	SH3 and F-BAR domain-containing protein DDB_G0274695 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274695 PE=4 SV=1
Q54NB6	2,157452591	0,0470	NSC	FK506-binding protein 4 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp4 PE=1 SV=1
P54638	2,151672628	0,0221	SC	Acetylornithine deacetylase OS=*Dictyostelium discoideum* OX=44689 GN=argE PE=1 SV=2
Q54M21	2,135167455	0,1242	NSC	DnaJ homolog subfamily C member 3 homolog OS=*Dictyostelium discoideum* OX=44689 GN=dnajc3 PE=3 SV=1
P26310	2,13182841	0,0362	C	Cytochrome c oxidase polypeptide 6, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cxfA PE=1 SV=2
Q55DV9	2,117223924	0,0047	SC	Cystathionine gamma-lyase OS=*Dictyostelium discoideum* OX=44689 GN=cysA PE=1 SV=1
Q76NW2	2,11484573	0,0396	SC	Histone H4 OS=*Dictyostelium discoideum* OX=44689 GN=H4a PE=1 SV=1
Q54CL0	2,108214715	0,0040	C	Apoptosis inhibitor 5 homolog OS=*Dictyostelium discoideum* OX=44689 GN=api5 PE=3 SV=1
Q557J6	2,100147928	0,0061	C	Drebrin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=abpE-1 PE=2 SV=1
Q556J0	2,091895114	0,0936	NSC	Transketolase OS=*Dictyostelium discoideum* OX=44689 GN=tkt-1 PE=1 SV=1
Q54HM2	2,088557826	0,0128	C	Uncharacterized protein DDB_G0289357 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289357 PE=4 SV=1
Q23915	2,083000583	0,0041	SC	Probable serine/threonine-protein kinase kinX OS=*Dictyostelium discoideum* OX=44689 GN=kinX PE=3 SV=2

Q76NV5	2,067322024	0,0093	SC	4-hydroxyphenylpyruvate dioxygenase OS=*Dictyostelium discoideum* OX=44689 GN=hpd PE=1 SV=1
Q550R2	2,063398743	0,0001	SC	Cortexillin-2 OS=*Dictyostelium discoideum* OX=44689 GN=ctxB PE=1 SV=1
Q54UJ0	2,061482437	0,0035	C	26S proteasome non-ATPase regulatory subunit 12 OS=*Dictyostelium discoideum* OX=44689 GN=psmD12 PE=2 SV=1
P46800	2,060190433	0,0147	SC	Guanine nucleotide-binding protein subunit beta-like protein OS=*Dictyostelium discoideum* OX=44689 GN=gpbB PE=1 SV=2
Q54JD4	2,042804568	0,0251	SC	Uncharacterized protein DDB_G0288133 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288133 PE=4 SV=1
P05095	2,038823047	0,0084	SC	Alpha-actinin A OS=*Dictyostelium discoideum* OX=44689 GN=abpA PE=1 SV=2
Q94464	2,027058693	0,0033	SC	Dynamin-A OS=*Dictyostelium discoideum* OX=44689 GN=dymA PE=1 SV=2
P22683	2,018307366	0,0157	SC	60S acidic ribosomal protein P2 OS=*Dictyostelium discoideum* OX=44689 GN=rplp2 PE=1 SV=3
O77082	2,014649021	0,0086	SC	40S ribosomal protein S10 OS=*Dictyostelium discoideum* OX=44689 GN=rps10 PE=1 SV=3
Q86HV4	2,007609889	0,0003	C	Oxysterol-binding protein 6 OS=*Dictyostelium discoideum* OX=44689 GN=osbF PE=3 SV=1
Q54PR9	1,989372103	0,0091	C	Counting factor 60 OS=*Dictyostelium discoideum* OX=44689 GN=cf60 PE=1 SV=1
Q54RD6	1,988740513	0,0622	NSC	Protein phosphatase 2A catalytic subunit B OS=*Dictyostelium discoideum* OX=44689 GN=pho2B PE=1 SV=1
Q86IV5	1,981834258	0,0142	C	Countin-1 OS=*Dictyostelium discoideum* OX=44689 GN=ctnA PE=1 SV=1
Q557E0	1,974304557	0,0009	SC	Heat shock cognate 70 kDa protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=hspE-1 PE=1 SV=1
Q55DR6	1,971216469	0,0250	SC	Fatty acyl-CoA synthetase A OS=*Dictyostelium discoideum* OX=44689 GN=fcsA PE=1 SV=1
Q55FR8	1,957815546	0,0909	NSC	Probable carboxypeptidase S-like 2 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267984 PE=3 SV=1
O15819	1,946594038	0,1214	NSC	Histone H3.3 type a OS=*Dictyostelium discoideum* OX=44689 GN=H3a PE=1 SV=1
Q9GPM4	1,942324425	0,0276	C	Phosphoglycerate kinase OS=*Dictyostelium discoideum* OX=44689 GN=pgkA PE=1 SV=2
Q54RQ1	1,940386383	0,0040	SC	Extracellular superoxide dismutase [Cu-Zn] 3 OS=*Dictyostelium discoideum* OX=44689 GN=sodC PE=2 SV=1
Q03409	1,937836325	0,0300	SC	40S ribosomal protein S25 OS=*Dictyostelium discoideum* OX=44689 GN=rps25 PE=3 SV=1
Q54DS3	1,931185698	0,0427	C	Transmembrane protein DDB_G0292058 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292058 PE=2 SV=1
Q54HG2	1,917613274	0,0029	SC	Cortexillin-1 OS=*Dictyostelium discoideum* OX=44689 GN=ctxA PE=1 SV=1
P46793	1,902405939	0,0114	SC	40S ribosomal protein S15a OS=*Dictyostelium discoideum* OX=44689 GN=rps15a PE=2 SV=3
Q86H60	1,889630246	0,2193	NSC	Small heat shock protein hspK OS=*Dictyostelium discoideum* OX=44689 GN=hspK PE=3 SV=1

Q54FD6	1,883816495	0,0023	C	Transcription initiation factor IIB OS=*Dictyostelium discoideum* OX=44689 GN=gtf2b PE=3 SV=1
Q54M70	1,870888091	0,0454	NSC	Aspartyl aminopeptidase OS=*Dictyostelium discoideum* OX=44689 GN=dnpep PE=1 SV=1
Q55AQ9	1,867275528	0,0074	SC	60S ribosomal protein L36 OS=*Dictyostelium discoideum* OX=44689 GN=rpl36 PE=3 SV=1
Q8MYF0	1,863390958	0,0065	C	Mitochondrial genome maintenance protein mgm101 homolog OS=*Dictyostelium discoideum* OX=44689 GN=mgm101 PE=3 SV=1
Q54MA6	1,847703853	0,0183	SC	40S ribosomal protein S5 OS=*Dictyostelium discoideum* OX=44689 GN=rps5 PE=1 SV=1
Q54X86	1,845351826	0,0251	C	Probable syntaxin-7B OS=*Dictyostelium discoideum* OX=44689 GN=syn7B PE=3 SV=1
P13021	1,843476858	0,0086	SC	F-actin-capping protein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=acpA PE=1 SV=1
Q54N17	1,842664816	0,0321	SC	40S ribosomal protein S15 OS=*Dictyostelium discoideum* OX=44689 GN=rps15 PE=3 SV=1
O77257	1,833705341	0,0279	SC	Protein gp17 OS=*Dictyostelium discoideum* OX=44689 GN=p17 PE=2 SV=1
Q54J34	1,833510868	0,0214	C	Adenylosuccinate lyase OS=*Dictyostelium discoideum* OX=44689 GN=purB PE=3 SV=1
Q54UB5	1,82735533	0,0058	C	26S proteasome non-ATPase regulatory subunit 11 OS=*Dictyostelium discoideum* OX=44689 GN=psmD11 PE=2 SV=1
P54648	1,824514342	0,0050	SC	V-type proton ATPase subunit C OS=*Dictyostelium discoideum* OX=44689 GN=vatC PE=2 SV=1
Q1ZXF5	1,824311606	0,0583	NSC	Probable cytochrome P450 508A4 OS=*Dictyostelium discoideum* OX=44689 GN=cyp508A4 PE=3 SV=1
P52922	1,824211522	0,0282	C	Leukotriene A-4 hydrolase homolog OS=*Dictyostelium discoideum* OX=44689 GN=lkhA PE=2 SV=2
Q54EW3	1,82306309	0,0225	C	Probable importin-5 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0291650 PE=3 SV=1
O76856	1,822800816	0,0038	SC	Cathepsin D OS=*Dictyostelium discoideum* OX=44689 GN=ctsD PE=1 SV=1
Q54UH8	1,822736797	0,0329	C	D-3-phosphoglycerate dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=serA PE=1 SV=1
P24639	1,810719713	0,0021	SC	Annexin A7 OS=*Dictyostelium discoideum* OX=44689 GN=nxnA PE=1 SV=1
P36415	1,803502573	0,0047	SC	Heat shock cognate 70 kDa protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=hspB PE=1 SV=2
Q54BC2	1,80304803	0,0981	NSC	Histone H2B.v1 OS=*Dictyostelium discoideum* OX=44689 GN=H2Bv1 PE=3 SV=1
O61122	1,800227965	0,0603	NSC	Serine/threonine-protein kinase svkA OS=*Dictyostelium discoideum* OX=44689 GN=svkA PE=1 SV=1
Q75JD4	1,800182755	0,1601	NSC	SH3 and F-BAR domain-containing protein DDB_G0271676 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271676 PE=4 SV=1
Q55EQ3	1,797725282	0,0085	SC	Uncharacterized abhydrolase domain-containing protein DDB_G0269086 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0269086 PE=1 SV=2
P14326	1,790592563	0,0482	NSC	Vegetative-specific protein H5 OS=*Dictyostelium discoideum* OX=44689 GN=cinB PE=2 SV=2
P28178	1,789188968	0,0227	C	Protein kinase 2 OS=*Dictyostelium discoideum* OX=44689 GN=pkgB PE=1 SV=2

Q54BM2	1,761363893	0,0059	SC	Polyadenylate-binding protein 1-A OS=*Dictyostelium discoideum* OX=44689 GN=pabpc1A PE=1 SV=1
P09402	1,754044429	0,0032	SC	Myosin, essential light chain OS=*Dictyostelium discoideum* OX=44689 GN=mlcE PE=2 SV=2
Q54NG2	1,743101648	0,0065	SC	60S ribosomal protein L17 OS=*Dictyostelium discoideum* OX=44689 GN=rpl17 PE=3 SV=1
Q54G42	1,739405883	0,0169	C	Chitinase domain-containing protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=chid1 PE=3 SV=1
P22684	1,739188376	0,0644	NSC	60S acidic ribosomal protein P1 OS=*Dictyostelium discoideum* OX=44689 GN=rplp1 PE=3 SV=1
Q54DU9	1,732396507	0,0672	NSC	Probable protein tyrosine phosphatase type IVA A OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292024 PE=3 SV=1
Q54HP3	1,71714788	0,0027	SC	Developmentally-regulated GTP-binding protein 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=drg1 PE=3 SV=1
Q54DF1	1,714897164	0,0299	SC	ATP synthase subunit gamma, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5C1 PE=1 SV=1
P42520	1,690897279	0,1234	NSC	40S ribosomal protein S17 OS=*Dictyostelium discoideum* OX=44689 GN=rps17 PE=3 SV=2
P34116	1,689292745	0,0536	NSC	Cell surface glycoprotein gp138B OS=*Dictyostelium discoideum* OX=44689 GN=GP138B PE=1 SV=1
Q54U07	1,689140501	0,0058	SC	Nascent polypeptide-associated complex subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=nacA PE=3 SV=1
Q1ZXP3	1,687362655	0,0055	C	Probable cytochrome b-c1 complex subunit 6 OS=*Dictyostelium discoideum* OX=44689 GN=uqcrh PE=3 SV=1
Q76P36	1,683778989	0,0592	NSC	40S ribosomal protein S29 OS=*Dictyostelium discoideum* OX=44689 GN=rps29 PE=3 SV=1
Q23911	1,681375503	0,0260	C	Protein 29C OS=*Dictyostelium discoideum* OX=44689 GN=29C PE=3 SV=2
P54639	1,675898199	0,0618	NSC	Cysteine proteinase 4 OS=*Dictyostelium discoideum* OX=44689 GN=cprD PE=2 SV=2
Q8MML6	1,670606108	0,0057	SC	V-type proton ATPase subunit H OS=*Dictyostelium discoideum* OX=44689 GN=vatH PE=1 SV=1
Q54S60	1,665637927	0,0456	NSC	Translation machinery-associated protein 16 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282655 PE=3 SV=1
Q869W6	1,658627897	0,0348	C	Probable myosin light chain kinase DDB_G0275057 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275057 PE=3 SV=1
Q54IX6	1,654480223	0,0460	NSC	Probable syntaxin-8B OS=*Dictyostelium discoideum* OX=44689 GN=syn8B PE=3 SV=1
Q54WR9	1,653107729	0,1133	NSC	Type-3 glutamine synthetase OS=*Dictyostelium discoideum* OX=44689 GN=glnA3 PE=1 SV=1
Q86H98	1,648208156	0,0302	C	Charged multivesicular body protein 4 OS=*Dictyostelium discoideum* OX=44689 GN=chmp4 PE=3 SV=1
Q54J47	1,644985003	0,1267	NSC	Probable pyridoxal 5'-phosphate synthase subunit pdx1 OS=*Dictyostelium discoideum* OX=44689 GN=pdx1 PE=1 SV=1
Q556U6	1,636910001	0,0346	SC	Luminal-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=bip1-1 PE=3 SV=1
Q54SV6	1,63498373	0,1520	NSC	Mitochondrial import inner membrane translocase subunit tim16 OS=*Dictyostelium discoideum* OX=44689 GN=timm16 PE=3 SV=1

Q54C24	1,630134255	0,0115	SC	Vacuolar protein sorting-associated protein 35 OS=*Dictyostelium discoideum* OX=44689 GN=vps35 PE=3 SV=1
Q54CK6	1,625027347	0,0411	C	Vesicle transport through interaction with t-SNAREs homolog 1A OS=*Dictyostelium discoideum* OX=44689 GN=vti1A PE=1 SV=1
P13022	1,621220534	0,0028	SC	F-actin-capping protein subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=acpB PE=1 SV=1
Q23921	1,619376281	0,0184	SC	Protein pkiA OS=*Dictyostelium discoideum* OX=44689 GN=pkiA PE=1 SV=2
P54872	1,619013165	0,0089	C	Hydroxymethylglutaryl-CoA synthase A OS=*Dictyostelium discoideum* OX=44689 GN=hgsA PE=1 SV=2
Q55D12	1,618240978	0,0514	NSC	Probable histidine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mhisS PE=3 SV=1
P34121	1,617882832	0,1580	NSC	Coactosin OS=*Dictyostelium discoideum* OX=44689 GN=coaA PE=1 SV=1
O00780	1,617182438	0,0163	SC	V-type proton ATPase subunit E OS=*Dictyostelium discoideum* OX=44689 GN=vatE PE=1 SV=1
P54657	1,615641532	0,0964	NSC	Calcium-dependent cell adhesion molecule 1 OS=*Dictyostelium discoideum* OX=44689 GN=cadA PE=1 SV=1
Q556Y4	1,614859193	0,0963	NSC	Casein kinase I OS=*Dictyostelium discoideum* OX=44689 GN=cak1-1 PE=1 SV=1
Q869Q8	1,614164906	0,2119	NSC	Probable serine carboxypeptidase CPVL OS=*Dictyostelium discoideum* OX=44689 GN=cpvl PE=3 SV=1
P27133	1,611894252	0,0177	SC	Coronin-A OS=*Dictyostelium discoideum* OX=44689 GN=corA PE=1 SV=2
Q54Y41	1,611668593	0,0047	SC	40S ribosomal protein S20 OS=*Dictyostelium discoideum* OX=44689 GN=rps20 PE=3 SV=1
Q555L5	1,6096183	0,0150	SC	Peroxiredoxin-4 OS=*Dictyostelium discoideum* OX=44689 GN=prdx4 PE=1 SV=2
Q86JD4	1,60798899	0,1033	NSC	Signal peptidase complex catalytic subunit sec11 OS=*Dictyostelium discoideum* OX=44689 GN=sec11 PE=3 SV=1
Q54PH8	1,603858431	0,0506	NSC	40S ribosomal protein S13 OS=*Dictyostelium discoideum* OX=44689 GN=rps13 PE=3 SV=1
Q869U7	1,599165547	0,0274	SC	40S ribosomal protein S18 OS=*Dictyostelium discoideum* OX=44689 GN=rps18 PE=3 SV=1
Q54XX1	1,587044131	0,0664	NSC	Signal recognition particle receptor subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=srprb PE=3 SV=1
O96626	1,585902865	0,0070	SC	Actin-related protein 2/3 complex subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=arcE PE=1 SV=1
Q55AH5	1,585212469	0,1663	NSC	V-type proton ATPase subunit F OS=*Dictyostelium discoideum* OX=44689 GN=vatF PE=3 SV=1
Q9TW32	1,578611311	0,0309	SC	Peptidyl-prolyl cis-trans isomerase B OS=*Dictyostelium discoideum* OX=44689 GN=cypB PE=1 SV=1
Q54ZW5	1,575386244	0,0149	SC	40S ribosomal protein S3a OS=*Dictyostelium discoideum* OX=44689 GN=rps3a PE=3 SV=1
Q54HL0	1,571445843	0,0303	C	Coatomer subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=copG PE=1 SV=1
Q55BN7	1,568800684	0,0015	SC	60S ribosomal protein L35a OS=*Dictyostelium discoideum* OX=44689 GN=rpl35a PE=3 SV=1
P13651	1,564253115	0,0789	NSC	Eukaryotic translation initiation factor 5A OS=*Dictyostelium discoideum* OX=44689 GN=eif5a PE=1 SV=2

Q54TR8	1,557132239	0,0852	NSC	Nascent polypeptide-associated complex subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=nacB PE=3 SV=1
Q8T1V6	1,554877533	0,1719	NSC	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufs4 PE=3 SV=2
Q9NKX1	1,553623272	0,0291	SC	Endoplasmin homolog OS=*Dictyostelium discoideum* OX=44689 GN=grp94 PE=2 SV=2
Q54PX9	1,551331695	0,0358	SC	40S ribosomal protein S12 OS=*Dictyostelium discoideum* OX=44689 GN=rps12 PE=1 SV=1
Q54VI6	1,540399752	0,0932	NSC	Translocon-associated protein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=ssr2 PE=2 SV=2
Q554H5	1,535917241	0,0157	C	Phospholipase B-like protein F OS=*Dictyostelium discoideum* OX=44689 GN=plbF PE=3 SV=1
Q869Z0	1,530033569	0,0513	NSC	Putative protein disulfide-isomerase DDB_G0275025 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275025 PE=1 SV=1
P34115	1,528488254	0,0425	C	Cell surface glycoprotein gp138A OS=*Dictyostelium discoideum* OX=44689 GN=GP138A PE=1 SV=1
Q23862	1,526552963	0,0025	SC	Rho-related protein racE OS=*Dictyostelium discoideum* OX=44689 GN=racE PE=1 SV=1
Q55BY1	1,526367643	0,0250	SC	40S ribosomal protein SA OS=*Dictyostelium discoideum* OX=44689 GN=rpsA PE=1 SV=1
O96624	1,524149846	0,0011	SC	Actin-related protein 2/3 complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=arcC PE=1 SV=1
O15757	1,523404244	0,0620	NSC	Serine/threonine-protein phosphatase PP1 OS=*Dictyostelium discoideum* OX=44689 GN=pppB PE=1 SV=1
Q54X51	1,523382774	0,1239	NSC	40S ribosomal protein S19 OS=*Dictyostelium discoideum* OX=44689 GN=rps19 PE=3 SV=1
Q8TA03	1,52145993	0,0059	SC	6-phosphogluconate dehydrogenase, decarboxylating OS=*Dictyostelium discoideum* OX=44689 GN=gnd PE=1 SV=1
Q54WH2	1,514770357	0,0451	NSC	Formin-A OS=*Dictyostelium discoideum* OX=44689 GN=forA PE=1 SV=1
Q75K27	1,512708718	0,0124	SC	40S ribosomal protein S24 OS=*Dictyostelium discoideum* OX=44689 GN=rps24 PE=3 SV=1
Q54PX7	1,509125952	0,0304	C	PCI domain-containing protein 2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=pcid2 PE=3 SV=1
Q54J23	1,500762701	0,0127	SC	60S ribosomal protein L35 OS=*Dictyostelium discoideum* OX=44689 GN=rpl35 PE=3 SV=1
Q5TJ65	1,497957737	0,0310	SC	Protein VASP homolog OS=*Dictyostelium discoideum* OX=44689 GN=vasp PE=1 SV=1
P15808	1,496450135	0,2044	NSC	Flavin-dependent thymidylate synthase OS=*Dictyostelium discoideum* OX=44689 GN=thyA PE=3 SV=2
Q556M4	1,496398493	0,1390	NSC	Probable cytochrome P450 508A2 OS=*Dictyostelium discoideum* OX=44689 GN=cyp508A2-1 PE=3 SV=1
Q54F42	1,491647792	0,1073	NSC	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=*Dictyostelium discoideum* OX=44689 GN=ndufa6 PE=3 SV=1
Q8T869	1,49129036	0,0424	SC	Luminal-binding protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=bip2 PE=1 SV=1
Q9NH03	1,489147529	0,2650	NSC	Farnesyl diphosphate synthase OS=*Dictyostelium discoideum* OX=44689 GN=fps PE=2 SV=1
Q6IMN8	1,487788162	0,1221	NSC	Aldose reductase A OS=*Dictyostelium discoideum* OX=44689 GN=alrA PE=2 SV=1

Q54KD9	1,48611233	0,2508	NSC	Ran-specific GTPase-activating protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=ranbp1 PE=1 SV=1
Q54WN8	1,480691098	0,0280	SC	Uncharacterized protein DDB_G0279527 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0279527 PE=1 SV=1
Q54SR7	1,479167817	0,1102	NSC	FK506-binding protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp2 PE=3 SV=1
Q54SE2	1,478554225	0,1047	NSC	1-Cys peroxiredoxin OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282517 PE=3 SV=1
Q54BQ3	1,478489545	0,0149	SC	60S ribosomal protein L23a OS=*Dictyostelium discoideum* OX=44689 GN=rpl23a PE=1 SV=1
Q54X53	1,477500971	0,0069	SC	60S ribosomal protein L21 OS=*Dictyostelium discoideum* OX=44689 GN=rpl21 PE=3 SV=1
Q86L05	1,473829519	0,0126	SC	60S ribosomal protein L10a OS=*Dictyostelium discoideum* OX=44689 GN=rpl10a PE=1 SV=1
Q8T191	1,470973447	0,0206	SC	Probable UDP-glucose:glycoprotein glucosyltransferase A OS=*Dictyostelium discoideum* OX=44689 GN=ggtA PE=1 SV=2
Q54RP6	1,468016829	0,0527	NSC	Hybrid signal transduction histidine kinase L OS=*Dictyostelium discoideum* OX=44689 GN=dhkL PE=3 SV=1
O77229	1,466985951	0,0120	SC	Catalase-A OS=*Dictyostelium discoideum* OX=44689 GN=catA PE=2 SV=2
P22685	1,445789517	0,0286	SC	60S acidic ribosomal protein P0 OS=*Dictyostelium discoideum* OX=44689 GN=rplp0 PE=1 SV=2
P02889	1,442114206	0,0876	NSC	Probable 26S proteasome non-ATPase regulatory subunit 8 OS=*Dictyostelium discoideum* OX=44689 GN=psmD8-1 PE=2 SV=2
Q7Z2B8	1,439993683	0,0831	NSC	Myosin-ID light chain OS=*Dictyostelium discoideum* OX=44689 GN=mlcD PE=1 SV=1
Q54WR2	1,436948693	0,0821	NSC	eIF-2-alpha kinase activator GCN1 OS=*Dictyostelium discoideum* OX=44689 GN=gcn1 PE=3 SV=1
Q54QF9	1,435775841	0,1818	NSC	GrpE protein homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=grpE PE=3 SV=1
Q54UU6	1,434799255	0,0996	NSC	KRR1 small subunit processome component homolog OS=*Dictyostelium discoideum* OX=44689 GN=krr1 PE=3 SV=1
Q54NC1	1,434733574	0,0640	NSC	NADH-cytochrome b5 reductase 1 OS=*Dictyostelium discoideum* OX=44689 GN=cyb5r1 PE=3 SV=1
Q54MK8	1,432537584	0,0479	NSC	60S ribosomal protein L18a OS=*Dictyostelium discoideum* OX=44689 GN=rpl18a PE=3 SV=2
Q54BC6	1,430165164	0,0429	C	26S proteasome non-ATPase regulatory subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=psmD2 PE=1 SV=1
Q54BK2	1,429794116	0,1776	NSC	Neutral ceramidase A OS=*Dictyostelium discoideum* OX=44689 GN=dcd2A PE=1 SV=1
P34149	1,426276629	0,1370	NSC	Rho-related protein racC OS=*Dictyostelium discoideum* OX=44689 GN=racC PE=1 SV=1
Q55CW5	1,424965471	0,0002	SC	60S ribosomal protein L36a OS=*Dictyostelium discoideum* OX=44689 GN=rpl36a PE=3 SV=2
Q55EX6	1,424452717	0,0426	C	Trafficking protein particle complex subunit 13 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0269062 PE=3 SV=2
Q54VN6	1,421009082	0,0252	SC	60S ribosomal protein L24 OS=*Dictyostelium discoideum* OX=44689 GN=rpl24 PE=1 SV=1

Q54K91	1,417733323	0,0368	C	Acetyl-CoA hydrolase OS=*Dictyostelium discoideum* OX=44689 GN=ach1 PE=3 SV=1
Q55EK2	1,416352687	0,1701	NC	Probable cytochrome P450 524A1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp524A1 PE=3 SV=1
Q54Z13	1,406981527	0,2398	NC	V-type proton ATPase subunit G OS=*Dictyostelium discoideum* OX=44689 GN=atp6v1g PE=1 SV=2
Q65YR7	1,406455524	0,2255	NC	Cystatin-A2 OS=*Dictyostelium discoideum* OX=44689 GN=cpiB PE=2 SV=1
P21900	1,402735431	0,0254	SC	Adenylosuccinate synthetase OS=*Dictyostelium discoideum* OX=44689 GN=purA PE=1 SV=1
P36410	1,39926424	0,1135	NSC	Ras-related protein Rab-14 OS=*Dictyostelium discoideum* OX=44689 GN=rab14 PE=1 SV=2
P34112	1,39490789	0,2611	NC	Cyclin-dependent kinase 1 OS=*Dictyostelium discoideum* OX=44689 GN=cdk1 PE=2 SV=1
Q54S90	1,394468387	0,1081	NSC	40S ribosomal protein S11 OS=*Dictyostelium discoideum* OX=44689 GN=rps11 PE=1 SV=1
Q54GK6	1,39439559	0,0089	SC	60S ribosomal protein L22 2 OS=*Dictyostelium discoideum* OX=44689 GN=rpl22a PE=3 SV=1
P54651	1,394216679	0,0615	NSC	Heat shock cognate 90 kDa protein OS=*Dictyostelium discoideum* OX=44689 GN=hspD PE=1 SV=2
Q55GE2	1,392552443	0,0550	NSC	Probable mitochondrial 2-oxodicarboxylate carrier OS=*Dictyostelium discoideum* OX=44689 GN=mcfT PE=3 SV=1
P18613	1,38864841	0,0194	SC	Ras-related protein rapA OS=*Dictyostelium discoideum* OX=44689 GN=rapA PE=1 SV=1
Q54UI0	1,3855668	0,1977	NC	Uncharacterized transmembrane protein DDB_G0281067 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0281067 PE=1 SV=1
Q54YZ4	1,380407196	0,0267	SC	Electron transfer flavoprotein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=etfb PE=3 SV=1
Q54F10	1,377646093	0,2047	NC	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufv2 PE=3 SV=1
P42528	1,375049773	0,0102	SC	Actin-related protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=arpC PE=1 SV=1
P13723	1,374927013	0,2354	NC	Beta-hexosaminidase subunit A1 OS=*Dictyostelium discoideum* OX=44689 GN=hexa1 PE=1 SV=1
Q54P71	1,362185038	0,1554	NC	Probable acid phosphatase DDB_G0284755 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284755 PE=3 SV=2
Q54SG3	1,360879374	0,2244	NC	Uncharacterized transmembrane protein DDB_G0282483 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0282483 PE=4 SV=1
Q54R04	1,357985372	0,2494	NC	ADP-ribosylation factor-like protein 8 OS=*Dictyostelium discoideum* OX=44689 GN=arl8 PE=3 SV=1
Q54CC5	1,357699594	0,0706	NC	Eukaryotic translation initiation factor 3 subunit E OS=*Dictyostelium discoideum* OX=44689 GN=eif3E PE=3 SV=1
Q559R0	1,357422818	0,1726	NC	GTP-binding protein Sar1A OS=*Dictyostelium discoideum* OX=44689 GN=sarA PE=1 SV=1
Q558Z0	1,348899912	0,2041	NC	Probable arginine--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=argS1 PE=3 SV=1
Q55G04	1,34808773	0,2885	NC	Proteasome subunit alpha type-5 OS=*Dictyostelium discoideum* OX=44689 GN=psmA5 PE=3 SV=1

P34123	1,347780425	0,0724	NC	26S proteasome regulatory subunit 6B homolog OS=*Dictyostelium discoideum* OX=44689 GN=psmC4 PE=1 SV=1
Q55E35	1,34535399	0,0624	NC	Signal peptidase complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=spcs2 PE=3 SV=2
Q54VA2	1,343894332	0,1296	NC	Fumarate hydratase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=fumH PE=3 SV=1
Q54RN1	1,339588839	0,0733	NC	Extracellular superoxide dismutase [Cu-Zn] 2 OS=*Dictyostelium discoideum* OX=44689 GN=sodB PE=2 SV=1
O15706	1,336859339	0,0976	NC	Vacuolin-A OS=*Dictyostelium discoideum* OX=44689 GN=vacA PE=1 SV=1
Q23892	1,332231683	0,1188	NC	Lysosomal beta glucosidase OS=*Dictyostelium discoideum* OX=44689 GN=gluA PE=1 SV=2
Q54Q51	1,328797084	0,1342	NC	40S ribosomal protein S16 OS=*Dictyostelium discoideum* OX=44689 GN=rps16 PE=3 SV=1
P51405	1,325668347	0,0039	SC	40S ribosomal protein S4 OS=*Dictyostelium discoideum* OX=44689 GN=rps4 PE=1 SV=3
Q9U9A3	1,324871225	0,0457	NC	Serine/threonine-protein phosphatase 6 catalytic subunit OS=*Dictyostelium discoideum* OX=44689 GN=ppp6c PE=2 SV=2
Q869Q2	1,322362745	0,1163	NC	Ribosome biogenesis regulatory protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=rrs1 PE=3 SV=1
Q86K94	1,318496716	0,2487	NC	Trafficking protein particle complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=trappc3 PE=3 SV=2
Q54XZ0	1,316232893	0,2119	NC	Probable enoyl-CoA hydratase 2 OS=*Dictyostelium discoideum* OX=44689 GN=mfeB PE=2 SV=1
P30815	1,313643478	0,0722	NC	Cytochrome c oxidase subunit 4, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cxdA PE=2 SV=2
O00897	1,312947884	0,1143	NC	Calmodulin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=calB PE=2 SV=1
Q54DS8	1,309396435	0,1641	NC	Protein SEC13 homolog OS=*Dictyostelium discoideum* OX=44689 GN=sec13 PE=3 SV=1
Q54EN4	1,309213909	0,0318	NC	Protein disulfide-isomerase 2 OS=*Dictyostelium discoideum* OX=44689 GN=pdi2 PE=3 SV=1
O96623	1,309058375	0,0249	NC	Actin-related protein 2/3 complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=arcB PE=1 SV=1
Q54M82	1,306273196	0,0648	NC	Probable cytochrome b-c1 complex subunit 7 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286171 PE=3 SV=1
Q54JV6	1,304082472	0,1410	NC	Protein transport protein Sec61 subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=sec61g PE=3 SV=1
P02599	1,303258228	0,2497	NC	Calmodulin OS=*Dictyostelium discoideum* OX=44689 GN=calA PE=1 SV=3
Q54NS3	1,303236954	0,2910	NC	TPR repeat-containing protein DDB_G0285095 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0285095 PE=4 SV=1
Q9GRF8	1,299202205	0,2230	NC	Elongation factor 1-beta OS=*Dictyostelium discoideum* OX=44689 GN=efa1B PE=1 SV=1
P90526	1,295566709	0,0258	NC	40S ribosomal protein S3 OS=*Dictyostelium discoideum* OX=44689 GN=rps3 PE=1 SV=1
Q94490	1,29432134	0,3321	NC	Ubiquitin conjugating enzyme E2 B OS=*Dictyostelium discoideum* OX=44689 GN=ubcB PE=1 SV=1

Q01501	1,294205162	0,1704	NC	Mitochondrial outer membrane protein porin OS=*Dictyostelium discoideum* OX=44689 GN=porA PE=1 SV=1
Q55GJ7	1,294177899	0,1343	NC	60S ribosomal protein L38 OS=*Dictyostelium discoideum* OX=44689 GN=rpl38 PE=3 SV=1
Q54HW8	1,292840417	0,2968	NC	Uncharacterized protein DDB_G0289171 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289171 PE=2 SV=1
Q23858	1,291448893	0,0356	NC	Calreticulin OS=*Dictyostelium discoideum* OX=44689 GN=crtA PE=1 SV=3
P15064	1,285432961	0,1146	NC	Ras-like protein rasG OS=*Dictyostelium discoideum* OX=44689 GN=rasG PE=1 SV=1
Q554S6	1,282417782	0,0368	NC	Actin-17 OS=*Dictyostelium discoideum* OX=44689 GN=act17 PE=3 SV=1
Q54JE3	1,281031055	0,0239	NC	60S ribosomal protein L22 1 OS=*Dictyostelium discoideum* OX=44689 GN=rpl22 PE=3 SV=1
P54632	1,273031344	0,0196	NC	14-3-3-like protein OS=*Dictyostelium discoideum* OX=44689 GN=fttB PE=1 SV=2
P16168	1,2711089	0,0951	NC	60S ribosomal protein L11 OS=*Dictyostelium discoideum* OX=44689 GN=rpl11 PE=1 SV=2
P29447	1,268240661	0,2631	NC	Thioredoxin-3 OS=*Dictyostelium discoideum* OX=44689 GN=trxC PE=3 SV=2
Q54VZ4	1,268207217	0,0530	NC	60S ribosomal protein L18 OS=*Dictyostelium discoideum* OX=44689 GN=rpl18 PE=1 SV=1
Q54VN2	1,267417488	0,2049	NC	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=coq5 PE=3 SV=1
Q55C21	1,266653465	0,1097	NC	Methionine aminopeptidase 2 OS=*Dictyostelium discoideum* OX=44689 GN=metap2 PE=3 SV=3
Q76P29	1,263992293	0,0487	NC	Importin subunit alpha-B OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272318 PE=3 SV=1
Q1ZXA8	1,262888981	0,1231	NC	Uncharacterized protein DDB_G0292160 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292160 PE=3 SV=1
Q86A77	1,26236531	0,1270	NC	V-type proton ATPase subunit D OS=*Dictyostelium discoideum* OX=44689 GN=atp6v1d PE=1 SV=1
Q54YA0	1,260995514	0,0887	NC	Probable ATP-citrate synthase OS=*Dictyostelium discoideum* OX=44689 GN=acly PE=1 SV=1
C7G046	1,252923034	0,0587	NC	von Willebrand factor A domain-containing protein DDB_G0286969 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286969 PE=4 SV=1
Q1ZXD3	1,252837011	0,0995	NC	26S proteasome non-ATPase regulatory subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=psmD3 PE=1 SV=1
Q54NQ0	1,25258032	0,2928	NC	26S proteasome non-ATPase regulatory subunit 13 OS=*Dictyostelium discoideum* OX=44689 GN=psmD13 PE=2 SV=1
Q54YJ6	1,245744355	0,2245	NC	Eukaryotic translation initiation factor 1A OS=*Dictyostelium discoideum* OX=44689 GN=eif1a PE=3 SV=1
Q54BN3	1,240980345	0,0907	NC	Probable replication factor C subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=rfc3 PE=3 SV=1
Q54UD0	1,234761228	0,2580	NC	Eukaryotic translation initiation factor 3 subunit H OS=*Dictyostelium discoideum* OX=44689 GN=eif3H PE=3 SV=1
Q54I41	1,232766399	0,0269	NC	40S ribosomal protein S7 OS=*Dictyostelium discoideum* OX=44689 GN=rps7 PE=1 SV=1

Q54JT7	1,232456738	0,3034	NC	Nicastrin OS=*Dictyostelium discoideum* OX=44689 GN=ncstn PE=3 SV=2
O96621	1,226877651	0,0283	NC	Actin-related protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=arpB PE=1 SV=1
Q86AV6	1,224202796	0,1037	NC	Citrate synthase OS=*Dictyostelium discoideum* OX=44689 GN=gltA PE=3 SV=1
Q54KA7	1,223589039	0,2128	NC	Ankyrin repeat, PH and SEC7 domain containing protein secG OS=*Dictyostelium discoideum* OX=44689 GN=secG PE=2 SV=1
Q55EX9	1,222405807	0,3429	NC	Putative methyltransferase DDB_G0268948 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268948 PE=1 SV=2
Q54D04	1,221691655	0,0880	NC	Probable malate dehydrogenase 2, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mdhB PE=1 SV=1
Q54RX9	1,217172635	0,1251	NC	Putative ras-related protein Rab-5B OS=*Dictyostelium discoideum* OX=44689 GN=rab5B PE=5 SV=1
Q554J3	1,216780662	0,2581	NC	FK506-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp1 PE=3 SV=1
Q54K74	1,214154583	0,2827	NC	Endoplasmic reticulum transmembrane protein YET-like OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0287543 PE=3 SV=2
Q75JR3	1,211220782	0,1645	NC	Isocitrate dehydrogenase [NADP] cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=idhC PE=1 SV=1
Q86IA3	1,210918448	0,1247	NC	Protein disulfide-isomerase 1 OS=*Dictyostelium discoideum* OX=44689 GN=pdi1 PE=1 SV=2
Q54HB4	1,209565516	0,2226	NC	Transcription and mRNA export factor ENY2 OS=*Dictyostelium discoideum* OX=44689 GN=eny2 PE=3 SV=1
Q76NU1	1,205874981	0,0776	NC	V-type proton ATPase subunit B OS=*Dictyostelium discoideum* OX=44689 GN=vatB PE=1 SV=1
Q54YT4	1,20484694	0,2146	NC	Enoyl-[acyl-carrier-protein] reductase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mecr PE=3 SV=1
O96552	1,193282242	0,2620	NC	Charged multivesicular body protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=chmp1 PE=3 SV=1
Q54E22	1,193154147	0,3116	NC	Acyl carrier protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufab1 PE=3 SV=1
Q54B68	1,192553357	0,1439	NC	Isocitrate dehydrogenase [NAD] regulatory subunit B, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=idhB PE=3 SV=1
Q86A92	1,182780061	0,2652	NC	Enhancer of rudimentary homolog OS=*Dictyostelium discoideum* OX=44689 GN=erh PE=3 SV=1
Q54W90	1,179104767	0,2025	NC	Protein SEY1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_0206311 PE=3 SV=1
Q54Q99	1,177831731	0,0349	NC	Serine/threonine-protein phosphatase 2A regulatory subunit phr2AB OS=*Dictyostelium discoideum* OX=44689 GN=phr2aB PE=3 SV=1
P11872	1,177410744	0,2189	NC	cAMP-regulated M3R protein OS=*Dictyostelium discoideum* OX=44689 GN=prtB PE=2 SV=4
P54660	1,176628151	0,3270	NC	Ponticulin OS=*Dictyostelium discoideum* OX=44689 GN=ponA PE=1 SV=1
Q86AD5	1,176183695	0,1136	NC	Pyruvate dehydrogenase complex subunit homolog DDB_G0271564, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhX PE=3 SV=1
Q54NI6	1,173731054	0,3139	NC	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufs7 PE=3 SV=1

Q55GH8	1,173164425	0,2695	NC	Small heat shock protein hspL OS=*Dictyostelium discoideum* OX=44689 GN=hspL PE=3 SV=1
Q54RA8	1,172986593	0,2576	NC	ATP synthase subunit O, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5O PE=3 SV=1
Q55F42	1,171957223	0,2775	NC	ATP synthase subunit delta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5D PE=3 SV=1
Q54VG1	1,17150276	0,3686	NC	Guanine nucleotide-binding protein alpha-12 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaL PE=1 SV=1
Q54HF1	1,170554945	0,0188	NC	Putative actin-24 OS=*Dictyostelium discoideum* OX=44689 GN=act24 PE=3 SV=1
Q54TL8	1,170271837	0,1864	NC	40S ribosomal protein S26 OS=*Dictyostelium discoideum* OX=44689 GN=rps26 PE=3 SV=1
P34144	1,170057583	0,1757	NC	Rho-related protein rac1A OS=*Dictyostelium discoideum* OX=44689 GN=rac1A PE=1 SV=2
Q86KZ5	1,16898952	0,1383	NC	Ribosome maturation protein SBDS OS=*Dictyostelium discoideum* OX=44689 GN=sbds PE=3 SV=2
P07829	1,166184819	0,0382	NC	Actin-3 OS=*Dictyostelium discoideum* OX=44689 GN=act3 PE=3 SV=3
Q55BS9	1,163876214	0,2275	NC	60S ribosomal protein L30 OS=*Dictyostelium discoideum* OX=44689 GN=rpl30 PE=3 SV=1
Q54C49	1,163629717	0,1375	NC	Eukaryotic translation initiation factor 3 subunit F OS=*Dictyostelium discoideum* OX=44689 GN=eif3f PE=3 SV=1
P34142	1,159855832	0,2817	NC	Ras-related protein Rab-21 OS=*Dictyostelium discoideum* OX=44689 GN=rab21 PE=1 SV=2
Q54EG3	1,158546357	0,1458	NC	40S ribosomal protein S14 OS=*Dictyostelium discoideum* OX=44689 GN=rps14 PE=3 SV=1
P29505	1,155307517	0,1380	NC	Cytochrome c oxidase subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=cxeA PE=1 SV=3
Q54UF3	1,150394619	0,2468	NC	Probable ornithine decarboxylase OS=*Dictyostelium discoideum* OX=44689 GN=odc PE=3 SV=1
Q55CW0	1,150114967	0,1092	NC	rRNA 2'-O-methyltransferase fibrillarin OS=*Dictyostelium discoideum* OX=44689 GN=fbl PE=3 SV=1
Q54NP6	1,149153078	0,2118	NC	Alpha-soluble NSF attachment protein OS=*Dictyostelium discoideum* OX=44689 GN=snpA PE=1 SV=1
Q54I98	1,148824741	0,1577	NC	Probable cycloartenol-C-24-methyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=smt1 PE=1 SV=1
Q55BI2	1,148609958	0,2333	NC	Isocitrate dehydrogenase [NAD] regulatory subunit A, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=idhA PE=3 SV=1
P54647	1,141085207	0,2142	NC	V-type proton ATPase catalytic subunit A OS=*Dictyostelium discoideum* OX=44689 GN=vatA PE=1 SV=2
Q54SF7	1,140990315	0,2363	NC	Aspartate aminotransferase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=aatB PE=3 SV=1
P34093	1,139121007	0,1610	NC	Nucleoside diphosphate kinase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndkM PE=1 SV=2
Q54ZD1	1,137704237	0,0401	NC	60S ribosomal protein L7a OS=*Dictyostelium discoideum* OX=44689 GN=rpl7a PE=1 SV=1
Q54NZ5	1,134292331	0,3863	NC	Cullin-3 OS=*Dictyostelium discoideum* OX=44689 GN=culC PE=3 SV=1
Q54G21	1,133842718	0,3780	NC	FK506-binding protein 5 OS=*Dictyostelium discoideum* OX=44689 GN=fkbp5 PE=1 SV=1

Q54DD3	1,131636399	0,3600	NC	Aminomethyltransferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcvT PE=3 SV=1
P26199	1,12980515	0,3036	NC	Profilin-1 OS=*Dictyostelium discoideum* OX=44689 GN=proA PE=2 SV=1
P11874	1,1290139	0,0267	NC	60S ribosomal protein L7 OS=*Dictyostelium discoideum* OX=44689 GN=rpl7 PE=1 SV=3
Q551M2	1,128295172	0,3905	NC	Eukaryotic translation initiation factor 6 OS=*Dictyostelium discoideum* OX=44689 GN=eif6 PE=1 SV=1
Q55AB5	1,124515009	0,1439	NC	60S ribosomal protein L32 OS=*Dictyostelium discoideum* OX=44689 GN=rpl32 PE=3 SV=1
Q54QS3	1,124469548	0,3110	NC	Probable ATP-dependent RNA helicase ddx3 OS=*Dictyostelium discoideum* OX=44689 GN=ddx3 PE=3 SV=1
Q75JI3	1,123928413	0,2288	NC	Vesicle-fusing ATPase OS=*Dictyostelium discoideum* OX=44689 GN=nsfA PE=1 SV=1
P83401	1,119539991	0,3699	NC	Putative aldehyde dehydrogenase family 7 member A1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0276821 PE=3 SV=2
Q54D99	1,118616516	0,3227	NC	Probable 39S ribosomal protein L53, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl53 PE=3 SV=1
Q54XK0	1,11801486	0,3554	NC	Probable 39S ribosomal protein L27, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl27 PE=3 SV=1
Q54PJ1	1,117981586	0,2912	NC	26S proteasome regulatory subunit 10B OS=*Dictyostelium discoideum* OX=44689 GN=psmC6 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P34123, P34124, Q54PN7; Additional IDs concatenated into MaxParsimony group: P34123, P34124, Q54PN7
P13023	1,11744312	0,0826	NC	60S ribosomal protein L8 OS=*Dictyostelium discoideum* OX=44689 GN=rpl8 PE=1 SV=2
Q86L14	1,116564622	0,3479	NC	Bifunctional purine biosynthesis protein purH OS=*Dictyostelium discoideum* OX=44689 GN=purH PE=1 SV=1
Q54UP4	1,116254232	0,3798	NC	Probable transaldolase OS=*Dictyostelium discoideum* OX=44689 GN=tal PE=3 SV=1
Q54WP3	1,115791398	0,3698	NC	Probable 39S ribosomal protein L22, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrpl22 PE=3 SV=1
P36408	1,114609414	0,2868	NC	Guanine nucleotide-binding protein subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=gpbA PE=1 SV=1
Q8I8U2	1,111462009	0,3483	NC	AP-1 complex subunit gamma OS=*Dictyostelium discoideum* OX=44689 GN=ap1g1 PE=1 SV=1
Q54CT8	1,111225718	0,4122	NC	Probable adenylate kinase B OS=*Dictyostelium discoideum* OX=44689 GN=adkB PE=3 SV=1
Q8IS15	1,108669809	0,4300	NC	Ras guanine nucleotide exchange factor I OS=*Dictyostelium discoideum* OX=44689 GN=gefI PE=2 SV=1
P42530	1,108209795	0,3570	NC	Discoidin-2 OS=*Dictyostelium discoideum* OX=44689 GN=dscE PE=1 SV=1
Q54FG5	1,106648731	0,3697	NC	Rho GTPase-activating protein gacJJ OS=*Dictyostelium discoideum* OX=44689 GN=gacJJ PE=3 SV=1
Q54MD4	1,106632615	0,2708	NC	Probable replication factor C subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=rfc4 PE=3 SV=1
Q8T2H0	1,105233853	0,3306	NC	Protein FAM49 homolog OS=*Dictyostelium discoideum* OX=44689 GN=fam49 PE=3 SV=2
P34098	1,100813224	0,0587	NC	Lysosomal alpha-mannosidase OS=*Dictyostelium discoideum* OX=44689 GN=manA PE=1 SV=2

Q54E24	1,095924458	0,2187	NC	40S ribosomal protein S8 OS=*Dictyostelium discoideum* OX=44689 GN=rps8 PE=1 SV=1
P10819	1,09162257	0,4472	NC	Adenosylhomocysteinase OS=*Dictyostelium discoideum* OX=44689 GN=sahA PE=1 SV=2
Q54J50	1,088538998	0,2964	NC	60S ribosomal protein L12 OS=*Dictyostelium discoideum* OX=44689 GN=rpl12 PE=1 SV=1
Q9GS21	1,087641903	0,2541	NC	60S ribosomal protein L28 OS=*Dictyostelium discoideum* OX=44689 GN=rpl28 PE=2 SV=1
Q54EW1	1,086536118	0,2496	NC	Serine hydroxymethyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=shmt2 PE=3 SV=1
Q55FI1	1,086462227	0,3286	NC	4-aminobutyrate aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=gabT PE=3 SV=1
Q55BJ9	1,083983614	0,3883	NC	Superoxide dismutase [Mn], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sod2 PE=3 SV=1
P33519	1,081194377	0,4117	NC	GTP-binding nuclear protein Ran OS=*Dictyostelium discoideum* OX=44689 GN=ranA PE=1 SV=1
Q54QQ0	1,080120559	0,3195	NC	Inosine-5'-monophosphate dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=impdh PE=1 SV=1
Q869S7	1,076629005	0,3654	NC	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=scsB PE=3 SV=1
Q54PA9	1,075800942	0,3800	NC	Ribose-phosphate pyrophosphokinase A OS=*Dictyostelium discoideum* OX=44689 GN=prsA PE=1 SV=1
Q54QJ9	1,075513555	0,4199	NC	Adenylate kinase OS=*Dictyostelium discoideum* OX=44689 GN=adkA PE=3 SV=1
Q54K32	1,07411471	0,3573	NC	Ras GTPase-activating-like protein rgaA OS=*Dictyostelium discoideum* OX=44689 GN=rgaA PE=1 SV=1
P34124	1,073506513	0,4297	NC	26S proteasome regulatory subunit 8 OS=*Dictyostelium discoideum* OX=44689 GN=psmC5 PE=1 SV=2
Q86K01	1,073058628	0,4164	NC	60S ribosomal protein L15 OS=*Dictyostelium discoideum* OX=44689 GN=rpl15-1 PE=1 SV=1
Q553P5	1,070990332	0,4316	NC	Syntaxin-8A OS=*Dictyostelium discoideum* OX=44689 GN=syn8A PE=1 SV=1
Q9NKW1	1,067173202	0,3545	NC	Peroxisomal multifunctional enzyme A OS=*Dictyostelium discoideum* OX=44689 GN=mfeA PE=2 SV=1
Q54Z69	1,065168982	0,2426	NC	60S ribosomal protein L4 OS=*Dictyostelium discoideum* OX=44689 GN=rpl4 PE=1 SV=1
Q54QW5	1,062659723	0,4134	NC	Ragulator complex protein LAMTOR5 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283567 PE=3 SV=1
Q54Y55	1,060643544	0,3901	NC	Dual specificity protein kinase shkC OS=*Dictyostelium discoideum* OX=44689 GN=shkC PE=3 SV=1
Q55GU3	1,060451447	0,3751	NC	Probable mitochondrial pyruvate carrier 2 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0268478 PE=3 SV=1
Q550H6	1,059792076	0,3420	NC	Ras-related protein Rab-11C OS=*Dictyostelium discoideum* OX=44689 GN=rab11C PE=1 SV=1
Q54Y72	1,059759016	0,3521	NC	Rho GTPase-activating protein gacA OS=*Dictyostelium discoideum* OX=44689 GN=gacA PE=3 SV=1
P54642	1,057033635	0,4566	NC	V-type proton ATPase proteolipid subunit OS=*Dictyostelium discoideum* OX=44689 GN=vatP PE=2 SV=1
Q54GE6	1,056680097	0,4207	NC	Probable malate dehydrogenase 1 OS=*Dictyostelium discoideum* OX=44689 GN=mdhA PE=1 SV=1

Q54G86	1,054578115	0,3691	NC	60S ribosomal protein L23 OS=*Dictyostelium discoideum* OX=44689 GN=rpl23 PE=1 SV=1
P32252	1,052052581	0,4086	NC	Ras-like protein rasB OS=*Dictyostelium discoideum* OX=44689 GN=rasB PE=1 SV=1
Q54U94	1,051580727	0,4020	NC	RNA exonuclease 4 OS=*Dictyostelium discoideum* OX=44689 GN=rexo4 PE=3 SV=1
Q54IT3	1,051119781	0,4347	NC	Probable flavin-containing monoamine oxidase A OS=*Dictyostelium discoideum* OX=44689 GN=maoA PE=3 SV=1
Q54YR4	1,050440823	0,4165	NC	Protein transport protein Sec61 subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=sec61b PE=3 SV=1
Q557D2	1,046977371	0,4340	NC	Glucose-6-phosphate 1-dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=g6pd-1 PE=3 SV=1
Q54KS4	1,045234393	0,3516	NC	Guanine nucleotide-binding protein-like 3 homolog OS=*Dictyostelium discoideum* OX=44689 GN=gnl3 PE=3 SV=1
Q75JD5	1,043977495	0,4257	NC	Phosphoenolpyruvate carboxykinase (ATP) OS=*Dictyostelium discoideum* OX=44689 GN=pckA PE=1 SV=1
Q557H1	1,043233569	0,4555	NC	Dipeptidyl peptidase 3 OS=*Dictyostelium discoideum* OX=44689 GN=dpp3-1 PE=3 SV=1
Q54WU3	1,040323782	0,1179	NC	Methionine aminopeptidase 1 OS=*Dictyostelium discoideum* OX=44689 GN=metap1 PE=3 SV=1
Q559Z0	1,037194587	0,4167	NC	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufa9 PE=3 SV=1
Q54KZ8	1,034605478	0,4379	NC	Eukaryotic translation initiation factor 3 subunit M OS=*Dictyostelium discoideum* OX=44689 GN=eif3m PE=1 SV=1
Q54DD2	1,034378781	0,4600	NC	Thimet-like oligopeptidase OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292362 PE=3 SV=1
P14329	1,034076381	0,3941	NC	60S ribosomal protein L19 OS=*Dictyostelium discoideum* OX=44689 GN=rpl19 PE=1 SV=1
Q54NS1	1,033374098	0,4365	NC	Putative transferase caf17 homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=caf17 PE=3 SV=1
O00899	1,032183325	0,4584	NC	Ras GTPase-activating-like protein gapA OS=*Dictyostelium discoideum* OX=44689 GN=gapA PE=1 SV=1
Q86A67	1,031202014	0,3156	NC	Fructose-bisphosphate aldolase OS=*Dictyostelium discoideum* OX=44689 GN=fba PE=3 SV=1
P36411	1,028712184	0,3717	NC	Ras-related protein Rab-7A OS=*Dictyostelium discoideum* OX=44689 GN=rab7A PE=1 SV=1
Q9UA41	1,027935447	0,4602	NC	Peptidyl-prolyl cis-trans isomerase D, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cypD PE=1 SV=1
Q54MR6	1,027927938	0,4688	NC	Heat shock 70-related protein 5 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0285709 PE=3 SV=1
Q54GW3	1,027691155	0,4448	NC	Coiled-coil domain-containing protein 124 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289893 PE=3 SV=1
Q58A42	1,026907187	0,3926	NC	Protein DD3-3 OS=*Dictyostelium discoideum* OX=44689 GN=DD3-3 PE=2 SV=1
Q553V1	1,024997499	0,3782	NC	Citrate synthase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cs PE=3 SV=1
Q54UU3	1,023415381	0,4504	NC	40S ribosomal protein S6 OS=*Dictyostelium discoideum* OX=44689 GN=rps6 PE=1 SV=1

Q869Z4	1,020961485	0,4524	NC	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pck2 PE=3 SV=1
Q54PV8	1,020354254	0,4824	NC	Inorganic pyrophosphatase OS=*Dictyostelium discoideum* OX=44689 GN=ppa1 PE=1 SV=1
Q86AV5	1,019845313	0,4760	NC	Mitochondrial substrate carrier family protein X OS=*Dictyostelium discoideum* OX=44689 GN=mcfX PE=3 SV=1
Q556J2	1,019723534	0,4667	NC	3-ketodihydrosphingosine reductase OS=*Dictyostelium discoideum* OX=44689 GN=ksrA-1 PE=3 SV=1
Q54T27	1,019546971	0,4606	NC	Eukaryotic translation initiation factor 2 subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=eif2s2 PE=3 SV=1
Q54CX6	1,019335728	0,4701	NC	Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=hibA PE=3 SV=1
Q94469	1,01929849	0,4671	NC	Glyceraldehyde-3-phosphate dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=gpdA PE=1 SV=2
Q54P23	1,016354432	0,4776	NC	Stromal cell-derived factor 2-like protein OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0284847 PE=3 SV=1
B0G104	1,013043223	0,4883	NC	60S ribosome subunit biogenesis protein NIP7 homolog OS=*Dictyostelium discoideum* OX=44689 GN=nip7 PE=3 SV=1
Q54XS2	1,010457844	0,4554	NC	Probable aconitate hydratase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aco2 PE=3 SV=1
Q54NX0	1,010163179	0,4856	NC	Putative rRNA methyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=fsjC PE=3 SV=1
P13833	1,009367175	0,4797	NC	Myosin regulatory light chain OS=*Dictyostelium discoideum* OX=44689 GN=mlcR PE=2 SV=1
Q65YR8	1,009122933	0,4886	NC	Cystatin-A1 OS=*Dictyostelium discoideum* OX=44689 GN=cpiA PE=2 SV=1
Q86KC1	1,006159753	0,4915	NC	Probable GH family 25 lysozyme 2 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274181 PE=3 SV=1
Q869R8	1,005949231	0,4873	NC	Triosephosphate isomerase OS=*Dictyostelium discoideum* OX=44689 GN=tpiA PE=3 SV=1
Q55BV5	1,005873706	0,4898	NC	26S proteasome regulatory subunit 4 homolog OS=*Dictyostelium discoideum* OX=44689 GN=psmC1 PE=1 SV=1
O96042	1,003820961	0,4969	NC	Differentiation-associated protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=dia2 PE=2 SV=1
Q54Z09	1,001237893	0,4972	NC	60S ribosomal protein L14 OS=*Dictyostelium discoideum* OX=44689 GN=rpl14 PE=3 SV=1
Q95VZ3	-1,000397831	0,4995	NC	Protein CARMIL OS=*Dictyostelium discoideum* OX=44689 GN=carmil PE=1 SV=1
Q8T1V4	-1,000507732	0,4995	NC	40S ribosomal protein S27 OS=*Dictyostelium discoideum* OX=44689 GN=rps27 PE=3 SV=2
Q54BN0	-1,004301985	0,4921	NC	Transmembrane emp24 domain-containing protein B OS=*Dictyostelium discoideum* OX=44689 GN=empB PE=3 SV=1
Q54WD9	-1,005366031	0,4958	NC	Probable tyrosine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mtyrS PE=3 SV=1
Q1ZXL7	-1,007616984	0,4892	NC	Probable cytochrome P450 508A3 OS=*Dictyostelium discoideum* OX=44689 GN=cyp508A3-1 PE=3 SV=1
Q54S03	-1,00958284	0,4576	NC	Probable ATP-dependent RNA helicase ddx18 OS=*Dictyostelium discoideum* OX=44689 GN=ddx18 PE=3 SV=1

Q54CE0	-1,010178489	0,4753	NC	Probable ATP-dependent RNA helicase ddx17 OS=*Dictyostelium discoideum* OX=44689 GN=ddx17 PE=3 SV=1
Q55C70	-1,010749013	0,4820	NC	Mitochondrial import inner membrane translocase subunit tim50 OS=*Dictyostelium discoideum* OX=44689 GN=timm50 PE=3 SV=1
Q54TU8	-1,010818306	0,4892	NC	Calcium load-activated calcium channel homolog OS=*Dictyostelium discoideum* OX=44689 GN=tmco1 PE=2 SV=1
Q75JK6	-1,013400313	0,4758	NC	ATP synthase subunit epsilon, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5e PE=3 SV=1
Q54J69	-1,013884266	0,4425	NC	60S ribosomal protein L10 OS=*Dictyostelium discoideum* OX=44689 GN=rpl10 PE=1 SV=2
O96759	-1,016100995	0,4855	NC	Alkyldihydroxyacetonephosphate synthase OS=*Dictyostelium discoideum* OX=44689 GN=eapA PE=1 SV=1
Q4W6B5	-1,016634204	0,4562	NC	Mitochondrial-processing peptidase subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=mppB PE=1 SV=1
Q55DJ3	-1,020880199	0,4705	NC	Protein MAK16 homolog OS=*Dictyostelium discoideum* OX=44689 GN=mak16l PE=3 SV=1
Q54QM8	-1,021935578	0,4512	NC	60S ribosomal protein L26 OS=*Dictyostelium discoideum* OX=44689 GN=rpl26 PE=3 SV=1
Q54WG0	-1,022209628	0,4774	NC	Density-regulated protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=denr PE=3 SV=1
Q54XC4	-1,025852316	0,4766	NC	Myeloid-derived growth factor homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0279047 PE=3 SV=2
Q54F47	-1,029514489	0,4629	NC	Probable cytochrome P450 513C1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp513C1 PE=3 SV=1
Q54MG6	-1,030188091	0,4259	NC	60S ribosomal protein L37 OS=*Dictyostelium discoideum* OX=44689 GN=rpl37 PE=3 SV=1
Q55BX3	-1,036472743	0,4194	NC	NDRG-like protein OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0270324 PE=3 SV=1
Q55BE6	-1,037873458	0,3946	NC	60S ribosomal protein L27 OS=*Dictyostelium discoideum* OX=44689 GN=rpl27 PE=3 SV=1
Q75JR2	-1,037943736	0,3960	NC	Isocitrate dehydrogenase [NADP], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=idhM PE=3 SV=1
Q9BKJ9	-1,041330089	0,3576	NC	Lysosome membrane protein 2-B OS=*Dictyostelium discoideum* OX=44689 GN=lmpB PE=1 SV=1
Q54UG4	-1,042441833	0,4357	NC	60S ribosomal protein L37a OS=*Dictyostelium discoideum* OX=44689 GN=rpl37A PE=3 SV=1
Q54QG4	-1,042779898	0,4618	NC	Uncharacterized protein DDB_G0283843 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283843 PE=4 SV=1
Q9GRX6	-1,04945222	0,4189	NC	Apoptosis-inducing factor 1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aif PE=2 SV=1
Q54YW1	-1,051249338	0,4301	NC	ELMO domain-containing protein A OS=*Dictyostelium discoideum* OX=44689 GN=elmoA PE=1 SV=1
P36412	-1,053864972	0,3640	NC	Ras-related protein Rab-11A OS=*Dictyostelium discoideum* OX=44689 GN=rab11A PE=1 SV=1
Q55AI5	-1,054460943	0,4107	NC	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=scsC PE=3 SV=1
Q23883	-1,055495172	0,4401	NC	NADH-ubiquinone oxidoreductase 49 kDa subunit OS=*Dictyostelium discoideum* OX=44689 GN=nad7 PE=1 SV=1

Q54PQ4	-1,057227021	0,4436	NC	Ras guanine nucleotide exchange factor A OS=*Dictyostelium discoideum* OX=44689 GN=gefA PE=1 SV=1
Q964D8	-1,057653719	0,4038	NC	Beta-ureidopropionase OS=*Dictyostelium discoideum* OX=44689 GN=pyd3 PE=1 SV=1
Q54LV3	-1,0589035	0,3587	NC	Elongation factor Ts, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=tsfm PE=3 SV=1
Q8T2J9	-1,065284503	0,3666	NC	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mccb PE=3 SV=2
Q8T2K9	-1,066609583	0,3798	NC	Malate synthase OS=*Dictyostelium discoideum* OX=44689 GN=masA PE=2 SV=2
Q54GI9	-1,07372378	0,3921	NC	Prohibitin-1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=phbA PE=3 SV=1
Q54N00	-1,073819251	0,4419	NC	Formin-H OS=*Dictyostelium discoideum* OX=44689 GN=forH PE=1 SV=1
Q54E20	-1,076900373	0,2256	NC	60S ribosomal protein L13 OS=*Dictyostelium discoideum* OX=44689 GN=rpl13 PE=1 SV=1
Q54GB3	-1,079606165	0,4138	NC	Synaptobrevin-B OS=*Dictyostelium discoideum* OX=44689 GN=sybB PE=3 SV=1
A0A0F6B980	-1,07960928	0,3827	NC	Thioredoxin OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=trxA PE=3 SV=1
Q55F21	-1,081081036	0,2993	NC	Aspartate aminotransferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aatA PE=3 SV=1
Q550U9	-1,08127335	0,3755	NC	Phospholipase B-like protein A OS=*Dictyostelium discoideum* OX=44689 GN=plbA PE=1 SV=1
Q54I10	-1,08147895	0,3806	NC	Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mmsdh PE=3 SV=1
Q54JV8	-1,088751072	0,3484	NC	Probable glycine cleavage system H protein 1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcvH1 PE=3 SV=1
Q54WZ2	-1,097362266	0,3839	NC	Vacuolin-B OS=*Dictyostelium discoideum* OX=44689 GN=vacB PE=1 SV=1
O96625	-1,100426978	0,2208	NC	Actin-related protein 2/3 complex subunit 4 OS=*Dictyostelium discoideum* OX=44689 GN=arcD PE=1 SV=1
Q86JA1	-1,10105045	0,3721	NC	26S proteasome regulatory subunit 7 OS=*Dictyostelium discoideum* OX=44689 GN=psmC2 PE=1 SV=1
Q54ME1	-1,101470849	0,3518	NC	Gamete and mating-type specific protein A OS=*Dictyostelium discoideum* OX=44689 GN=gmsA PE=2 SV=1
Q54ST4	-1,118314791	0,3383	NC	Probable replication factor C subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=rfc5 PE=3 SV=1
Q54Q94	-1,118501179	0,3770	NC	Probable ATP-dependent RNA helicase ddx10 OS=*Dictyostelium discoideum* OX=44689 GN=ddx10 PE=3 SV=1
Q54GE3	-1,118573414	0,3393	NC	Vacuolar protein sorting-associated protein 45 OS=*Dictyostelium discoideum* OX=44689 GN=vps45 PE=1 SV=1
Q54JD2	-1,119789454	0,3215	NC	Putative uncharacterized protein DDB_G0288137 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288137 PE=4 SV=1
Q6UK63	-1,119899986	0,3606	NC	Protein pirA OS=*Dictyostelium discoideum* OX=44689 GN=pirA PE=1 SV=1
P0C7B6	-1,123118215	0,3275	NC	Type-1 glutamine synthetase 2 OS=*Dictyostelium discoideum* OX=44689 GN=glnA2 PE=1 SV=1

Q54EQ1	-1,123646589	0,3263	NC	Eukaryotic translation initiation factor 3 subunit K OS=*Dictyostelium discoideum* OX=44689 GN=eif3K PE=3 SV=2
Q86HX0	-1,124649934	0,3141	NC	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhB PE=1 SV=1
Q54R41	-1,128167195	0,3058	NC	Guanine nucleotide-binding protein alpha-9 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaI PE=2 SV=1
P32256	-1,130256659	0,2021	NC	Tubulin beta chain OS=*Dictyostelium discoideum* OX=44689 GN=tubB PE=1 SV=2
Q54M18	-1,130547112	0,2862	NC	Bifunctional protein argC, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=argC PE=1 SV=1
Q54KB7	-1,131281117	0,2335	NC	Glutamate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gluD PE=1 SV=1
Q55CS9	-1,134183416	0,1589	NC	ATP synthase subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp5b PE=1 SV=1
Q54X04	-1,134891961	0,3171	NC	Probable cysteine desulfurase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=nfs1 PE=1 SV=1
Q86I43	-1,136205084	0,3586	NC	Uncharacterized protein DDB_G0275161 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275161 PE=2 SV=1
Q54XI5	-1,136847904	0,3290	NC	60S ribosomal protein L9 OS=*Dictyostelium discoideum* OX=44689 GN=rpl9 PE=1 SV=2
Q869Y7	-1,137735715	0,0595	NC	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=odhB PE=1 SV=1
P34136	-1,14274108	0,3168	NC	3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 OS=*Dictyostelium discoideum* OX=44689 GN=hmgB PE=2 SV=2
Q55G75	-1,148829959	0,3041	NC	PH domain-containing protein DDB_G0267786 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267786 PE=4 SV=1
Q54JC2	-1,149189094	0,2498	NC	Uncharacterized protein DDB_G0288155 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288155 PE=1 SV=1
Q54MT2	-1,149198863	0,3350	NC	Nucleolar protein 56 OS=*Dictyostelium discoideum* OX=44689 GN=nop56 PE=3 SV=1
Q54DF7	-1,156457357	0,1974	NC	Probable serine/threonine-protein kinase DDB_G0292354 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0292354 PE=3 SV=1
Q54NU0	-1,159420982	0,3675	NC	Flap endonuclease 1 OS=*Dictyostelium discoideum* OX=44689 GN=repG PE=3 SV=1
P36413	-1,160297444	0,1877	NC	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhC PE=1 SV=2
P34139	-1,16338943	0,2431	NC	Ras-related protein Rab-1A OS=*Dictyostelium discoideum* OX=44689 GN=rab1A PE=2 SV=2; Additional IDs concatenated into MaxParsimony group: P20790, P34140, Q54NU2; Additional IDs concatenated into MaxParsimony group: P20790, P34140, Q54NU2
Q54DG1	-1,164744673	0,3130	NC	Aldehyde dehydrogenase family 3 comG OS=*Dictyostelium discoideum* OX=44689 GN=comG PE=3 SV=1
Q54E21	-1,168050948	0,3192	NC	Probable replication factor C subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=rfc2 PE=3 SV=1
Q54C70	-1,16934402	0,1542	NC	Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=pdhA PE=1 SV=1
Q54I58	-1,170887431	0,2771	NC	Protein NipSnap homolog OS=*Dictyostelium discoideum* OX=44689 GN=nipsnap PE=3 SV=1

Q54U31	-1,172696868	0,3521	NC	Dual specificity protein kinase shkD OS=*Dictyostelium discoideum* OX=44689 GN=shkD PE=3 SV=1
Q95YL5	-1,181845106	0,3253	NC	Penta-EF hand domain-containing protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=pefA PE=1 SV=1
P54641	-1,18419959	0,0341	NC	V-type proton ATPase subunit d OS=*Dictyostelium discoideum* OX=44689 GN=vatD-1 PE=1 SV=2
Q8I0H7	-1,190429565	0,2145	NC	Heat shock 70 kDa protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mhsp70 PE=1 SV=1
Q559Z4	-1,193318919	0,2531	NC	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=*Dictyostelium discoideum* OX=44689 GN=ndufa5 PE=3 SV=1
Q54XE6	-1,194584741	0,3146	NC	Probable H/ACA ribonucleoprotein complex subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=gar1 PE=3 SV=1
P02887	-1,19743567	0,1828	NC	Discoidin-1 subunit B/C OS=*Dictyostelium discoideum* OX=44689 GN=dscC-1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P02886, P02888, P42530; Additional IDs concatenated into MaxParsimony group: P02886, P02888, P42530
Q54DK1	-1,199616674	0,3132	NC	Sulfide:quinone oxidoreductase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sqor PE=3 SV=1
Q869N6	-1,202926445	0,0790	NC	3-hydroxybutyryl-CoA dehydratase-like protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271866 PE=3 SV=1
Q54Q31	-1,203396321	0,2550	NC	Prohibitin-2 OS=*Dictyostelium discoideum* OX=44689 GN=phbB PE=3 SV=1
Q54RB9	-1,203403755	0,1982	NC	Calcium-binding mitochondrial carrier protein OS=*Dictyostelium discoideum* OX=44689 GN=mcfO PE=3 SV=1
Q86B05	-1,20431016	0,3622	NC	Probable ribosome biogenesis protein RLP24 OS=*Dictyostelium discoideum* OX=44689 GN=rlp24 PE=2 SV=1
Q55D66	-1,204637737	0,2789	NC	Proteasome subunit beta type-3 OS=*Dictyostelium discoideum* OX=44689 GN=psmB3 PE=3 SV=1
Q54LV8	-1,20508016	0,2234	NC	60S ribosomal protein L34 OS=*Dictyostelium discoideum* OX=44689 GN=rpl34 PE=3 SV=1
Q54RA2	-1,206573184	0,1443	NC	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0283293 PE=3 SV=1
Q86L04	-1,207162073	0,2763	NC	TNF receptor-associated protein 1 homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=trap1 PE=2 SV=1
Q54XM6	-1,208325927	0,2924	NC	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=etfdh PE=3 SV=1
Q54D07	-1,210707343	0,2535	NC	Cytochrome c1, heme protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=cyc1 PE=3 SV=1
P09556	-1,211235775	0,1788	NC	Uridine 5'-monophosphate synthase OS=*Dictyostelium discoideum* OX=44689 GN=pyr56 PE=1 SV=2
Q54B67	-1,214561762	0,2215	NC	Mitochondrial substrate carrier family protein Z OS=*Dictyostelium discoideum* OX=44689 GN=mcfZ PE=2 SV=1
Q54J68	-1,215307468	0,1714	NC	10 kDa heat shock protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=hspe1 PE=3 SV=1
Q54YZ0	-1,217465544	0,0630	NC	UTP--glucose-1-phosphate uridylyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=ugpB PE=2 SV=1
Q54IN6	-1,221535315	0,1644	NC	Uncharacterized protein DDB_G0288629 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0288629 PE=4 SV=1

Q02720	-1,223317433	0,3518	NC	Casein kinase II subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=casK PE=2 SV=1
O00909	-1,225972202	0,3029	NC	ADP-ribosylation factor 1 OS=*Dictyostelium discoideum* OX=44689 GN=arfA PE=1 SV=3
Q54IF7	-1,22880024	0,2376	NC	Vacuolar protein sorting-associated protein 29 OS=*Dictyostelium discoideum* OX=44689 GN=vps29 PE=3 SV=1
P54671	-1,231621778	0,1115	NC	Histone H1 OS=*Dictyostelium discoideum* OX=44689 GN=H1 PE=1 SV=3
P02886	-1,232485871	0,1694	NC	Discoidin-1 subunit A OS=*Dictyostelium discoideum* OX=44689 GN=dscA-1 PE=1 SV=3
Q54G58	-1,238200511	0,0536	NC	Uncharacterized protein DDB_G0290387 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0290387 PE=3 SV=1
P08800	-1,242095894	0,0860	NC	UTP--glucose-1-phosphate uridylyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=uppA PE=2 SV=2
Q54KN7	-1,243878596	0,1492	NC	Putative thioredoxin-5 OS=*Dictyostelium discoideum* OX=44689 GN=trxE PE=3 SV=1
Q54PN7	-1,244655859	0,3498	NC	26S proteasome regulatory subunit 6A homolog OS=*Dictyostelium discoideum* OX=44689 GN=psmC3 PE=1 SV=1
Q9NGQ2	-1,24588041	0,1561	NC	Kinesin-related protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=kif1 PE=1 SV=1
Q54N47	-1,246095909	0,1768	NC	Branched-chain-amino-acid aminotransferase OS=*Dictyostelium discoideum* OX=44689 GN=bcaA PE=3 SV=1
Q55BP5	-1,248690546	0,3380	NC	Probable DNA topoisomerase 2 OS=*Dictyostelium discoideum* OX=44689 GN=top2 PE=3 SV=1
Q54DJ0	-1,253137306	0,0626	NC	Ribosome production factor 2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=bxdc1 PE=3 SV=1
Q54EX7	-1,253147576	0,2040	NC	Glutaredoxin-like protein OS=*Dictyostelium discoideum* OX=44689 GN=grxB PE=3 SV=1
P26200	-1,254234378	0,2930	NC	Profilin-2 OS=*Dictyostelium discoideum* OX=44689 GN=proB PE=1 SV=1
Q54QB1	-1,254695814	0,2837	NC	Extracellular signal-regulated kinase 2 OS=*Dictyostelium discoideum* OX=44689 GN=erkB PE=1 SV=1
Q54NS7	-1,257756426	0,2221	NC	PRA1 family protein 2 OS=*Dictyostelium discoideum* OX=44689 GN=prafB PE=3 SV=2
Q54JN0	-1,262100612	0,0842	NC	Ribosome biogenesis protein BRX1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=bxdc2 PE=3 SV=1
Q54K35	-1,265108936	0,2829	NC	Mitochondrial import inner membrane translocase subunit tim17 OS=*Dictyostelium discoideum* OX=44689 GN=timm17 PE=3 SV=1
P54659	-1,26777401	0,0651	NC	Major vault protein beta OS=*Dictyostelium discoideum* OX=44689 GN=mvpB PE=1 SV=1
Q54ZM4	-1,274494814	0,2368	NC	Probable cytochrome P450 518A1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp518A1 PE=3 SV=1
Q54JD9	-1,274987276	0,0157	NC	Probable succinyl-CoA:3-ketoacid coenzyme A transferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=oxct1 PE=3 SV=1
Q1ZXG4	-1,276600099	0,0250	NC	Proliferation-associated protein A OS=*Dictyostelium discoideum* OX=44689 GN=prlA PE=2 SV=1
Q553M7	-1,277450302	0,0799	NC	60S ribosomal protein L13a OS=*Dictyostelium discoideum* OX=44689 GN=rpl13a PE=1 SV=1

Q54QK7	-1,278807541	0,0655	NC	Probable dimethyladenosine transferase OS=*Dictyostelium discoideum* OX=44689 GN=dimt1 PE=3 SV=1
Q54HB2	-1,279580624	0,1189	NC	Elongation factor Tu, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=tufm PE=1 SV=2
Q54BM3	-1,281612062	0,2787	NC	Mitochondrial substrate carrier family protein G OS=*Dictyostelium discoideum* OX=44689 GN=mcfG PE=2 SV=1
P34118	-1,288386904	0,0984	NC	Major vault protein alpha OS=*Dictyostelium discoideum* OX=44689 GN=mvpA PE=1 SV=1
Q55C75	-1,288630478	0,0734	NC	26S proteasome non-ATPase regulatory subunit 6 OS=*Dictyostelium discoideum* OX=44689 GN=psmD6 PE=1 SV=1
P14797	-1,296962778	0,0379	NC	Ubiquitin-40S ribosomal protein S27a OS=*Dictyostelium discoideum* OX=44689 GN=ubqC PE=1 SV=2
Q54VI3	-1,302057592	0,0466	NC	Glutamate dehydrogenase 2 OS=*Dictyostelium discoideum* OX=44689 GN=glud2 PE=1 SV=2
P54654	-1,30653811	0,1473	NC	Adenylyl cyclase-associated protein OS=*Dictyostelium discoideum* OX=44689 GN=cap PE=1 SV=1
Q55CC2	-1,306880763	0,0521	NC	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sdhB PE=3 SV=1
Q75JL2	-1,312041152	0,2896	NC	Mitochondrial DNA repair protein recA homolog OS=*Dictyostelium discoideum* OX=44689 GN=recA PE=3 SV=1
Q86AQ7	-1,319135491	0,0228	SC	Vesicle-associated membrane protein 7B OS=*Dictyostelium discoideum* OX=44689 GN=vamp7B PE=3 SV=1
Q86AD9	-1,321152609	0,1517	NC	Probable acetyl-CoA acetyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271544 PE=2 SV=1
Q54F93	-1,323614365	0,1561	NC	Mitochondrial-processing peptidase subunit alpha-2 OS=*Dictyostelium discoideum* OX=44689 GN=mppA2 PE=1 SV=1
Q54KM7	-1,327617847	0,2855	NC	Glycine dehydrogenase (decarboxylating), mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcvP PE=3 SV=1
Q86CR8	-1,33074292	0,0225	C	Autophagy-related protein 8 OS=*Dictyostelium discoideum* OX=44689 GN=atg8 PE=2 SV=1
Q54X82	-1,330844934	0,0816	NC	AP-1 complex subunit beta OS=*Dictyostelium discoideum* OX=44689 GN=ap1b1 PE=3 SV=1
Q54JE4	-1,331823001	0,1609	NC	2-oxoglutarate dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ogdh PE=3 SV=1
Q54WM4	-1,35255154	0,1964	NC	Eukaryotic translation initiation factor 3 subunit G OS=*Dictyostelium discoideum* OX=44689 GN=eif3G PE=3 SV=1
Q553V2	-1,356963017	0,0957	NC	Methylmalonyl-CoA epimerase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mcee PE=3 SV=1
Q554U9	-1,359281137	0,0328	SC	Eukaryotic translation initiation factor 3 subunit D OS=*Dictyostelium discoideum* OX=44689 GN=eif3d PE=3 SV=1
P48160	-1,359297378	0,0281	SC	60S ribosomal protein L27a OS=*Dictyostelium discoideum* OX=44689 GN=rpl27a PE=3 SV=1
Q54LT2	-1,361191205	0,1262	NC	Uricase OS=*Dictyostelium discoideum* OX=44689 GN=uox PE=3 SV=1
P32253	-1,363357247	0,1146	NC	Ras-like protein rasC OS=*Dictyostelium discoideum* OX=44689 GN=rasC PE=2 SV=1
Q54XF7	-1,364331548	0,0684	NC	Cullin-5 OS=*Dictyostelium discoideum* OX=44689 GN=culE PE=3 SV=1

Q54T46	-1,364624197	0,2553	NC	Probable Xaa-Pro aminopeptidase 3 OS=*Dictyostelium discoideum* OX=44689 GN=xpnpep3 PE=2 SV=1
Q54VG0	-1,366156594	0,1219	NC	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1 homolog, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=odhA PE=3 SV=1
Q54QR3	-1,390828678	0,1306	NC	Ras-related protein Rab-32A OS=*Dictyostelium discoideum* OX=44689 GN=rab32A PE=1 SV=1
Q54HG9	-1,396750547	0,1606	NC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit swp1 OS=*Dictyostelium discoideum* OX=44689 GN=swp1 PE=3 SV=1
P34046	-1,407825023	0,0550	NSC	Guanine nucleotide-binding protein alpha-8 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaH PE=2 SV=2
Q54BF6	-1,409204464	0,1783	NC	Mitochondrial substrate carrier family protein N OS=*Dictyostelium discoideum* OX=44689 GN=mcfN PE=1 SV=2
Q54UU8	-1,417405863	0,2130	NC	Thioredoxin reductase OS=*Dictyostelium discoideum* OX=44689 GN=trrA PE=3 SV=1
Q86J23	-1,424692195	0,1369	NSC	Ragulator complex protein LAMTOR3 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274833 PE=3 SV=1
Q54P26	-1,426585637	0,2182	NC	Probable serine/threonine-protein kinase samkB OS=*Dictyostelium discoideum* OX=44689 GN=samkB PE=3 SV=1
Q54K93	-1,427257902	0,0228	C	Putative uncharacterized protein DDB_G0287517 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0287517 PE=4 SV=1
P24005	-1,428498297	0,0992	NSC	Calcium-regulated actin-bundling protein OS=*Dictyostelium discoideum* OX=44689 GN=abpB PE=1 SV=1
Q55GJ6	-1,433618813	0,1087	NSC	Proteasome subunit beta type-6 OS=*Dictyostelium discoideum* OX=44689 GN=psmB6 PE=1 SV=1
Q1ZXF1	-1,434747965	0,1081	NSC	Probable enoyl-CoA hydratase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=echs1 PE=3 SV=1
Q86HD3	-1,435607923	0,0042	SC	Ribosome assembly factor mrt4 OS=*Dictyostelium discoideum* OX=44689 GN=mrt4 PE=3 SV=1
Q559X6	-1,435751655	0,1090	NSC	Ras-related protein Rab-2B OS=*Dictyostelium discoideum* OX=44689 GN=rab2B PE=3 SV=1
Q54R47	-1,436386157	0,1691	NSC	Glutaryl-CoA dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gcdh PE=3 SV=1
P54644	-1,441564447	0,1863	NSC	RAC family serine/threonine-protein kinase homolog OS=*Dictyostelium discoideum* OX=44689 GN=pkbA PE=1 SV=1
Q37315	-1,445409216	0,0768	NSC	ATP synthase subunit 9, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp9 PE=3 SV=1
Q7KWL3	-1,447154064	0,1407	NSC	DDB1- and CUL4-associated factor 13 OS=*Dictyostelium discoideum* OX=44689 GN=wdsof1 PE=3 SV=1
Q554Z5	-1,447764982	0,1316	NSC	Acyl-CoA synthetase short-chain family member B, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=aslB PE=3 SV=1
Q54WA4	-1,454040823	0,0817	NSC	Probable 28S ribosomal protein S10, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps10 PE=3 SV=1
Q54I90	-1,47056584	0,0910	NSC	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=ndufv1 PE=2 SV=1
Q86IV4	-1,474421298	0,0528	NSC	PH domain-containing protein DDB_G0274775 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0274775 PE=4 SV=1

P0C7W5	-1,482519601	0,1841	NSC	Uncharacterized protein DDB_G0281707 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0281707 PE=4 SV=1
Q555C8	-1,485458929	0,1338	NSC	Monothiol glutaredoxin-5, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=grx5 PE=3 SV=1
Q54M22	-1,492904951	0,0326	C	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=bkdA PE=3 SV=1
Q55CV5	-1,498626321	0,0820	NSC	Probable tetraspanin tspA OS=*Dictyostelium discoideum* OX=44689 GN=tspA PE=2 SV=1
Q54LP3	-1,507277698	0,0620	NSC	Dolichol-phosphate mannosyltransferase subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=dpm1 PE=3 SV=1
P36967	-1,512032349	0,1560	NSC	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=scsA PE=1 SV=3
Q54FL2	-1,516063408	0,1570	NSC	Ras-related protein RabG2 OS=*Dictyostelium discoideum* OX=44689 GN=rabG2 PE=3 SV=2
Q86IC8	-1,529109999	0,0386	C	Probable caffeoyl-CoA O-methyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=omt6 PE=1 SV=1
Q556Q3	-1,541904114	0,0592	NSC	Probable serine/threonine-protein kinase irlF OS=*Dictyostelium discoideum* OX=44689 GN=irlF-1 PE=3 SV=1
Q5V9F0	-1,542382668	0,0702	NSC	Cytosol aminopeptidase OS=*Dictyostelium discoideum* OX=44689 GN=lap PE=1 SV=1
Q9U641	-1,542403423	0,0200	SC	Conditioned medium factor receptor 1 OS=*Dictyostelium discoideum* OX=44689 GN=cmfB PE=1 SV=1
Q55FL5	-1,544110503	0,1514	NSC	Serine palmitoyltransferase 1 OS=*Dictyostelium discoideum* OX=44689 GN=sptA PE=3 SV=1
Q9U9R7	-1,546205318	0,0212	C	Gamma-soluble NSF attachment protein OS=*Dictyostelium discoideum* OX=44689 GN=snpC PE=1 SV=1
P08799	-1,54743033	0,0001	SC	Myosin-2 heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=mhcA PE=1 SV=3
P36416	-1,553101924	0,0480	NSC	N-terminal acetyltransferase complex ARD1 subunit homolog OS=*Dictyostelium discoideum* OX=44689 GN=natA PE=2 SV=1
B0G159	-1,557215673	0,1605	NSC	Mitochondrial substrate carrier family protein C OS=*Dictyostelium discoideum* OX=44689 GN=mcfC PE=2 SV=1
Q54KE6	-1,557896788	0,1072	NSC	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mccA PE=3 SV=1
Q55FN7	-1,558242209	0,0417	C	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=bkdB PE=3 SV=1
P53766	-1,562896072	0,1693	NSC	Uracil-DNA glycosylase OS=*Dictyostelium discoideum* OX=44689 GN=uglA PE=2 SV=2
P21837	-1,581299431	0,0753	NSC	Crystal protein OS=*Dictyostelium discoideum* OX=44689 GN=cryS PE=1 SV=1
Q7KWK5	-1,60634228	0,0212	C	Pre-mRNA-processing factor 19 OS=*Dictyostelium discoideum* OX=44689 GN=prp19 PE=3 SV=1
Q54FW9	-1,609570852	0,0553	NSC	WD repeat-containing protein DDB_G0290555 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0290555 PE=4 SV=1
Q552P9	-1,613187109	0,0887	NSC	Uncharacterized protein DDB_G0275933 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0275933 PE=3 SV=1
Q9U3X4	-1,620692782	0,0097	SC	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sdhA PE=3 SV=1

Q55GW4	-1,624865957	0,1185	NSC	Putative uncharacterized protein DDB_G0267482 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0267482 PE=4 SV=1
Q54C27	-1,650668829	0,1319	NSC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=ost1 PE=2 SV=1
Q76NU3	-1,650846545	0,0913	NSC	T-complex protein 1 subunit zeta OS=*Dictyostelium discoideum* OX=44689 GN=cct6 PE=1 SV=1
Q54GY8	-1,654404306	0,0669	NSC	Ras-related protein Rab-18 OS=*Dictyostelium discoideum* OX=44689 GN=rab18 PE=3 SV=1
Q8T2T5	-1,68329469	0,0479	NSC	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=sdhC PE=3 SV=1
Q54NU2	-1,689134744	0,0410	C	Ras-related protein Rab-1D OS=*Dictyostelium discoideum* OX=44689 GN=rab1D PE=1 SV=1
Q54YN3	-1,716629199	0,1110	NSC	ER membrane protein complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=emc3 PE=3 SV=1
O77203	-1,736526082	0,1578	NSC	Protein pianissimo A OS=*Dictyostelium discoideum* OX=44689 GN=piaA PE=1 SV=1
P34113	-1,738758158	0,0928	NSC	60S ribosomal protein L3 OS=*Dictyostelium discoideum* OX=44689 GN=rpl3 PE=1 SV=2
Q75JB5	-1,7408977	0,1320	NSC	Transmembrane protein 14 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0271790 PE=3 SV=1
Q55E60	-1,755951983	0,0489	NSC	Xaa-Pro dipeptidase OS=*Dictyostelium discoideum* OX=44689 GN=pepd PE=1 SV=1
O15736	-1,761655841	0,0277	C	Protein tipD OS=*Dictyostelium discoideum* OX=44689 GN=tipD PE=3 SV=1
Q54DW2	-1,79627937	0,0093	C	Probable endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=*Dictyostelium discoideum* OX=44689 GN=ergic3 PE=3 SV=1
Q54E49	-1,797069661	0,0728	NSC	Probable ATP-dependent RNA helicase ddx6 OS=*Dictyostelium discoideum* OX=44689 GN=ddx6 PE=3 SV=1
B0G180	-1,802906605	0,0580	NSC	Signal peptidase complex subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=spcs3 PE=3 SV=1
Q23887	-1,802975573	0,0357	C	Ribosomal protein S7, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mrps7 PE=3 SV=1
Q54RV6	-1,805196957	0,1318	NSC	Trafficking protein particle complex subunit 2 OS=*Dictyostelium discoideum* OX=44689 GN=trappc2 PE=3 SV=1
Q55BU8	-1,80539918	0,1072	NSC	Protein erg2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=erg2 PE=3 SV=1
Q54J97	-1,820505639	0,0367	SC	60 kDa heat shock protein, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=hspA PE=2 SV=1
Q55G10	-1,826464836	0,0649	NSC	Nicotinate phosphoribosyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=naprt PE=2 SV=1
Q54XX3	-1,829655641	0,0051	SC	60S ribosomal protein L5 OS=*Dictyostelium discoideum* OX=44689 GN=rpl5 PE=1 SV=1
Q54V77	-1,862554881	0,0178	C	CTP synthase OS=*Dictyostelium discoideum* OX=44689 GN=ctps PE=3 SV=1
Q55BF2	-1,867935404	0,0548	NSC	60S ribosomal export protein NMD3 OS=*Dictyostelium discoideum* OX=44689 GN=nmd3 PE=3 SV=1
Q55DT8	-1,883762647	0,0204	C	Probable acetylornithine aminotransferase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=argD PE=3 SV=1

Q54IP4	-1,904993545	0,0165	C	Dual specificity protein kinase shkB OS=*Dictyostelium discoideum* OX=44689 GN=shkB PE=3 SV=1
P54661	-1,905749991	0,1222	NSC	Small aggregate formation protein OS=*Dictyostelium discoideum* OX=44689 GN=smlA PE=2 SV=2
Q03380	-1,932774341	0,0235	SC	Comitin OS=*Dictyostelium discoideum* OX=44689 GN=comA PE=1 SV=1
P34092	-1,937850583	0,0684	NSC	Myosin IB heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=myoB PE=1 SV=2
P20790	-1,943414709	0,0068	SC	Ras-related protein Rab-8A OS=*Dictyostelium discoideum* OX=44689 GN=rab8A PE=3 SV=1
Q54G18	-2,040363869	0,0629	NSC	Rho GTPase-activating protein gacW OS=*Dictyostelium discoideum* OX=44689 GN=gacW PE=3 SV=1
Q54B10	-2,040434319	0,1246	NSC	NADPH oxidoreductase A OS=*Dictyostelium discoideum* OX=44689 GN=redA PE=2 SV=1
Q54C94	-2,1014763	0,1189	NSC	Ras guanine nucleotide exchange factor F OS=*Dictyostelium discoideum* OX=44689 GN=gefF PE=2 SV=1
Q54LT7	-2,132317946	0,0860	NSC	Probable cytochrome P450 519E1 OS=*Dictyostelium discoideum* OX=44689 GN=cyp519E1 PE=3 SV=1
O96622	-2,132791882	0,0015	SC	Actin-related protein 2/3 complex subunit 1 OS=*Dictyostelium discoideum* OX=44689 GN=arcA PE=1 SV=1
Q54NW7	-2,137152808	0,0336	C	Vesicle-associated membrane protein 7A OS=*Dictyostelium discoideum* OX=44689 GN=vamp7A PE=1 SV=1
Q54EW8	-2,147342144	0,0008	SC	Dihydrolipoyl dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=lpd PE=3 SV=1
P16894	-2,150092326	0,0008	SC	Guanine nucleotide-binding protein alpha-1 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaA PE=2 SV=1
P08796	-2,159676719	0,0566	NSC	Contact site A protein OS=*Dictyostelium discoideum* OX=44689 GN=csaA PE=1 SV=3
O15818	-2,170607895	0,0043	SC	Clustered mitochondria protein homolog OS=*Dictyostelium discoideum* OX=44689 GN=clua PE=1 SV=2
Q54IM8	-2,194947522	0,0061	C	Isobutyryl-CoA dehydrogenase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=acad8 PE=3 SV=1
Q54I92	-2,213500083	0,0205	C	Protein psiI OS=*Dictyostelium discoideum* OX=44689 GN=psiI PE=3 SV=1
Q54ET0	-2,225162906	0,0684	NSC	Metabotropic glutamate receptor-like protein E OS=*Dictyostelium discoideum* OX=44689 GN=grlE PE=2 SV=2
O21049	-2,232499996	0,0398	C	Cytochrome c oxidase subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=cox3 PE=3 SV=1
Q54H97	-2,23428648	0,0216	C	CBS domain-containing protein DDB_G0289609 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289609 PE=2 SV=1
Q54E62	-2,237751689	0,0246	SC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=*Dictyostelium discoideum* OX=44689 GN=ddost PE=3 SV=1
Q54L98	-2,2448923	0,0213	C	Protein KRTCAP2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286759 PE=3 SV=1
Q54HG7	-2,285827306	0,1053	NSC	Methylglutaconyl-CoA hydratase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=auh PE=3 SV=1
Q54E04	-2,288214637	0,0004	SC	Vacuolar proton translocating ATPase 100 kDa subunit OS=*Dictyostelium discoideum* OX=44689 GN=vatM PE=1 SV=2

Q54D63	-2,301528089	0,0008	SC	60S ribosomal protein L6 OS=*Dictyostelium discoideum* OX=44689 GN=rpl6 PE=1 SV=1
Q7YXD4	-2,327025083	0,0467	NSC	Protein P80 OS=*Dictyostelium discoideum* OX=44689 GN=p80 PE=2 SV=1
Q55A19	-2,351442488	0,0006	SC	40S ribosomal protein S23 OS=*Dictyostelium discoideum* OX=44689 GN=rps23 PE=3 SV=1
Q54N72	-2,355611276	0,0005	C	Probable nucleolar GTP-binding protein 1 OS=*Dictyostelium discoideum* OX=44689 GN=nog1 PE=1 SV=1
Q54KB8	-2,359812709	0,1311	NSC	Probable glutamate--tRNA ligase, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=gluS PE=2 SV=1
Q8MY12	-2,376676554	0,0299	C	Myosin heavy chain kinase C OS=*Dictyostelium discoideum* OX=44689 GN=mhkC PE=1 SV=1
Q94502	-2,413235869	0,0292	C	Neutral alpha-glucosidase AB OS=*Dictyostelium discoideum* OX=44689 GN=modA PE=3 SV=1
Q86KI1	-2,418565754	0,0171	C	AP-2 complex subunit alpha-2 OS=*Dictyostelium discoideum* OX=44689 GN=ap2a1-1 PE=3 SV=1
P0CE94	-2,46289571	0,0420	C	Talin-A OS=*Dictyostelium discoideum* OX=44689 GN=talA PE=3 SV=1
Q55CT1	-2,474983594	0,0634	NSC	NADPH--cytochrome P450 reductase OS=*Dictyostelium discoideum* OX=44689 GN=redB PE=2 SV=1
P15112	-2,492550847	0,0009	SC	Elongation factor 2 OS=*Dictyostelium discoideum* OX=44689 GN=efbA PE=1 SV=2
Q86C65	-2,503175005	0,1703	NSC	Serine/threonine-protein kinase tor OS=*Dictyostelium discoideum* OX=44689 GN=tor PE=1 SV=1
Q54LY8	-2,506038689	0,0158	C	Uncharacterized protein DDB_G0286299 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0286299 PE=4 SV=1
Q54GN8	-2,567995156	0,0118	C	Ribosome biogenesis protein NSA2 homolog OS=*Dictyostelium discoideum* OX=44689 GN=nsa2 PE=3 SV=1
Q86LA2	-2,571325423	0,0002	C	Eukaryotic translation initiation factor 3 subunit L OS=*Dictyostelium discoideum* OX=44689 GN=eif3L PE=3 SV=1
Q54TS4	-2,599739129	0,0017	C	Protein YIPF1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=yipf1 PE=3 SV=1
Q55EL3	-2,652870805	0,0030	C	Uridine-cytidine kinase A OS=*Dictyostelium discoideum* OX=44689 GN=udkA PE=3 SV=1
Q769F9	-2,65432857	0,0194	SC	Transmembrane emp24 domain-containing protein A OS=*Dictyostelium discoideum* OX=44689 GN=empA PE=3 SV=1
Q86A68	-2,682576267	0,0018	C	Phenylalanine--tRNA ligase, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=mpheS PE=3 SV=1
Q54WN5	-2,685233607	0,0017	C	U3 small nucleolar RNA-associated protein 6 homolog OS=*Dictyostelium discoideum* OX=44689 GN=utp6 PE=1 SV=1
Q54QE4	-2,693346571	0,0014	SC	Bifunctional purine synthesis protein purC/E OS=*Dictyostelium discoideum* OX=44689 GN=purC/E PE=1 SV=1
Q553B6	-2,766806942	0,0040	C	Glycylpeptide N-tetradecanoyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=nmt PE=3 SV=2
Q1ZXH9	-2,811160111	0,0425	SC	Probable lanosterol 14-alpha demethylase OS=*Dictyostelium discoideum* OX=44689 GN=cyp51 PE=3 SV=1
Q54JH4	-2,835940286	0,0070	C	P2X receptor E OS=*Dictyostelium discoideum* OX=44689 GN=p2xE PE=3 SV=2

P34045	-2,837615596	0,0018	C	Guanine nucleotide-binding protein alpha-7 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaG PE=2 SV=3
Q869N1	-2,935746802	0,0044	SC	Cytochrome c OS=*Dictyostelium discoideum* OX=44689 GN=cytC PE=3 SV=1
P34140	-2,982567539	0,0003	SC	Ras-related protein Rab-1B OS=*Dictyostelium discoideum* OX=44689 GN=rab1B PE=2 SV=2
Q54RR5	-3,009798902	0,0010	C	Probable short/branched chain specific acyl-CoA dehydrogenase OS=*Dictyostelium discoideum* OX=44689 GN=acadsb PE=3 SV=1
Q86JP3	-3,072974337	0,0070	SC	Ras-related protein Rab-5A OS=*Dictyostelium discoideum* OX=44689 GN=rab5A PE=3 SV=1
P18142	-3,148998064	0,0026	SC	cAMP-regulated D2 protein OS=*Dictyostelium discoideum* OX=44689 GN=D2 PE=2 SV=3
A0A0F6AZN3	-3,199933186	0,0547	NSC	Outer membrane protein A OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=ompA PE=1 SV=1
Q54XD8	-3,208498579	0,0008	SC	Eukaryotic translation initiation factor 2 subunit 3 OS=*Dictyostelium discoideum* OX=44689 GN=eif2s3 PE=2 SV=1
Q54K66	-3,248698386	0,0244	C	RNA-binding protein pno1 OS=*Dictyostelium discoideum* OX=44689 GN=pno1 PE=3 SV=1
P36409	-3,265601916	0,0009	SC	Ras-related protein Rab-2A OS=*Dictyostelium discoideum* OX=44689 GN=rab2A PE=2 SV=2
Q55DW4	-3,373166038	0,0081	C	ABC transporter G family member 1 OS=*Dictyostelium discoideum* OX=44689 GN=abcG1 PE=3 SV=1
O97470	-3,381696528	0,0024	SC	Mitochondrial substrate carrier family protein ancA OS=*Dictyostelium discoideum* OX=44689 GN=ancA PE=1 SV=1
Q54VF1	-3,427588275	0,0040	C	Probable ATP-dependent RNA helicase ddx56 OS=*Dictyostelium discoideum* OX=44689 GN=ddx56 PE=3 SV=1
Q7YTA6	-3,497276329	0,0055	C	Putative phagocytic receptor 1c OS=*Dictyostelium discoideum* OX=44689 GN=phg1c PE=2 SV=1
A0A0F6B0X1	-3,555428833	0,0158	SC	Murein lipoprotein OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=lpp PE=4 SV=1
Q55E94	-3,581127026	0,0215	C	Elongation factor G, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=gfm1 PE=3 SV=1
Q9XXV8	-3,591315383	0,0099	C	Myosin-K heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=myoK PE=2 SV=1
Q54XK2	-3,649262903	0,0018	SC	Protein transport protein Sec61 subunit alpha OS=*Dictyostelium discoideum* OX=44689 GN=sec61a PE=3 SV=1
Q54J42	-3,677076872	0,0240	C	Dolichyl-phosphate beta-glucosyltransferase OS=*Dictyostelium discoideum* OX=44689 GN=alg5 PE=2 SV=1
Q9U1M8	-3,882780808	0,0303	SC	Myosin-I heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=myoI PE=1 SV=1
Q54PV7	-3,918188077	0,0006	C	Eukaryotic translation initiation factor 2A OS=*Dictyostelium discoideum* OX=44689 GN=eif2a PE=3 SV=1
Q869Q3	-3,942781646	0,0732	NSC	Nck-associated protein 1 homolog OS=*Dictyostelium discoideum* OX=44689 GN=napA PE=1 SV=1
Q54KD0	-3,964452334	0,0342	C	TPR repeat-containing protein DDB_G0287407 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0287407 PE=4 SV=1
Q86JM5	-4,020475848	0,0005	C	Putative elongation of fatty acids protein DDB_G0272012 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0272012 PE=3 SV=1

Q54BU4	-4,14523001	0,0304	C	ABC transporter B family member 1 OS=*Dictyostelium discoideum* OX=44689 GN=abcB1 PE=3 SV=1
Q54RV9	-4,23283192	0,0076	C	Sphingosine-1-phosphate lyase OS=*Dictyostelium discoideum* OX=44689 GN=sglA PE=2 SV=1
Q869L3	-4,24280032	0,0342	C	Midasin OS=*Dictyostelium discoideum* OX=44689 GN=mdn1 PE=3 SV=2
Q55FP0	-4,28468568	0,0000	SC	Putative phagocytic receptor 1a OS=*Dictyostelium discoideum* OX=44689 GN=phg1a PE=2 SV=1
Q9NGP5	-4,343519437	0,0084	C	ABC transporter G family member 2 OS=*Dictyostelium discoideum* OX=44689 GN=abcG2 PE=1 SV=2
Q55FK2	-4,400324078	0,0005	SC	Ras-related protein Rab-6 OS=*Dictyostelium discoideum* OX=44689 GN=rab6 PE=3 SV=1
Q55FI4	-4,521388211	0,0023	SC	Nucleolar protein 58 OS=*Dictyostelium discoideum* OX=44689 GN=nop58 PE=3 SV=1
Q55CE0	-4,676113724	0,0260	C	Probable serine/threonine-protein kinase mkcF OS=*Dictyostelium discoideum* OX=44689 GN=mkcF PE=3 SV=1
Q54EX5	-4,706183925	0,0404	C	Serine palmitoyltransferase 2 OS=*Dictyostelium discoideum* OX=44689 GN=sptB PE=1 SV=1
P34036	-5,111829744	0,0002	SC	Dynein heavy chain, cytoplasmic OS=*Dictyostelium discoideum* OX=44689 GN=dhcA PE=1 SV=2
Q54X97	-5,169420368	0,0009	C	Eukaryotic translation initiation factor 3 subunit C OS=*Dictyostelium discoideum* OX=44689 GN=eif3C PE=3 SV=1
Q9NIV0	-5,205858486	0,0023	C	Rhesus-like glycoprotein A OS=*Dictyostelium discoideum* OX=44689 GN=rhgA PE=1 SV=1
P54679	-5,301494171	0,0002	C	Probable plasma membrane ATPase OS=*Dictyostelium discoideum* OX=44689 GN=patB PE=2 SV=2
Q86B20	-5,303606094	0,0027	C	Eukaryotic translation initiation factor 3 subunit A OS=*Dictyostelium discoideum* OX=44689 GN=eif3A PE=1 SV=1
Q55CA0	-5,382448087	0,0002	C	Vacuolar protein sorting-associated protein 26 OS=*Dictyostelium discoideum* OX=44689 GN=vps26 PE=2 SV=1
Q55DA0	-5,496624344	0,0008	C	ABC transporter G family member 22 OS=*Dictyostelium discoideum* OX=44689 GN=abcG22 PE=2 SV=1
Q54HJ2	-5,759838926	0,0090	C	Pescadillo homolog OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0289415 PE=3 SV=1
Q54HS9	-5,902420989	0,0002	C	AP-1 complex subunit mu OS=*Dictyostelium discoideum* OX=44689 GN=apm1 PE=1 SV=1
Q03479	-5,932926685	0,0020	C	Myosin IE heavy chain OS=*Dictyostelium discoideum* OX=44689 GN=myoE PE=1 SV=2
Q54QW1	-5,946407059	0,0004	SC	Eukaryotic translation initiation factor 3 subunit B OS=*Dictyostelium discoideum* OX=44689 GN=eif3B PE=3 SV=2
P34042	-6,038682623	0,0012	SC	Guanine nucleotide-binding protein alpha-4 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaD PE=1 SV=1
Q54EW2	-6,288784356	0,0011	SC	Putative bifunctional amine oxidase DDB_G0291301 OS=*Dictyostelium discoideum* OX=44689 GN=DDB_G0291301 PE=1 SV=1
P54678	-6,357153168	0,0000	SC	Calcium-transporting ATPase PAT1 OS=*Dictyostelium discoideum* OX=44689 GN=patA PE=2 SV=2
P16051	-6,555802333	0,0106	SC	Guanine nucleotide-binding protein alpha-2 subunit OS=*Dictyostelium discoideum* OX=44689 GN=gpaB PE=1 SV=3

Q54NM9	-6,752847337	0,0051	SC	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 OS=*Dictyostelium discoideum* OX=44689 GN=stt3 PE=3 SV=1
Q9XPJ9	-6,825225524	0,0000	SC	ATP synthase subunit alpha, mitochondrial OS=*Dictyostelium discoideum* OX=44689 GN=atp1 PE=1 SV=1
Q869W9	-7,23562643	0,0001	C	Probable polyketide synthase 16 OS=*Dictyostelium discoideum* OX=44689 GN=pks16 PE=2 SV=1
Q54BT3	-7,414002916	0,0025	C	ABC transporter B family member 2 OS=*Dictyostelium discoideum* OX=44689 GN=abcB2 PE=3 SV=1
Q54TJ4	-7,559986973	0,0009	C	Probable ATP-dependent RNA helicase ddx27 OS=*Dictyostelium discoideum* OX=44689 GN=ddx27 PE=3 SV=1
A0A0F6B9X6	-8,229960598	0,0001	SC	Elongation factor Tu OS=*Salmonella* Typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=tuf_2 PE=3 SV=1
P20054	-8,914405047	0,0001	SC	Protein PYR1-3 OS=*Dictyostelium discoideum* OX=44689 GN=pyr1-3 PE=1 SV=3
Q54ET6	-9,654732873	0,0529	NSC	Actin-binding protein F OS=*Dictyostelium discoideum* OX=44689 GN=abpF PE=1 SV=1