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Investigating the Mode of Action of a Novel N-sec-butylthiolated Beta-lactam Against Staphylococcus aureus

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Investigating the Mode of Action of a Novel *N-sec*-butylthiolated Beta-lactam Against *Staphylococcus aureus*

by

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TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

ABSTRACT

N-sec-butylthioloated β-lactam (NsβL) is a novel beta-lactam antimicrobial with a mechanism of action proposed to inhibit 3-oxoacyl-acyl carrier protein synthase (ACP) III (FabH), resulting in the inhibition of fatty acid synthesis. It has been suggested that NsβL inhibits FabH indirectly by inactivating coenzyme-A (CoA). CoA is an essential cofactor for numerous proteins involved in glycolysis, the citric acid cycle (TCA), and pyruvate metabolism, in addition to fatty acid biosynthesis. This study aimed to determine the effects of NsβL on a diverse array of laboratory and clinical *Staphylococcus aureus* isolates by analyzing the mode of resistance in spontaneous and adaptive mutant NsβL-resistant mutants. Phenotypic analysis of the mutants was performed, as well as sequence analysis of *fabH*; along with comparative proteomic analysis of intracellular proteomes. Our results indicate that NsβL resistance is mediated by drastic changes in the cell wall, oxidative stress response, virulence regulation, and those pathways associated with CoA. It is our conclusion that NsβL has activity towards CoA, resulting in wide-spread effects on metabolism, virulence factor production, stress response, and antimicrobial resistance.

INTRODUCTION

Staphylococcus aureus

Staphylococcus aureus is a Gram-positive coccoid bacterium that is facultatively anaerobic, non-motile, and non-sporeforming. It has a relatively small genome of 2.8 to 2.9 Mb with an approximate G+C content of 32%. *S. aureus* is part of the normal microflora of the nose, skin, gastrointestinal tract, and genitourinary tract of humans, and colonizes approximately one-third of the US population. It is an opportunistic pathogen, causing disease in immunocompromised individuals, such as children, the elderly, HIV/AIDS patients, severe burn victims, and intravenous drug users[37].

Besides being a human pathogen, *S. aureus* is also known to colonize and infect most other mammals, which can in turn serve as a reservoir for human inoculation. Indeed, there are a number of documented cases where companion animals have been shown to be a source of recurrent human infection. Bovine and equine infections are a concern for the agricultural industry, with infections often caused by human-associated strains[98]. Alternatively, a recent report describes the case of a young, healthy girl infected with the ST398 livestock-associated strain bearing the community acquired MRSA (CA-MRSA)-associated Panton-Valentine leukocidin (PVL) toxin. This infection resulted in fatal necrotizing pneumonia, and illustrates the zoonotic potential of *S. aureus*[90].

Infections caused by *S. aureus*. *S. aureus* is able to cause disease in almost every niche of the human body. It is the major cause of skin and soft tissue infections (SSTIs) in the United States, causing 76% of all purulent SSTIs seen in hospitals between 2001 and 2003[76]. SSTIs can be uncomplicated (uSSTIs) and typically involve infection of the epidermis and/or hair follicles, resulting in pimples, boils, abscesses, carbuncles, furuncles, folliculitis, tendonitis, and impetigo. Complicated SSTIs (cSSTIs) stem from uSSTIs and typically exhibit systemic symptoms; for example, *S. aureus* is also known as a 'flesh-eating bug' due to its ability to cause necrotizing fasciitis. *S. aureus* can also cause invasive illnesses, including septic arthritis, endocarditis, osteomyelitis, and pneumonia[54]. *S. aureus* is also a leading cause of surgical wound infections[41] and infections of foreign bodies, such as prosthetic joints, catheters, and pacemakers. Foreign body infections can be difficult to treat because they are often caused by biofilms forming on the indwelling device or implant[101]. The reasons for difficulty in treatment are not well elucidated, but have been attributed to reduced penetration of antibiotics into the aggregate matrix, or via the presence of persister cells, which resist antimicrobial treatment and remain after treatment to re-establish the biofilm, leading to recurrent infection. Often, the only effective treatment is to remove the implanted or indwelling device altogether[61].

Virulence factors

S. aureus has an impressive array of toxins which are involved in causing illnesses that range from mild to severe. It is differentiated from other members of its family by its ability to cause disease despite the fact that 50% of the core genome is common to all

staphylococci[10]. Indeed, the genomes of individual strains of *S. aureus* vary by only 22%. These variable accessory regions contain mobile genetic elements (MGE) such as staphylococcal cassette chromosomes (SCC), pathogenicity islands (PI), bacteriophages (φ), transposons (TN), and plasmids, and often encode virulence factors, toxins, and resistance genes[64].

Adhesins, immune modulation, and evasion. A factor in the pathogenic success of *S. aureus*' stems in part from its versatile adhesion molecules. Collectively, these are known as the microbial surface components recognizing adhesive matrix molecules (MSCRAMM). The host extracellular matrix (ECM) has many components which *S. aureus* is able to target for the purpose of adhesion. Collagen, a component of cartilage, is a target for the collagen-binding adhesin (Cna), which has been implicated in osteomyelitis[33]. Fibronectin-binding proteins (FnBP) allow for attachment to platelets and, subsequently, activation of clot formation, which has been associated with endocarditis[35]. *S. aureus* also binds to fibrinogen, the precursor to fibrin, through clumping factor A (ClfA), effectively coating the bacterial cell in fibrinogen and acting as camouflage against phagocytic cells[42]. Staphylokinase (SAK) binds to plasminogen and is responsible for cleaving fibrin, allowing *S. aureus* the opportunity to move to a new site within the host[15]. Another factor in its success is the presence of several immunomodulatory and immune evasion proteins. Surface protein A (SpA) has anti-phagocytic activity; it binds the Fc region of immunoglobulin G (IgG), preventing opsonization and, consequently, recognition by phagocytes[4]. Another IgG-binding protein, the staphylococcal binder of immunoglobulin (Sbi), is secreted and forms

insoluble IgG complexes, reducing opportunities for opsonization. Sbi also has proteolytic activity towards complement factor 3 (C3), which is a key component of the complement system and important for the initial immune response to bacterial infection[18]. The combination of these surface-associated and secreted proteins affords *S. aureus* the ability to manipulate their host environment.

Cytolytic toxins. A number of staphylococcal secreted toxins have lytic activity towards different cell types present in the host. Generally, they have pore-forming activity which can lead to osmotic disregulation and cell lysis at high concentrations. Alpha-hemolysin (Hla) is strongly lytic towards rabbit erythrocytes, but also has activity towards human erythrocytes, monocytes, epithelial cells, and endothelial cells. Hla also has dermonecrotic and neurotoxic activity. Beta-hemolysin (Hlb) displays activity similar to Hla, but is less active in *S. aureus* isolates causing human disease. This is typically due to integration of a prophage within the *hlb* structural encoding gene. Delta toxin (Hld) has a mechanism different from that of either Hla or Hlb, both of which use polymers to form pores in cell membranes; instead, Hld monomers aggregate on a cell's surface until they are heavy enough to sink into the host cell, resulting in holes in the membrane and causing the release of intracellular components and cell death. Gamma-hemolysin is a bicomponent toxin with hemolytic and leukolytic activity. The level of lytic activity depends on the combination of S and F components which make up all staphylococcal bicomponent toxins. The S components of gamma-hemolysin are encoded by *hlgA* or *hlgC* and the single F component is encoded by *hlgB*. Similarly, Panton-Valentine leukocidn (PVL) is a bicomponent toxin, encoded by *lukF*-PV and *lukS*-PV, which is

significantly more leukotoxic than gamma-hemolysin[14, 29]. The phenol soluble modulins (PSM) have been recently described and appear to have formed two major classes, α-PSMs and β-PSMs, with the former class having the most leukocytic and inflammatory activity[106]. Both PVL and PSM-α are strongly associated with the hypervirulence of CA-MRSA infections, as detailed below. These cytolytic toxins have the overall effect of dampening the efficacy of the host immune response by destroying vital immune cells and misdirecting the immune response through the release of pro-inflammatory cytokines from lysed cells.

Staphylococcal superantigens. Superantigens are molecules which initiate a non-specific interaction between the T-cell receptor (TCR) on CD4+ T-cells and the major histocompatbility complex class II (MHC-II) on antigen presenting cells (APC). This interaction leads to a robust immune response, resulting in a cytokine storm that can lead to multi-system organ failure and death. Different isolates of *S. aureus* may carry any number of genes encoding superantigens. Toxic shock syndrome toxin 1 (TSST-1) is a bacteriophage-encoded superantigen most often linked to tampon-associated toxic shock syndrome. Scalded skin syndrome, seen almost exclusively in newborns, is caused by exfoliative toxins, which degrade desmoglein 1 and result in burn-like lesions[77]. A range of staphylococcal enterotoxins (SEA – SEG) cause food poisoning, which is often self-limiting and not associated with the more serious affects caused by the other staphylococcal superantigens[60, 77].

Clonal variation of *S. aureus*

S. aureus has historically been considered an opportunistic pathogen, infecting primarily the elderly, the hospitalized or otherwise immunocompromised patients. However, recently, so-called CA-MRSA isolates have been causing infection in young, healthy individuals with no history of *S. aureus* infection or previous contact with the healthcare environment. CA-MRSA infections have been steadily increasing in both the community and hospital settings, while the occurrence of hospital-acquired MRSA (HA-MRSA) infections is declining[25, 107]. CA-MRSA strains are characterized by enhanced virulence compared to the classical HA-MRSA isolates. The CA-MRSA strain USA 300 is the major cause of the alteration in epidemiology of MRSA infections in the United States, and now accounts for the majority of SSTIs presenting in emergency rooms[53]. USA 300 is emerging as a major cause of prosthetic joint infections[56] and blood stream infections[95] in hospitals, and has been associated with necrotizing pneumonia[58] and necrotizing fasciitis[63]. The necrotizing diseases in particular have been attributed to the presence of the PVL toxin. The association of CA-MRSA virulence with PVL remains controversial, as a number of reports have questioned whether PVL is the mediator of necrotic activity, or merely an indicator of the presence of other, as yet undefined, toxins[104]. Diep, et. al. have suggested that PVL plays a transitory role in CA-MRSA pathogenesis, being beneficial (to the bacteria) only at the onset of infection[28]. Furthermore, the expression of PSM-α was recently shown to be enhanced in CA-MRSA strains, and have been associated with eliciting a strong immune response in animal models of bacteremia (USA 400) and cSSTIs (USA 300), recruiting neutrophils to the site of infection, causing cell lysis leading to extensive tissue damage[106].

It has recently been suggested that regulation of virulence factors encoded as part of the core genome, as opposed to the acquisition of various MGEs encoding toxins or resistance genes (e.g. PVL), is the reason for the increased virulence of CA-MRSA. Li et. al. have shown that *agr*-regulated virulence factors such as HLA and PSM-α are significantly upregulated in USA 300 and USA 500 (CA-MRSA isolates) in comparison to USA 100 and USA 200 (HA-MRSA isolates); however, they also indicated that, as staphylococcal regulation is so complex, it is highly likely that this process is multifactorial[62].

Antimicrobial therapies and resistance

S. aureus is a remarkably versatile and adaptable pathogen, in part due to its multifactorial mode of pathogenesis, but also because it has developed resistance to every therapy introduced in the last 60 years. Here, we discuss the major classes of antimicrobials used for the clinical treatment of *S. aureus* and the mechanisms of resistance it has developed to cope with challenges posed by these various therapies.

Cell-wall synthesis inhibitors. With the release of penicillin in the 1940s, previously fatal bacterial infections became treatable, heralding a new era of infection control. However, within a few short years, strains of *S. aureus* appeared that were completely resistant to this drug, and it became apparent that controlling bacterial diseases would become more complex than first perceived. Specific analysis revealed that resistance was

mediated by penicillinase, which cleaves the active β-lactam ring of this class of drugs, inactivating them entirely[19].

Methicillin, a derivative of penicillin, was introduced onto the market in 1959 as one of the first semi-synthetic β-lactams, and a potential solution to penicillin-resistant strains of bacteria. The reason methicillin was considered to be so important was that its β-lactam ring is chemically buried, and is thus protected from access to β-lactamases. Unfortunately, the first reported case of resistance occurred by 1961[19] and ushered in the demise of β-lactam antibiotics. Methicillin-resistance is mediated by a novel penicillin-binding protein (PBP2a), encoded by the *mecA* gene. The *mecA* gene may have been acquired from *S. sciuri* and incorporated into the staphylococcal chromosome cassette (SCC), resulting in the SCC*mec* mobile genetic element[108]. There are currently eight known types of SCCmec, I – VIII[19]. Each type is associated with a different range and level of antimicrobial resistance. SCC*mecs* I – III are associated with HA-MRSA, and SCC*mecs* IV, V, and VI are associated with CA-MRSA[25, 53]. In addition to methicillin/β-lactam resistance, SCC*mec* can confer resistance to other antimicrobial classes, such as aminoglycosides, heavy metals, macrolides, and polyketides[19].

Another commonly used class of β-lactams is the cephalosporins, which also inhibit cell-wall synthesis by a mechanism similar to the penicillins. Cephalosporins are divided into "generations" based on the time they were discovered and their spectrum of activity, with the older generations being the most limited and the newer generations being the most broadly active. They were first introduced into the clinical environment in 1962, 17 years

after their discovery in 1945[93]. Strains resistant to methicillin are also resistant to cephalosporins, so their therapeutic use is only indicated for known methicillin-susceptible *S. aureus* (MSSA) strains[19].

There are currently only a few effective antimicrobials available to treat highly resistant MRSA infections. The antibiotic most commonly used in such situations is vancomycin, a glycopeptide that has poor solubility, high toxicity, and can only be administered intravenously. Its mode of action, like β-lactams, affects bacterial cell wall synthesis, although via a slightly different mechanism. Reduced susceptibility to vancomycin in clinical isolates was first reported in 1997 in Japan, 39 years after its introduction in 1958[43]. Since this time, so-called vancomycin-intermediate *S. aureus* (VISA) has become distributed worldwide. They are characterized by a diminished sensitivity to the drug, requiring increasing concentrations to produce positive therapeutic outcomes. Fully vancomycin resistant *S. aureus* (VRSA) was first reported in 2002 and appears to be conferred by acquisition of the *vanA* resistance gene from vancomycin-resistant Enterococci (VRE). Specifically, a study from 2003 describes a diabetes patient co-infected with methicillin-susceptible *S. aureus* (MSSA) and VRE. The patient was treated with a wide array of antibiotics, including vancomycin, and VRSA cells were isolated before the course of treatment was completed. Sulfamethoxazole-trimethoprim and metronidazole were successful in eradicating the infection, but only after the infection had disseminated to bacteremia and the patient's foot was amputated. This was the first time a clinical strain of *S. aureus* was demonstrated to carry the *vanA* gene[20]. Another point for concern has been the appearance of heterogenous vancomycin-

intermediate strains (hVISA). These strains will appear to be susceptible to treatment by vancomycin, but a subset of the bacterial population (less than 1 in 10^{-5} – 10^{-6}) will be resistant. The presence of hVISA is typically associated with repeated MRSA infection and exposure to vancomycin, and is often difficult to detect. Most VISA and hVISA strains do not carry *vanA*; instead, they display thickened cell walls and may have altered transcription of regulatory elements[44].

Membrane disruption. Daptomycin is one of the few novel antimicrobials that targets methicillin-resistant strains of *S. aureus*, and was approved by the FDA in 2003. It works by disrupting the charge of the cell envelope, thus weakening membrane stability. The first reported case of reduced susceptibility to daptomycin occurred in 2004 in Boston, Massachusetts[69], and resistance often occurs during a failed course of treatment for an infection previously shown to be daptomycin-susceptible[69, 71]. The resistance mechanism, whilst not completely understood at this time, has been associated with changes in membrane fluidity and increased positive charge of the bacterial membrane[49, 79].

DNA synthesis inhibition. Fluoroquinolones such as ciprofloxacin, levofloxacin, and moxifloxacin inhibit bacterial DNA gyrase and topoisomerase IV. Many MRSA strains are resistant to fluoroquinolones, thus, they are infrequently used[27]; however, many MSSA isolates are still susceptible. Even so, fluoroquinolones are known to have negative side effects, and are rarely a first-line choice for treatment. As with other therapeutics, resistance can develop during the course of treatment; as such, ciprofloxacin

is often used in combination therapy with rifampicin. Fluoroquinolone resistance is mediated by the quinolone resistance determining regions (QRDR) that are present in the genes encoding the protein targets of fluoroquinolones. Specific mutations leading to resistance have been shown to occur in *gyrAB* (DNA gyrase) and *grlAB* (topoisomerase IV), which interferes with quinolone binding whilst still allowing enzymatic function[87]. The efflux pumps NorA[51] and QacBIII[78] have also been shown to play a role in decreased susceptibility to these drugs.

Trimethoprim-sulfamethoxazole (TMP-SMX), a pyrimidine-sulfonamide combination drug, inhibits folic acid synthesis, an essential precursor for purines and thymine, by competitively binding dihydrofolate reductase (DHFR). TMP-SMX is typically used only for the treatment of MSSA and non-multiply resistant MRSA (nmrMRSA), as multiply-drug resistant MRSA (mdrMRSA) typically demonstrate TMP-SMX resistance[34, 91]. Resistance is caused by point mutations in the DHFR gene, or by acquisition of a plasmid-encoded accessory DHFR. These accessory DHFRs often have very little sequence homology with other prokaryotic DHFRs, rendering them unrecognizable to TMP-SMX[24, 47].

Transcription inhibition. A common technique used to combat multiple-drug resistant infections is combination drug therapy. Rifampicin, a transcription inhibitor, is commonly used in combination with ciprofloxacin, vancomycin, daptomycin, or linezolid for such a purpose. Rifampicin binds to the RNA polymerase β subunit, encoded by *rpoB*, interfering with transcription of DNA to RNA. While many strains of MRSA are

resistant to rifampicin[5], it can be effective in combination with fusidic acid or vancomycin[50, 73]. Despite reported successes of vancomycin-rifampicin therapy, there remains a strong possibility of rifampicin resistance developing during treatment[67, 89].

Translation inhibition. There are a number of antimicrobial classes available that target different components of protein synthesis. Aminoglycosides (e.g. gentamycin, kanamycin, neomycin) and macrolides (e.g. erythromycin, clarithromycin, azithromycin) are classes that bind to either the 30S or 50S subunit of the ribosome and interfere with translation. These antimicrobial agents are typically used only to treat MSSA infections due to the high prevalence of resistance found in mdrMRSA isolates. Lincosamides (lincomycin and clindamycin) also bind to the 50S ribosomal subunit and inhibit translational initiation, and are also only indicated for the treatment of MSSA infections[91]. The streptogramin B group includes the combination therapy quinupristin/dalfopristin, which work synergistically to inhibit the elongation of polypeptides. Resistance to any member of the MLS (Macrolides, Lincosamides, and Streptrogramin B) group of antibiotics often results in cross-resistance to the remaining members, and, specifically, improper use of erythromycin can induce resistance to clindamycin[109].

Tetracycline antibiotics of the polyketide class target the 30S subunit of ribosomes, blocking translational elongation. Strains of *S. aureus* often carry the tetracycline resistance genes *tetK* and *tetL*, encoding efflux pumps, and *tetM* and *tetO*, encoding ribosomal protection proteins, both of which confer high levels of resistance to

tetracycline antibiotics[86]. A new class of protein synthesis inhibitors, the glycylcyclines, has been derived from tetracyclines, and includes tigecycline, which was approved by the FDA in 2005 to treat MRSA infections. Tigecycline blocks the A-site of the ribosome by binding to the 30S ribosomal subunit with five times greater affinity than tetracycline. The reason for this increased binding affinity is probably due to structural differences between tetracycline and tigecycline, with tigecycline forming stronger and more numerous bonds with the ribosome[26, 84]. In 2004, an initiative was taken to establish the Tigecycline Evaluation and Surveillance Trial (TEST) whose purpose was to monitor tigecycline susceptibility and compare it to other clinically relevant drugs. As reported in 2008, there has been no change in MSSA or MRSA MICs, making tigecycline an attractive therapeutic option for otherwise untreatable infections[30].

Linezolid is a synthetic oxazolidinone which binds the 23s rRNA component of the 50S ribosomal subunit, and was approved in 2000 to treat multiply-drug resistant infections. Because it is completely synthetic, it was expected that there would be no reservoir for resistance. However, the first clinical isolate of linezolid-resistant MRSA was reported in 2001 in Massachusetts[102], while the first clinical outbreak, consisting of 12 patients, occurred in 2008 in Madrid, Spain[75]. Resistance has been associated with the presence of the *cfr* gene, which is carried on a plasmid, and confers resistance to chloramphenicol, florfenicol, and clindamycin. The mechanism of resistance involves altering the target of linezolid by introducing a mutation into the gene encoding the 23s rRNA[75]. A specific resistance-inducing mutation, G2576T, in the same gene has also been reported to occur

spontaneously in 1 x 10^{-9} isolates. However, because *S. aureus* has multiple copies of the 23s rRNA gene, the occurrence of *in vivo* resistance is still rare[88].

Novel therapeutics

With a remarkable number of antibiotics no longer proving effective in the clinic, it appears troublesome at best to keep pace with staphylococcal drug resistance. Very few new antimicrobial classes have been developed in the past 50 years; however, there are a number of new drugs in the pipeline that display improved antimicrobial activity.

Next generation β-lactams. Two new cephalosporins with broad-spectrum, anti-MRSA activity are being investigated. The first, ceftobiprole and its prodrug ceftobiprole medocaril, are being developed by Basilea Pharmaceutica AG and Johnson & Johnson Pharmaceutical Research and Development LLC. Unlike other β-lactam antimicrobials, ceftobiprole has a very high affinity for PBP2a, the protein encoded on SCC*mec* which confers methicillin-resistance, and has a chemical structure more resistant to cleavage by β-lactamases. Furthermore, ceftobiprole has also shown good activity against completely vancomycin-resistant strains[111]. *In vitro* experimentation has demonstrated that resistance is rare, although not impossible. To date, Phase III trials for SSTIs and pneumonias, alongside comparison to vancomycin efficacy, have been completed, with ceftobiprole showing similar cure rates and patient tolerance to vancomycin[110]. Ceftaroline and its prodrug ceftaroline fosamil act by a mechanism similar to ceftobiprole and have been compared favorably to imipenem (a carbapenem) and nitrocefin (a cephalosporin). The spontaneous mutation frequency in MSSA and MRSA is ≤1 in 10^{-9}

– 10^{-10}. One Phase III trial has been completed, studying the usefulness and safety of ceftaroline for the treatment of SSTIs as compared to vancomycin, and was found to be equally effective and well tolerated[112].

Membrane disruption. The majority of drugs available and in the pipeline today target growing bacteria, with no antimicrobials specifically targeting stationary-phase bacteria currently available. HT61 is a very early-phase, narrow-spectrum compound currently being tested by Helperby Therapeutics for its use as a topical therapeutic in humans. Its mode of action appears to be concentration-dependent membrane disruption by rapid depolarization, causing leaking of intracellular contents at low concentrations and cell wall nicking at high concentrations. *In vivo*, HT61-imbued gel completely prevented colonization of mouse skin by stationary-phase *S. aureus* cultures, as compared to mupirocin, which had no inhibitory effect. HT61 was also shown to be effective in eradicating both MSSA and MRSA in a mouse infection model using log-phase cultures, and was, again, significantly more effective than mupirocin. Interestingly, HT61 is considerably more active towards non-multiplying cells than actively growing cells, although the precise reason for this has not yet been determined. Significantly, *in vitro* experiments show that no resistance occurs in either stationary- or log-phase cultures after 50 passages at sub-MIC concentrations[45].

DNA synthesis inhibition. Iclaprim, like trimethoprim, prevents DNA synthesis by binding DHFR. Unlike TMP, it is active against those strains of MSSA, MRSA, VISA, and VRSA which are TMP resistant[93]. *In vitro*, resistance has not been observed thus far,

and the side effects for this drug appear to be negligible, making it a very attractive therapeutic prospect. It also shows, like TMP, synergistic activity with SMX[94], and has completed Phase II trials for the treatment of SSTIs[57].

Fatty acid synthesis inhibition. Currently, triclosan is the only inhibitor of Type II fatty acid synthesis clinically available. It has more than one mode of action, but seems to function by binding to the enoyl-acyl carrier protein (FabI), and preventing initiation of fatty acid synthesis. Recently, more interest has emerged in this pathway, as it is believed to be essential to bacterial growth and is distinct from mammalian Type I fatty acid synthesis[6]. Despite the attractiveness of this pathway as a therapeutic target, there has been controversy concerning its suitability[6, 16, 17]. Brinster, et. al. showed that *Streptococcus agalactiae*, a causative agent of neonatal meningitis, was able to survive the activity of both triclosan and cerulenin (an inhibitor of b-ketoacyl carrier protein synthetase [FabF/B]) when culture media was supplemented with long-chain fatty acids[17]. *S. aureus* was also demonstrated to survive cerulenin activity in the presence of both short-chain and long-chain fatty acids[2], but both of these claims have recently been contested by Balemans, et. al[6]. Despite this controversy, Merck & Co, Inc. is investigating the potential use of two fatty acid synthesis inhibitors, platensimycin and platencin. Platensimycin inhibits β-ketoacyl-[acyl-carrier protein (ACP)] synthase II (FabF), while platencin inhibits both FabF and β-ketoacyl-[ACP] synthase III (FabH). Both have broad-spectrum *in vitro* and *in vivo* activity against Gram-positive pathogens, including MRSA. The rate of resistance for platencin was between 2×10^{-8} and 1×10^{-9} depending on the strain tested and concentration of exposure[105].

Mode of Action	Antimicrobial	Class	Date of Release	First Reported Date of Resistance	Gene/Source of Resistance	Mode of Resistance
Cell wall synthesis inhibition	Penicillin	β-lactam	1940s	1940s	production of a β-lactamase	penicillinase cleaves β-lactam ring, inactivating penicillin
	Methicillin	β-lactam	1959	1961	acquisition of *mecA*	PBP2a
	Vancomycin	Glycopeptide	1958	1997	acquisition of *vanA*	altered cell wall prevents antimicrobial binding
Membrane disruption	Daptomycin	Lipopeptide	2003	2004	mutations in *mprF* or *yycG*	membrane's positive charge increases, preventing drug binding
DNA synthesis inhibition	Ciprofloxacin	Fluoroquinolone	1987	1997	mutations in *gyrAB* or *grlAB*	structure of DNA gyrase is altered, preventing drug binding
Transcription inhibition	Rifampicin	Rifamycin	1989	2004	mutations in *rpoB*	structure of β-subunit of RNA polymerase is altered, reducing drug binding
Translation inhibition	Erythromycin	Macrolide	1952	1957	acquisition of *ermA* or *ermC*	structure of 23s rRNA is altered, reducing drug binding
	Gentamicin	Aminoglycoside	1963	1976	acquisition of *rmtC*	enzymatic inactivation of the drug
	Linezolid	Oxazolidinone	2000	2001	acquisition of *cfr*	mutation in gene encoding 23s subunit of 50S ribosome prevents drug binding
	Tigecycline	Glycylcycline	2005	Not yet detected	NA	NA

Table 1. Overview of relevant antimicrobials and *S. aureus* resistance.

***N*-thiolated β-lactams.** A novel β-lactam, which forms the focus of this study, has been developed, and displays a mode of action unlike any other β-lactam previously investigated. *N*-thiolated β lactams have shown strong activity towards MRSA, *Bacillus anthracis*, and *Micrococcus luteus*, weak activity towards *Neisseria gonorrhoeae,*

Bacteroides fragilis, and *Haemophilus influenza*, but no activity towards *Listeria monocytogenes, Streptococcus pyogenes, S. pneumoniae, Klebsiella pneumoniae, Vibrio cholerae, Escherichia coli, Salmonella typhimurium, Pseudomonas aeruginosa,* or *Mycobacterium smegmatis*[103]. Instead of targeting cell wall synthesis, it has been suggested that NsβL interacts with coenzyme A (CoA) by thiolating the active site cysteine residue, and similarly sulfenylating the active site cysteine of FabH[103], thus both directly and indirectly interfering with Type II fatty acid synthesis[92]. Because of the possible interaction with CoA, other pathways dependent on this intermediate may also be affected by this drug. All analogs of *N*-thiolated β lactams are unaffected by β-lactamases at every concentration tested, and activity appears to be dependent on both low intracellular concentrations of glutathione (GSH) and high concentrations of CoA, indicating that *N*-thiolated β lactams may act as a thiolating agent[92].

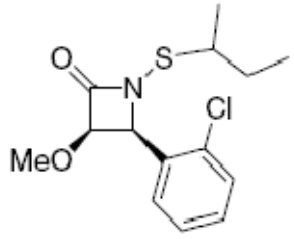

Figure 1. *N-sec*-butylthiolated β-lactam (NsβL). This analog has the highest antimicrobial activity of all NβL analogs tested.

The activity of NsBL against a variety of laboratory and clinical *S. aureusu* isolates was determined, including strains methicillin-, multidrug-, and vancomycin-resistant. Additionally, the affects of different *in vitro* conditions mimicking physiological on the activity of NsβL were explored. In an effort to clarify the mechanism(s) of action of NsβL, we generated mutants resistant to this drug by two different methods in three

strains. By determining the phenotypic and proteomic changes that resulted from the gain of resistance in these isolates, we hope to elucidate the primary target of NsβL.

MATERIALS AND METHODS

Bacterial strains

Because there is a wide range of clonal variation amongst *S. aureus* strains, a variety of laboratory and clinical isolates were used in this study (Table 2).

Strain	Source	Significant Characteristics
***S. epidermidis* RP62A**	NARSA*	MRSE clinical isolate
***S. aureus* 8325-4**	Simon Foster	Defective in *rsbU*
***S. aureus* RN6390**	Mark Smeltzer	Derived from 8325-4
***S. aureus* SH1000**	Simon Foster	Functional *rsbU* derivative of 8325-4
***S. aureus* Newman**	Mark Smeltzer	Laboratory strain
***S. aureus* COL**	Lab stock	Early clinical MRSA isolate
***S. aureus* UAMS-1**	Mark Smeltzer	Well studied biofilm-former
***S. aureus* USA 100 635**	Tampa General Hospital	HA-MRSA
***S. aureus* USA 100 Mu50**	NARSA	VISA
***S. aureus* USA 200 MRSA252**	NARSA	HA-MRSA
***S. aureus* USA 300 Houston**	Mark Smeltzer	CA-MRSA
***S. aureus* USA 300 LAC**	Kelly Rice	CA-MRSA
***S. aureus* USA 300 FPR3757**	Mark Smeltzer	CA-MRSA
***S. aureus* USA 400 MW2**	NARSA	CA-MRSA

Table 2. Bacterial strains used. *Network on Antimicrobial Resistance in *Staphylococcus aureus*.

Culture media

Tryptic soy broth (TSB) and brain-heart infusion broth (BHI). Tryptic soy broth (Teknova) and BHI (Bacto) were prepared according to the manufacturer's specifications. Agar was added at 15 gL^{-1} as needed for plates. All media was autoclaved for 30 minutes at 121°C and 15 psi, unless otherwise noted.

Top Agar. Top agar was prepared by adding 0.7 g agar to 100 mL TSB and autoclaving as described.

Biofilm media (BIO). TSB was supplemented with 0.5% dextrose and 3% NaCl prior to autoclaving.

Purple broth. Purple broth was purchased from Fisher Scientific and prepared according to the manufacturer's specifications.

Chemically-defined media (CDM). Different types of chemically-defined media were prepared by combining separately prepared limiting solutions (CL# or CDM#). Refer to the appendix for the complete lists of the components of the CL and CDM solutions.

Non-Limiting CDM. Combine the following solutions:

CL1	50%
CL2	10%
CL3	1%
CL4	0.2%
CDM4	0.1%
CDM5	10%
MilliQ dH_2O	28.7%

Non-limiting CDM plates (CDM-A). Combine CL1, CL2, CL3, CDM4, and MilliQ dH2O in the proportions described and add 15 gL^{-1} agar, then autoclave and cool to 55°C. Add CL4 and CDM5 in the proportions described.

Amino acid-limiting CDM (AA-CDM). Combine the following solutions, then filter sterilize:

CDM1	0.07%
CDM2	0.02%
CDM3	0.05%
CDM4	0.001%
CDM5	0.1%

Glucose-limiting CDM (G-CDM). Reduce the concentration of glucose in CDM5 by ten-fold and follow the recipe for amino acid-limiting CDM.

Phosphate-limiting CDM (PO_4-CDM). Reduce the concentration of Na_2HPO_4 and KH_2PO_4 in CDM1 by five-fold and follow the recipe for amino-acid limiting CDM.

Limiting CDM plates ([L]-CDMA). Combine CDM1, CDM3, CDM4, and dH_2O in the proportions described, and 15 gL^{-1} agar, then autoclave and cool to 55°C. Add CDM2 and CDM5 in the proportions described. Do this for any type of CDM needed.

Metal ion-limiting media (ML). All glassware used for metal ion-limiting solutions was washed in 0.1M HCl overnight, rinsed thoroughly with dH_2O, and autoclaved prior to use. All solutions used in metal ion-limiting media were treated with Chelex-100 to remove trace metal ions.

Combine the following solutions:

CL1	50%
CL2	10%
CL3	1%
CL4	0.2%
MilliQ dH_2O	38.8%

Add $10gL^{-1}$ Chelex-100 and stir for 4 hours. Filter sterilize, then add 0.4 mLL^{-1} sterile 1M $MgSO_4$ in Chelex-treated MilliQ dH_2O.

Metal ion-limiting plates (MLA). Combine CL1, CL2, CL3, and MilliQ dH2O in the proportions described, and add 10 gL^{-1} agar, then autoclave and cool to 55°C. Add $MgSO_4$ in the proportion described. Do not treat with Chelex-100.

Milk plates. Milk plates were prepared by preparing TSA as normal, but with the addition of 2% dry skim milk and autoclaving for 10 minutes at 121°C and 15 psi. Plates were streaked from an isolated colony on a TSA plate and incubated at 37°C overnight.

Blood plates. Remel blood plates containing 5% sheep's blood were purchased from Fisher Scientific. Plates were streaked from an isolated colony on a TSA plate and incubated at 37°C overnight.

Sodium nitrate and sodium nitrite plates. Sodium nitrite plates were prepared by adding sterile 1M $NaNO_2$ to a final concentration of 1mM $NaNO_2$ or 2M $NaNO_3$ to a final concentration of 20mM $NaNO_3$ to TSA after autoclaving. Plates were streaked from an isolated colony on a TSA plate and incubated in an anaerobic GasPak chamber at 37°C overnight.

Congo red agar (CRA). Congo red agar was prepared by supplementing TSA with 5% sucrose and 0.8 gL^{-1} congo red before autoclaving.

Maintenance and growth of bacterial cultures

Glycerol stocks. Glycerol stocks were prepared from 1 mL of overnight culture grown in 100 mL TSB in a 250 mL Erlenmeyer flask at 37°C with shaking at 250 rpm. The 1 mL aliquot was centrifuged at 13,300 x g for 10 minutes, the supernatant was discarded, and the pellet was resuspended in 1 mL TSB containing 12% glycerol. Stocks were stored at -80°C until needed, when they were streaked on TSA and incubated at 37°C overnight. Stock plates were used for a maximum of seven days before new plates were prepared.

Synchronized cultures. Two hundred-fifty mL Erlenmeyer flasks containing 100 mL TSB were inoculated with one colony from stock plates and incubated at 37°C overnight with shaking at 250 rpm. A fresh flask was inoculated with 1 mL of the overnight culture and further incubated for 3 hours. Another fresh flask was inoculated to ~OD^{600nm} 0.05 and incubated until the desired growth phase was reached. Synchronized cultures were used unless otherwise stated.

Direct plate count. Cultures were serially diluted 1:10 in sterile PBS up to a 10^{-7} dilution. 100 µL of the 10^{-6} and 10^{-7} dilutions were spread-plated in triplicate and incubated overnight at 37°C. Individual colonies were counted and the colony forming units per milliliter (CFU/mL) was calculated for each plate. The average was taken to give the final CFU/mL.

Determination of minimum inhibitory concentrations

Minimum inhibitory concentrations (MIC) were determined using a microbroth 96-well plate method. TSB containing the drug of interest was prepared in aliquots of at least 1 mL, then 100 µL of the antibiotic-containing TSB was added to each well of a sterile 96-well flat-bottomed plate (Greiner Bio-One). Cultures grown overnight in 10 mL TSB in a 50 mL Falcon tube were diluted 1:100 before adding 10 µL to each prepared well, resulting in a final dilution of 1:1000. At least three wells containing TSB were left uninoculated to serve as negative controls. Each MIC was performed in triplicate.

Disk diffusion assays

Pre-warmed TSA plates were overlaid with 5mL top agar inoculated with 5 uL of overnight culture. The plates were allowed to dry before sterile Whatman paper disks imbued with the chemical stressor of interest were place on the plates. Plates were incubated right-side up at 37°C overnight. Zones of inhibition were measured in millimeters the next day. After the first round of assays, only those stressors which resulted in a significant difference between the wild-type and mutant strains were repeated.

Fatty acid 96-well assays

Flat-bottomed 96-well plates were prepared with 200 µL per well TSB containing 0.05% bovine serum albumin (BSA, Fisher BioReagents), 0.1% tween 80 (Fisher Scientific), or 0.01% oleic acid (Fisher Scientific). Tween 80 was prepared as a 10% solution in sterile 5% BSA. Oleic acid was prepared as a 1% solution in sterile 5% BSA. A range of antibiotic concentrations were tested from sub-MIC up to 100x MIC. Each well was inoculated with an overnight culture diluted to ~$OD_{600\ nm}$ 0.05, and plates were incubated at 37°C overnight. Plates were examined for growth in the different media at each antibiotic concentration. To quantify, 100 µL was removed from each well and diluted in 900 µL diH_2O in a cuvette and the absorbance was measured at 600 nm.

Antimicrobial susceptibility of biofilms

A sterile flat-bottom 96-well plate was treated with 150 µL human plasma per well (20% human plasma in bicarbonate/sodium bicarbonate buffer) and incubated at 4°C overnight.

The plasma was gently aspirated from each well, and each prepared well was inoculated with 150 µL culture grown overnight in 100 mL TSB-Bio in a 250 mL Erlenmeyer flask. Each culture was arbitrarily standardized to ~$OD_{600\ nm}$ 0.05. The plate was incubated at 37°C for 24 hours, then the plate was gently rinsed three times with sterile phosphate buffered saline (PBS). 150 µL TSB-Bio containing an antibiotic of interest in a range of concentrations was added to each well, and the plate was further incubated at 37°C for 24 hours. The plate was gently rinsed three times with sterile PBS and each well was fixed with 200 µL 100% ethanol. The ethanol was removed and the plate was allowed to air dry. Each well was then filled with 200 µL staining solution (41% crystal violet w/v, 12% ethanol) and allowed to stain for 2 minutes. The stain was gently aspirated, and each well was washed three times with sterile PBS. The plate was covered and allowed to air dry overnight. The stain was eluted with 100 µL of 100% ethanol for 10 minutes. The absorbance was read using a BioTek Synergy2 plate reader at 590 nm. Samples were further diluted in 100% ethanol as necessary to get a reading within range. Biofilms of interest were compared to biofilms formed by the strains *S. aureus* 8325-4 (negative control) and *S. aureus* SH1000 (positive control).

Generation of spontaneous mutants

TSA plates were supplemented with 5 µg/mL NsβL after autoclaving. 1 mL of a 10 mL overnight culture was centrifuged at full speed and all the supernatant except for 100 µL was discarded. The pellet was resuspended and spread-plated on the NsβL-TSA plates. At the same time, the CFU/mL of the inoculating culture was calculated (2.3). The plates were incubated ~36 hours at 37°C, and any colonies were counted and patched onto

NsβL-TSA plates. The patched plates were incubated at 37°C overnight, and glycerol stocks were made from each patch.

Calculation of spontaneous mutation frequency. The spontaneous mutation frequency of each spontaneous mutant was calculated using the following equation:

$$Spontaneous\ Mutation\ Frequency = \frac{\Sigma R}{\Sigma N}$$

Where R is the number of resistant colonies obtained and N is the number of cells screened.

Generation of adaptive mutants

4 µL of a synchronized culture was used to inoculate a 15 mL Falcon tube containing 2 mL BHI with 0.125 µg/mL NsβL (sub-MIC). The Falcon was incubated at 37°C for 24 h with shaking. A 4 uL aliquot was used to inoculate a new 15 mL Falcon tube containing 2 mL BHI with 0.25 µg/mL NsβL, which was incubated as previously. This process was repeated, doubling the NsβL concentration until no growth was observed. A 1 mL aliquot from each day was spun down and stored in glycerol at -80°C as described.

Growth curve assays

Standard conditions. Synchronized cultures were used to inoculate 100 mL TSB or CDM in a 250 mL Erlenmeyer flask to ~OD_{600nm} 0.05. For CDM, cells were washed twice with sterile PBS before inoculation. Absorbance readings were taken once every hour for 8 hours.

Nutrient limiting conditions. Synchronized cultures were used to inoculate [L]-CDM to ~OD_{600nm} 0.05 by first measuring the absorbance then calculating the volume needed to reach the desired optical density, then washing twice with sterile PBS. Absorbance readings were taken once every hour for 8 hours.

Metal ion-limiting conditions. Isolated colonies from TSA were used to streak MLA. Isolated colonies from MLA were used to inoculate 5 mL ML in a 50 mL Falcon tube, which was incubated at 37°C for 36 – 48 hours. An Erlenmeyer flask containing 25 mL CL was inoculated to ~OD600 nm 0.005 and incubated at 37°C with shaking. After 12 hours, an identical set of flasks was set up and incubated at 37°C with shaking. Twelve hours from that point is when absorbance measurements were begun, once an hour for 12 hours, resulting in a total time-point range from 12 hours to 32 hours.

Alternative sugar fermentation assay

A flat-bottomed 96-well plate was prepared with 200 µL purple broth per well. Wells were supplemented with 1% of an alternative sugar and inoculated with 5 µL overnight culture standardized to ~$OD_{600\ nm}$ 1.0. Each sugar stock was prepared at a concentration of 100 mg/mL. Alternative sugars used were dextrose, fructose, galactose, *D*-glucosamine, lactose, maltose, mannose, ribose, sucrose, trahalose, raffinose, and xylose. Plates were incubated at 37°C overnight, then examined for a change in color from purple to yellow. The color change indicated fermentation of the alternative carbon source. Each assay was performed in triplicate.

Autolysis assays

Triton X-100 lysis. Synchronized cultures were used to calculate the volume needed to inoculate a 10 mL solution to ~OD_{600nm} 2.0. The required volume was aliquoted and washed twice with ice cold diH_2O, then resuspended in 10 mL sterile 0.05M Tris-HCl (pH 7.6) with or without 0.05% Triton X-100. Absorbance measurements were recorded every 30 minutes for 3 hours. Each assay was performed in triplicate.

Penicillin G lysis. Synchronized cultures were used to inoculate 100 mL TSB containing 0.4 μg/mL Penicillin G in a 250 mL Erlenmeyer flask to an ~$OD_{600\ nm}$ 0.05. Absorbance measurements were recorded every 30 minutes for 5 hours. Each assay was performed in triplicate.

Gene sequencing

Solutions. All solutions used for gene sequencing were made according to the following formulas:

TE buffer

Tris-HCl	1 mM
EDTA	0.1 mM

Adjust pH to 7.5 and autoclave. Store at room temperature.

50x TAE buffer

Trisma base	242 g
Glacial acetic acid	57.1 mL
0.5 M Na_2EDTA, pH 8.0	100 mL

Bring up to 1L in diH_2O.

Dilute 1:10 in diH_2O before use.

DNA extraction

A 5 mL overnight culture was spun down and the pellet was resuspended in 600 µL TE buffer in a snap-cap Eppendorf tube. ~0.5 cm of 0.1mm glass beads were added, and the tube was bead beaten for six 10 second intervals. The samples were spun for 5 minutes at full speed and the supernatant was transferred to a new snap-cap Eppendorf. 200 µL 1.6% sarkosyl and 5 µL proteinase K were added, and the samples were incubated at 60°C for 60 minutes. 800 µL of phenol/chloroform was added, the samples were vortexed, and spun for 5 minutes at full speed. The upper aqueous layer was transferred to a 1.5 mL Eppendorf tube, and 500 µL 100% isopropanol and 100 µL 3M sodium acetate were added and mixed by inversion. The sample was incubated at -80°C for 30 minutes. The sample was spun at full speed for 5 minutes, the supernatant was discarded, and 500 µL 70% ethanol was added. The sample was again spun at full speed for 5 minutes and the supernatant was discarded. The pellet was air-dried at room temperature, gently resuspended in 200 µL diH_2O, then allowed to fully resuspend at 4°C overnight.

Polymerase chain reaction (PCR) conditions. Extracted DNA was prepared in PCR tubes as described and placed in a thermocycler (DNAEngine, BioRad). The following conditions were used:

Initiation: 94°C for 2 minutes

30 cycles of

- Denaturation: 94°C for 1 minute
- Annealing: 55°C for 30 seconds
- Extension: 72°C for 1 minute

Final elongation: 72°C for 7 minutes

Hold at 14°C

Primers for *fabH*

Forward primer:

5'-CCT ACC TCT GAC TTG AGT-3'

- Melting temperature: 50.1°C
- GC content: 50%
- MW: 5425.6 g/mol

Reverse primer:

5'-GAC ATC ATT ACC GAT TGG AG-3'

- Melting temperature: 50.5°C
- GC content: 45%
- MW: 6141.0 g/mol

PCR sample preparation

12.5 µL ExTaq

2 µL forward primer

2 µL reverse primer

2 µL template DNA

6.5 µL diH_2O

Electrophoresis conditions. Gels containing 1% agarose in TAE were prepared depending on the size of the gel tank. Enough TAE buffer was added to completely cover the gel, and 5 - 10 µL of 10 µg/mL ethidium bromide was added to the solution. Each well was loaded with the total PCR product, and the gel was run at 110 V and 400 mA for 40 minutes. The gel was placed under ultraviolet light and photographed using the GelDoc-It System to visualize the DNA.

Gel extraction. The QIAquick gel extraction kit (Qiagen, California) was used to extract DNA from the agarose gel. Briefly, the gel was placed on a UV transilluminator and a clean scalpel was used to excise the DNA bands. The gel was placed in a microcentrifuge tube and 1 mL of Buffer QG was added. The tube was placed in a 50°C water bath and occasionally vortexed until the gel was completely dissolved. An equal volume of isopropanol was added to the solution. The solution was transferred to a QIAquick spin column in a 2 mL collection tube and spun for 1 minute. The flow through was discarded and 5 µL Buffer QG was added, and the sample was again spun for 1 minute. The flow through was discarded, and 750 µL Buffer PE was added to the

column, allowed to stand for 3 minutes, then spun for 1 minute. The flow through was discarded and the column was spun for 2 minutes, then the spin column was transferred to a clean 1.5 mL Eppendord tube. 50 µL diH2O was added to the column, allowed to stand for 1 minute, and spun for 1 minute. Eluted DNA was stored at 4°C until needed.

Gene sequencing. PCR products extracted from gels were sent to Eurofins MWG Operon (Huntsville, Alabama) for sequencing. Samples containing 2 µL of the appropriate primer, 8 µL diH_2O, and 10 µL of the DNA sample were combined in 1.5 mL Eppendorf tubes. A set for both the forward and reverse primers were each prepared in separate Eppendorf tubes. The tubes were double-sealed in parafilm, wrapped in bubble wrap, and shipped overnight via FedEx.

Sequence analysis. Sequence massager was used to obtain the complement of reverse primer sequences. Clustal W2 (European Bioinformatics Institue, EMBL-EBI) was used to align the forward and reverse primer sequences, resulting in the whole sequenced gene. The same program was used to compare the parent and mutant sequences to determine the presence of any mutations at the genetic level.

Proteomic analysis

Solutions. All solutions used for proteomic analysis were made according to the following formulas:

Dissolution buffer

Triethylammonium bicarbonate	500 mM
Sodium dodecyl sulfate, ultrapure	0.1%

Bring up to volume in HPLC-grade diH_2O and store at 4°C in the dark.

Cytoplasmic protein extraction. A synchronized culture was used to inoculate a 1 L Erlenmeyer flask containing 400 mL TSB to ~$OD_{600\ nm}$ 0.05. The flask was incubated until the culture reached the phase of interest. The entire culture was spun down at full speed for 10 minutes. The pellet was resuspended in PBS, transferred to a 50 mL Falcon tube, and washed in PBS three times. The pellet was resuspended in 1 mL dissolution buffer, and 500 µL aliquots were transferred to screw-cap tubes, and 0.01mm glass beads were added. The tubes were subjected to vigorous bead beating using a MiniBeadbeater-16 (Biospec Products) for four 1 minute intervals. The tubes were spun at full speed in a tabletop microcentrifuge for 10 minutes, and the supernatants were combined in an Eppendorf tube. The tubes were spun again, and the supernatant was transferred to another Eppendorf tube. Extracted proteins were stored at -80°C until needed.

Concentrating proteins. The required concentration for iTRAQ analysis was 5 – 100 µg per 20 µL. Millipore concentration tubes were used to concentrate extracted proteins to the desired concentration as needed, following the manufacturer's recommendations. Protein samples were centrifuged for 30 minutes at 13,300 x g for concentration and recovered by centrifuging for 2 minutes at 2000 x g.

Protein precipitation. Concentrated proteins were precipitated by suspending overnight in a 1:10 volume of 100% trichloroacetic acid at 4°C. The resulting pellet was washed twice with ice cold 100% ethanol by centrifuging at 8500 x g for 70 minutes. The pellet was allowed to air dry then resuspended by sonication in 1 mL dissolution buffer. The samples were spun for 30 minutes at full speed, the supernatants discarded, and the pellets resuspended in 100 µL dissolution buffer. The Pierce assay was performed following manufacturer's recommendations to determine the final protein concentration.

Trypsin digest. The volume of protein sample needed to contain 100 µg of protein was calculated and aliquoted to a 1.5 mL Eppendorf tube, and 20 µL dissolution buffer and 1 µL denaturant was added. The tube was vortexed and 2 µL reducing agent was added, and the tube was vortexed again. The tube was incubated at 60°C for 1 hour and briefly centrifuged. 1 µL cysteine blocking reagent was added, vortexed to mix, and briefly centrifuged. The tube was incubated at room temperature for 10 minutes. Trypsin was provided with the iTRAQ kit and reconsitituted with 25 µL MilliQ water. 10 µL was added to each protein sample, vortexed, and briefly centrifuged. The tube was incubated at 37°C for 16 hours then briefly centrifuged. The next step was begun immediately.

iTRAQ labeling. The iTRAQ reagents required for all the protein samples were allowed to reach room temperature before use, briefly centrifuged, and 70 µL ethanol was added to each tube. The reagents were vortexed, briefly centrifuged, and the contents of one vial was transferred to one protein sample. Samples were vortexed, briefly centrifuged,

and incubated at room temperature for 1 hour. All protein samples were combined into a single fresh 1.5 mL Eppendorf tube, vortexed, and briefly centrifuged.

Desalt. A MacroSpin column placed in a 2 mL Eppendorf tube was activated by adding 50 µL acetonitrile and centrifuging at 110 x g for 1 minute. The eluent was discarded and the column was dried with a Kim wipe. The column was equilibrated by adding 500 µL 0.1% formic acid and centrifuged as previously. The eluent was discarded and the column was washed with 0.1% formic acid again. The labeled protein sample was added to the column and centrifuged as previously, and the eluent was discarded. The MacroSpin column was transferred to a new 2 mL Eppendorf tube, and the labeled protein sample was eluted by adding 250 µL acetonitrile/water (90:10). The sample was spun as previously and the eluent was transferred to a 1.5 mL Eppendorf tube. Samples were dried in a speed vac for ~1 hour and resuspended in 0.1% formic acid to a final concentration of 1 µg/µL. The desalted, labeled protein sample was sonicated for 10 – 15 minutes, or until completely solubilized, then stored at 4°C until needed.

Evaluation of proteins by mass spectrometry. The sonicated protein samples were transferred to cylindrical glass tubes and placed in the autosampler, which injects 5 µL aliquots of the samples into the LTQ Orbitrap XL (ThermoFinnigan) for analysis. The program used to evaluate the labeled peptides called for two injections at 180 minutes each.

Analysis of iTRAQ data. Raw iTRAQ data was first run through Mascot. This allowed the identified fractions to be compared to a known database and compiled into a single file. The condensed files were processed by Scaffold Q+ and used to compare parent strains and mutants.

SDS-PAGE

Solutions. All solutions used for sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) were made according to the following formulas:

SP buffer

Raffinose	30%
$MgCl_2$	20 mM

Laemmli sample buffer

diH_2O	4.0 mL
0.5M Tris, pH 6.8	1.0 mL
100% glycerol	0.8 mL
10% sodium dodecyl sulfate	1.6 mL
β-mercaptoethanol	0.4 mL
Bromophenol blue	0.05%

Store at -20°C.

Coomassie blue staining solution

Methanol	50%
Acetic acid	10%
Coomassie blue	0.25%

Destain solution

Methanol	10%
Acetic acid	5%

Separating gel

diH_2O	3.35 mL
1.5M Tris-HCl, pH 8.8	2.5 mL
10% SDS	100 µL
Acrylamide*	4.0 mL
10% APS	50 µL
TEMED	7 µL

ProtoGel acrylamide was purchased from National Diagnostics. It consisted of 30% w/v acrylamide and 0.8% w/v *bis*-acrylamide.

Stacking gel

diH_2O	3.05 mL
0.5M Tris-HCl, pH 6.8	1.25 mL
10% SDS	50 µL
Acrylamide*	650 µL
10% APS	25 µL
TEMED	5 µL

ProtoGel acrylamide was purchased from National Diagnostics. It consisted of 30% w/v acrylamide and 0.8% w/v *bis*-acrylamide.

10x Electrophoresis buffer

Glycine	144 gL^{-1}
Tris base	30.3 gL^{-1}
SDS	10 gL^{-1}

Solution was diluted 1:10 in diH_2O before use.

Extraction of cell-wall associated proteins. The absorbance of overnight cultures were measured at $OD_{600\ nm}$, and the volume calculated to result in an ~OD_{600nm} 50.0 in 100 mL was calculated. The calculated volume was aliquoted and spun down at full speed for 10 minutes. The supernatant was discarded, and the pellet was resuspended in 100 µL SP buffer. Twenty-five µL lysostaphin and 8µL protease inhibitor was added to the sample, and the suspension was incubated at 37°C for 20 minutes. Following incubation, the

samples were spun at full speed for 10 minutes, and the supernatants containing the proteins were collected in an Eppendorf tube to be stored at -20°C until needed for SDS-PAGE analysis. This protocol was also followed for cultures standardized to ~$OD_{600\ nm}$ 100.0 or 150.0. The addition of lysostaphin was increased accordingly. An aliquot of the protein sample was mixed with an equal volume of laemmli sample buffer and boiled for 5 minutes before loading on a gel.

Extraction of secreted proteins. Cultures grown overnight for 10 - 15 hours were standardized so that all cultures had the same arbitrary absorbance. Cultures were spun down at full speed for 10 minutes, and the supernatant containing the proteins was stored at -80°C until needed. Upon need, the samples were thawed on ice, and 1 mL was transferred to a locking-cap Eppendorf tube. 100 µL 100% trichloroacetic acid was added, and the samples were mixed by inversion and incubated on ice for 30 minutes. The samples were spun at full speed for 5 minutes and washed twice with 500 µL acetone. Each time, the pellet was broken with a pipette tip. Following the final wash, the pellet was air-dried before adding 30 µL laemmli sample buffer, then boiled for 10 minutes and cooled before loading on a gel.

Electrophoresis conditions. BioRad's Mini-Protean TETRAcell system was used to run up to four protein gels at a time. The length of time per run was increased proportionate to the number of gels being run, from ~40 minutes for one gel up to ~2 hours for four gels. The power source was set to 300 V and 30 mA.

RESULTS

Activity of NsβL against a diverse array of laboratory and clinical strains of *S. aureus*. *S. aureus* is a clinically relevant human pathogen with a high level of clonal variation, resulting in a wide range of antimicrobial resistances. Accordingly, we screened a variety of different laboratory and clinical strains for susceptibility to NsβL using a disk diffusion assay (**Fig. 2**). The zones of inhibition (ZOI) were found to be comparable for all strains tested, regardless of their origin or existing antimicrobial resistance. NsβL was dissolved in dimethylsulfoxide (DMSO). DMSO was not found to have any effect on the growth of *S. aureus* in this assay (data not shown).

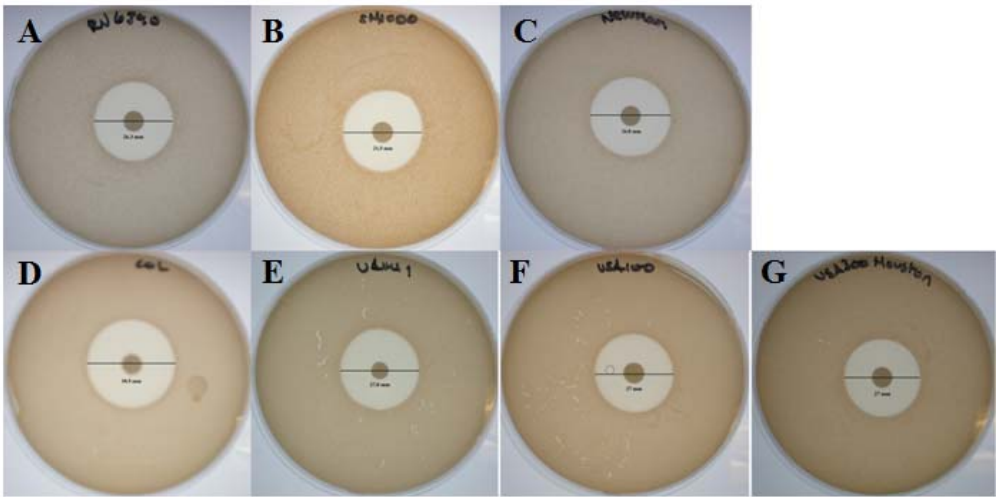

Figure 2. Disk diffusion assays using NsβL with multiple laboratory and clinical strains of *S. aureus*. (A) RN6390; (B) SH1000; (C) Newman; (D) COL; (E) UAMS-1; (F) USA100; (G) USA 300 Houston.

In order to quantify the activity of NsβL, the minimum inhibitory concentration (MIC) was determined for each of these strains using a 96-well plate microbroth dilution method, which allows for quick and efficient screening of multiple samples at a range of concentrations. The MIC is defined as the lowest drug concentration at which there is no visible growth, and was found to be between 0.4 µg/mL and 1 µg/mL for all strains tested (**Fig. 3; Table 3**).

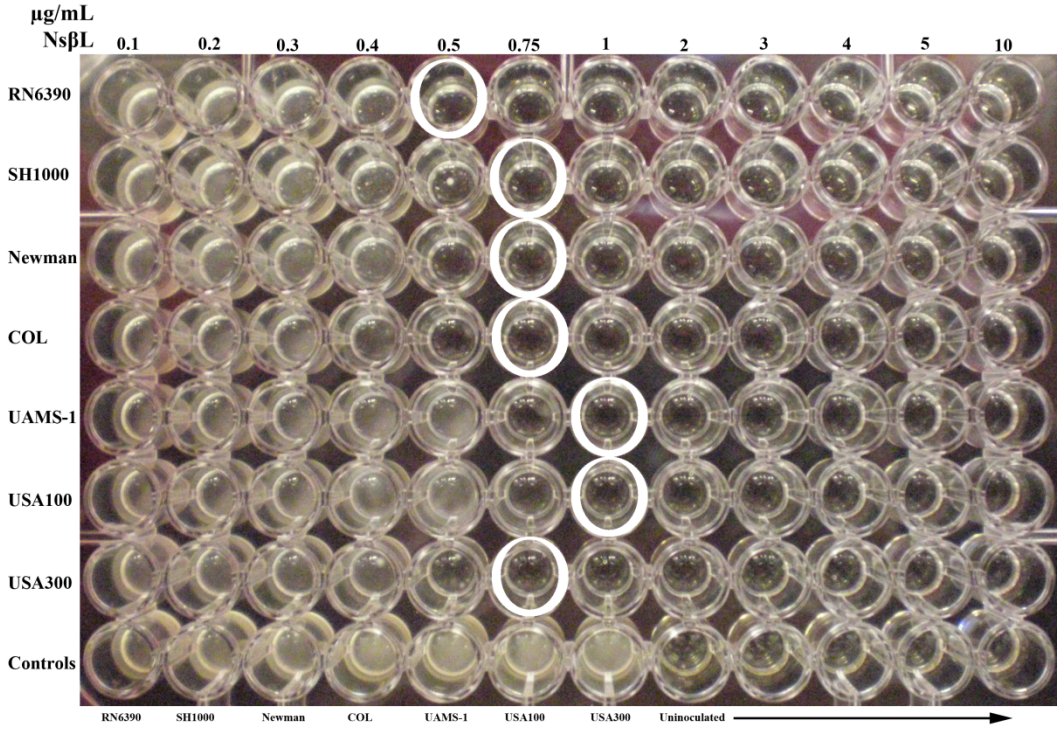

Figure 3. Microbroth dilution assay to determine MIC of NsβL using a variety of *S. aureus* and clinical isolates. Circles indicate the lowest concentration with no visible turbidity; ie the MIC.

Strain	MIC (µg/mL)
RN6390	0.5
SH1000	0.75
Newman	0.75
COL	0.75
UAMS-1	1
USA 100 635	1
USA 300 Houston	0.75

Table 3. Minimum inhibitory concentrations for laboratory and clinical *S. aureus* strains as determined using a microbroth dilution assay.

Investigation into the effects of fatty acids on the activity of NsβL. As a result of these studies, the effect of fatty acids on the activity of NsβL was first tested using a disk diffusion assay. There has been conflicting evidence concerning the effect of fatty acids on the growth of *S. aureus* and other Gram-positive pathogens in the presence of antimicrobials targeting fatty acid synthesis. Specifically, it has been suggested that the fatty acids can rescue growth, despite the presence of antimicrobial agents[2, 6, 16, 17]. As previous work has indicated that NsβL may target fatty acid synthesis[92], 0.01% oleic acid (a long chain unsaturated fatty acid) or 0.1% Tween 80 (an oleic acid surrogate) was added to TSA to determine if there was a similar effect on NsβL activity. As a control, NsβL ZOIs were compared to those for vancomycin (a cell wall synthesis inhibitor). The assay was performed for *S. epidermidis* RP62A and the *S. aureus* strains SH1000, Newman, COL, USA 100 Mu50, USA 200 MRSA252, USA 300 Houston, and USA 400 MW2 (**Fig. 4**). For all strains tested, the NsβL ZOIs were significantly and consistently reduced in the presence of Tween 80. For SH1000, COL, and USA 300 Houston, the vancomycin ZOIs were also reduced in the presence of Tween 80, but all other strains had consistent ZOIs.

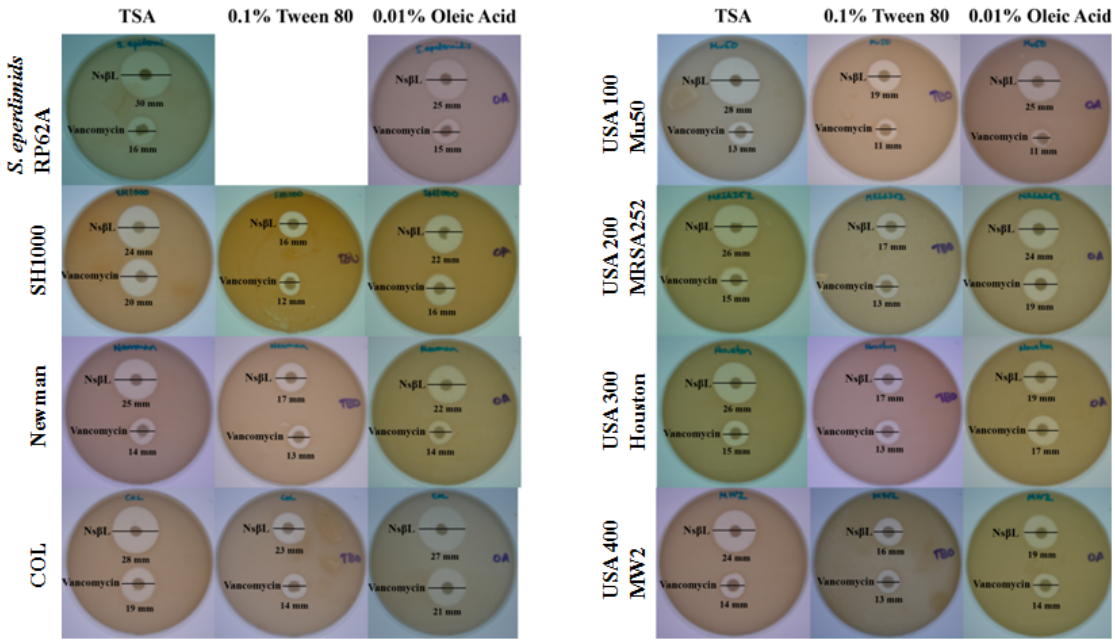

Figure 4. Disk diffusion assays comparing the effects of fatty acids on the activity of NsβL and vancomycin against a variety of laboratory and clinical *S. aureus* isolates.

Quantification of the effects of fatty acids on antimicrobial activity was further evaluated by adding 0.1% Tween 80, 0.01% oleic acid, or 0.5% BSA to TSB and measuring the growth of *S. aureus* isolates in the presence of NsβL, vancomycin, or triclosan (a commercially used fatty acid synthesis inhibitor). Both Tween 80 and oleic acid were dissolved in BSA, so this was included in the assay as a control. BSA, Tween 80, and oleic acid significantly reduced the MIC for vancomycin, indicating that these additives may work synergistically with vancomcyin to inhibit cell wall synthesis. The MIC for triclosan was increased by Tween 80 20- to 50-fold for all strains tested; however, oleic acid did not have significant rescue activity for cultures treated with triclosan. The presence of Tween 80 allowed growth in the presence of NsβL concentrations equal to the MIC, but not at the concentrations tested above the MIC. Cultures treated with BSA were also able to grow in the presence of NsβL, but at a level significantly lower than the

untreated culture. These results were comparable for all strains tested, suggesting that the diverse isolates tested had similar responses to the presence of fatty acids (only USA 300 data shown: **Fig. 5**).

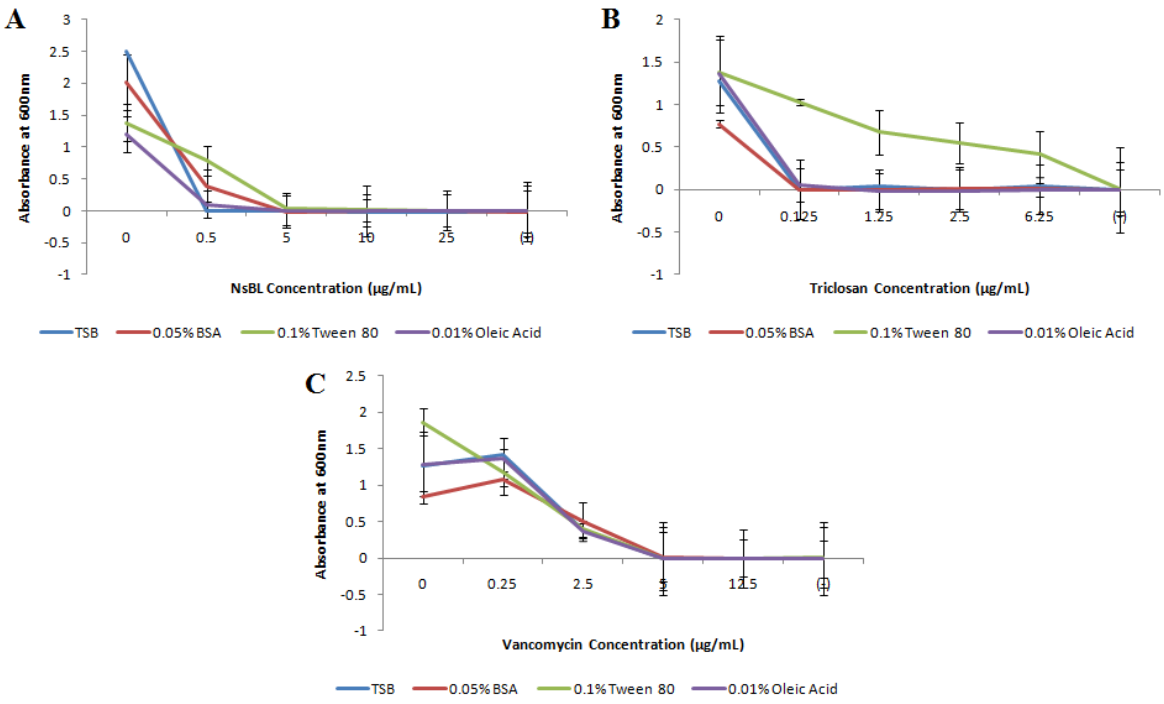

Figure 5. The effects of fatty acids on the antimicrobial activity of NsβL towards *S. aureus* USA 300 Houston. (A) NsβL; (B) Triclosan; (C) Vancomycin.

Comparison of the effects of NsβL and other antibiotics on *S. aureus* biofilms. *S. aureus* biofilms are difficult to treat due to a lack of antimicrobial diffusion through the biofilm matrix and because not all of the cells are in an actively growing state[61]. The effects of NsβL, triclosan, vancomycin, and tetracycline (a protein synthesis inhibitor) on UAMS-1 biofilms were analyzed using a 96-well plate method previously described by Beenken, et. al. UAMS-1 was chosen as it is a biofilm-forming strain that has previously been well characterized for this aggregate lifestyle[11]. SH1000 was also used as a positive control, and 8325-4 as a negative control. Biofilms were allowed to establish for 24

hours before fresh media containing the relevant antimicrobial was added. Antimicrobial exposure lasted an additional 24 hours before the biofilms were stained with crystal violet for evaluation (**Fig. 6**).

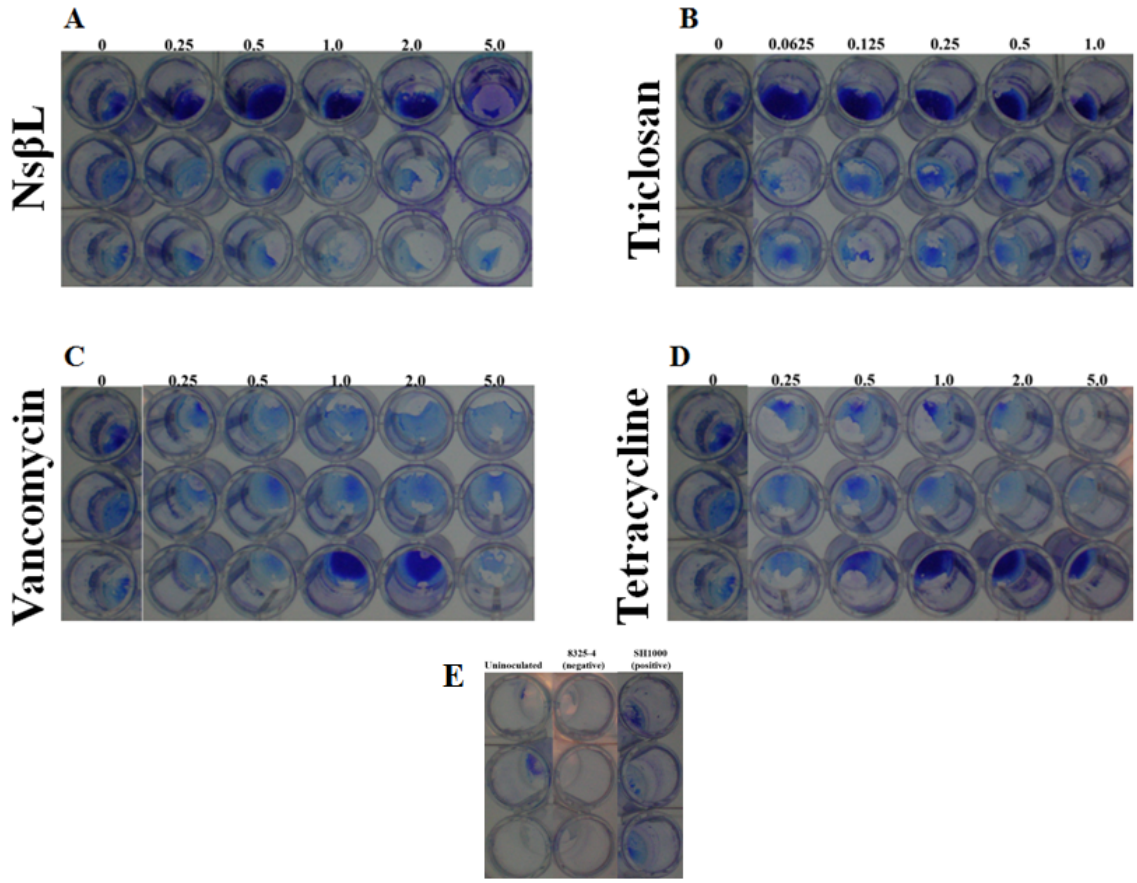

Figure 6. The effect of selected antimicrobials on *S. aureus* UAMS-1 biofilms. Biofilms were exposed to the antimicrobials in the concentrations indicated (μg/mL) for 24 hours before staining with crystal violet. (A) NsβL; (B) Triclosan; (C) Vancomycin; (D) Tetracycline; (E) Untreated controls.

Quantitative analysis was performed by measuring the absorbance of eluted crystal violet at 595 nm in a BioTek Synergy2 96-well plate reader and the percent change from the untreated biofilms was calculated (**Fig. 7**). Tetracycline and NsβL had the greatest effect on biofilm formation, reducing the absorbance at 595 nm by approximately 30% and 40%, respectively. Triclosan had only a slight effect on biofilms, reducing their

formation by 13 – 21%. Biofilms were unaffected by treatment with vancomycin, and had levels of formation comparable to or exceeding the untreated UAMS-1 control.

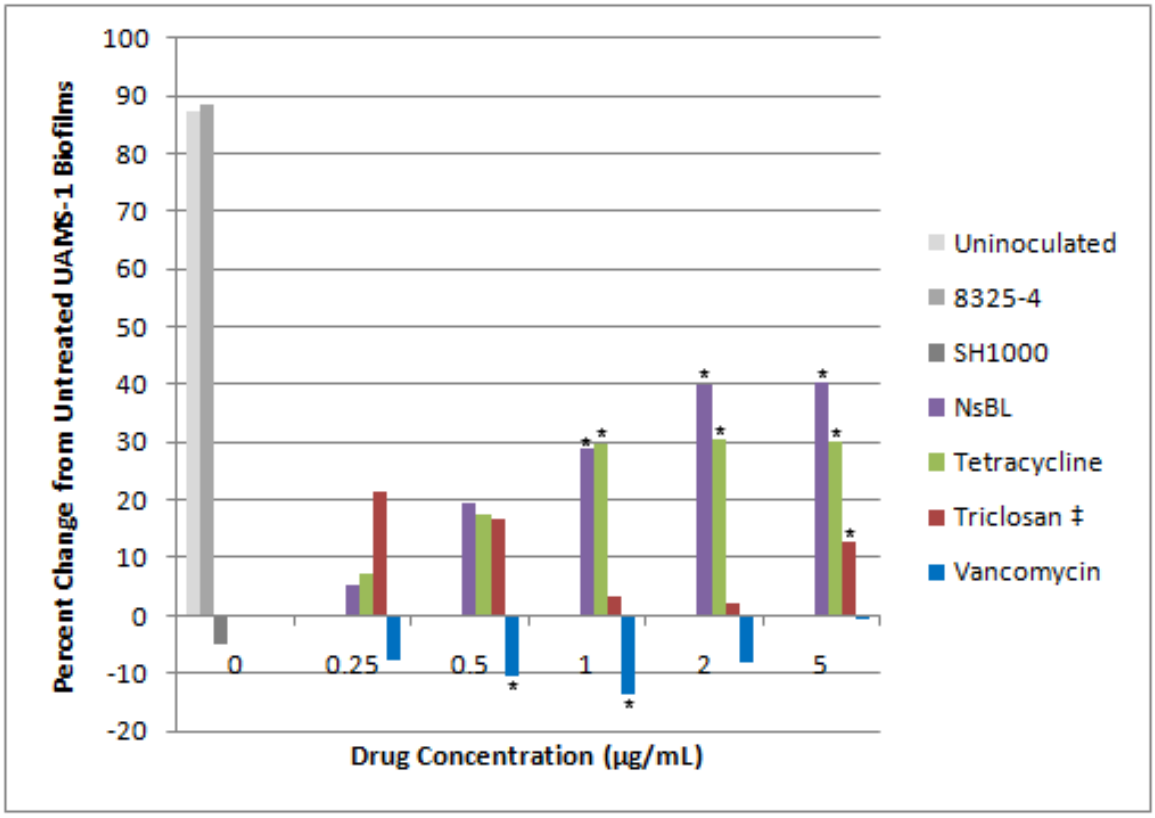

Figure 7. Quantative analysis and comparison of antimicrobial-treated biofilms. Biofilms were stained with crystal violet as described and the absorbance of a 1:100 dilution was measured with a BioTek Synergy2 plate reader at 590 nm. The percent change as compared to the untreated UAMS-1 biofilms was calculated. * $p < 0.1$ using the Student's t-test comparing the antimicrobial-treated biofilms to the untreated UAMS-1 biofilms. ‡Triclosan concentrations were 0, 0.0625, 0.125, 0.25, 0.5, and 1 µg/mL.

Analysis of spontaneous mutation frequencies for NsβL. Spontaneous mutation leading to resistance is a problem with all clinically available antimicrobials. Knowing the rate of mutation is vital in order to determine the minimum dosage required to prevent resistance. In addition, it gives a sense of the suitability of a given compound for use in treating infections. As such, TSA was supplemented with seven times the NsβL MIC and inoculate with 3 x 10^9 SH1000 cells in order to determine the spontaneous mutation

frequency, calculated as the number of resistant colonies per cells screened. Four replicates were performed for this assay (**Fig. 8**), yielding a total of 98 colonies from a total inoculum of 1.38 x 10^{10} cells yielded a spontaneous mutation rate of 7.1 x 10^{-9}. The NsβL MICs of all colonies obtained were determined by the microbroth dilution method as described, and found to be 1.5-fold to 67-fold greater than the parent strain. A total of 26 of the isolated spontaneous mutants had MICs less than 5 µg/mL. When this is taken into account, the spontaneous mutation rate becomes 5.2 x 10^{-9}. Two isolates, SH-11 and SH-32, were chosen to use for further experimentation because they had the highest MICs (**Table 4**).

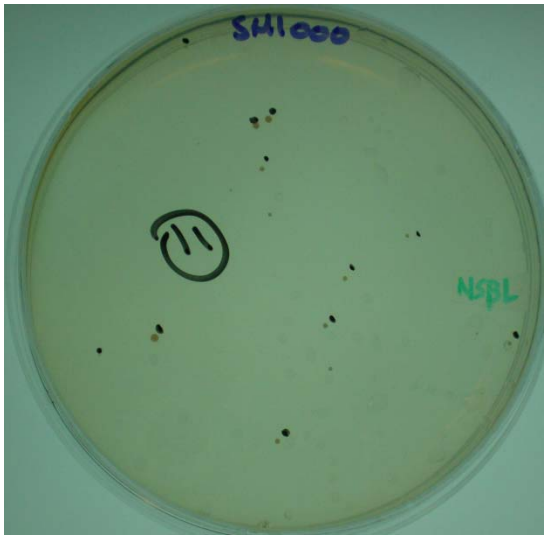

Figure 8. Spontaneous mutagenesis of *S. aureus* SH1000 using 7X MIC of NsβL. TSA supplemented with NsβL was inoculated with 1 x 10^9 SH1000 cells and incubated at 37°C for 30 hours. Plates yielded between 11 and 49 colonies. A representative example is shown.

Isolate	MIC µg/mL	Isolate	MIC µg/mL
SH-11	50	**SH-60**	20
SH-15	X	**SH-62**	20
SH-22	30	**SH-64**	20
SH-32	30	**SH-69**	10
SH-38	10	**SH-74**	10
SH-56	20	**SH-75**	20
SH-58	10	**SH-77**	X
SH-59	X	**SH-85**	X

Table 4. MICs for spontaneous NsβL SH1000 mutants. These values were determined using the microbroth dilution method, and are shown for randomly selected isolates. NsβL concentrations tested were 0, 10, 20, 30, 40, and 50 µg/mL. X indicates no visible growth at all NsβL concentrations. The isolates used for further experimentation in this study are highlighted.

Analysis of the effect of NsβL on a nitrosoguanidine mutant library of *S. aureus*. We set out to determine if prior DNA mutagenesis would affect the spontaneous mutation rate of *S. aureus* to NsβL. As such, SH1000 was treated with nitrosoguanidine (NTG), a

DNA alkylating agent, and the spontaneous mutation frequency was determined as previously described (**Fig. 9**; **Table 5**). Twelve colonies were isolated from the 4 x 10^8 NTG-treated cells plated, yielding a spontaneous mutation rate of 3 x 10^{-9}. However, four of the twelve NTG-treated NsβL-resistant isolates had MICs equal to 1 µg/mL, significantly lower than the concentration used to generate them, and changes the spontaneous mutation rate to 2 x 10^{-8}, which is 3.85 times greater than the spontaneous mutation rate of the untreated cells.

Figure 9. Spontaneous mutagenesis of an NTG-treated SH1000 mutant library An inoculum of 4 x 10^8 cells yielded 12 colonies on a 5 µg/mL NsβL plate.

Isolate	MIC µg/mL	Isolate	MIC µg/mL
NTG-A	10	**NTG-G**	1
NTG-B	1	**NTG-H**	10
NTG-C	10	**NTG-I**	10
NTG-D	10	**NTG-J**	1
NTG-E	10	**NTG-K**	10
NTG-F	1	**NTG-L**	10

Table 5. MICs for the spontaneous NTG-treated SH1000 mutants. The MICs for library mutants were determined using the microbroth dilution method. NsβL concentrations tested were 0, 1, 10, 15, and 20 µg/mL.

The adaptation of *S. aureus* to prolonged growth in the presence of NsβL. In contrast to the spontaneous mutant analysis, we also set out to determine the effect of prolonged NsβL exposure on *S. aureus* cells. Therefore, *S. aureus* strains USA 100 and USA 300 were subjected to increasingly higher concentrations of NsβL in order to obtain highly resistant adaptive mutants. Overnight exposure began at 0.125 µg/mL in 2 mL brain-heart infusion (BHI) broth. A 4 µL aliquot of the culture was transferred to a fresh tube

containing 2 mL BHI with double the NsβL concentration and exposed for 24 hours. This process was repeated, making a glycerol stock of the exposed cells as previously described, and transferring a 4 µL aliquot to fresh BHI with double the NsβL concentration each day until no growth was obtained at 64 µg/mL. The MICs were confirmed by the microbroth dilution method as previously described (**Table 6**).

Strain	MIC (µg/mL)
USA 100 WT	0.75
USA 100 AM	65
USA 300 WT	0.75
USA 300 AM	55

Table 6. MICs of adaptive mutants (AM) and their wild-type (WT) parents.

Phenotypic characterization of the NsβL-resistant mutants. Previous studies on the mode of action of NsβL have indicated that this drug may target FabH, an essential component of fatty acid biosynthesis. The study also speculated that NsβL may have an effect on coenzyme-A (CoA), which is a cofactor for a number of fatty acid synthesis, pyruvate metabolism, and the citric acid cycle (TCA) enzymes[92]. Thus far, the mode of action of NsβL has not been fully characterized. In an effort to extrapolate the mechanism of activity of NsβL, two of the SH1000 spontaneously generated mutants, SH-11 and SH-32, and the adaptive mutants of USA 100 and USA 300 were evaluated for phenotypic changes from their parental strains.

Growth analysis of the NsβL-resistant mutants. Standard growth curves were performed in TSB and chemically-defined media (CDM) in order to determine if there were changes in growth of the various mutant strains (**Fig. 10**). No changes were observed for the SH-11 or SH-32 spontaneous mutants or for the USA 100 adaptive

mutant in TSB. However, the USA 300 adaptive mutant showed decreased levels of growth in TSB in comparison to its parent. In CDM, the SH-11 spontaneous mutant showed decreased growth during lag phase in comparison to both SH1000 and the SH-32 spontaneous mutant. The USA 100 adaptive mutant had increased growth levels during lag and early-exponential phase, but decreased growth during stationary phase. The USA 300 adaptive mutant had increased growth during all phases tested.

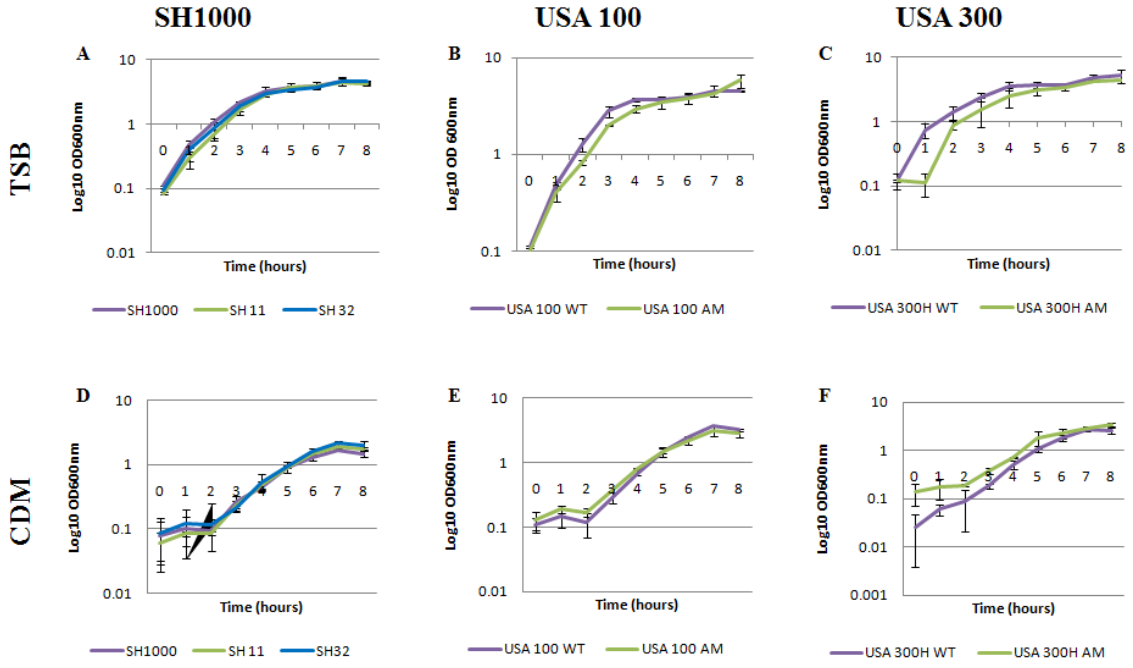

Figure 10. Growth curve analysis of the NsβL-resistant mutants in both TSB (top) and CDM (bottom). (A, D) SH1000 and its spontaneous mutants; (B, E) USA 100 and its adaptive mutants; (C, F) USA 300 Houston and its adaptive mutants. All assays were performed in triplicate.

Nutrient limiting derivatives of CDM were also used to determine if there were defects in response to nutrient starvation in the spontaneous and adaptive mutants. For amino acid-limiting CDM, no significant differences were seen for either spontaneous mutant. The USA 100 adaptive mutant showed increased growth levels in early-exponential phase, but

decreased growth in late-exponential and stationary phase. The USA 300 adaptive mutant showed decreased growth only during exponential phase (**Fig. 11**).

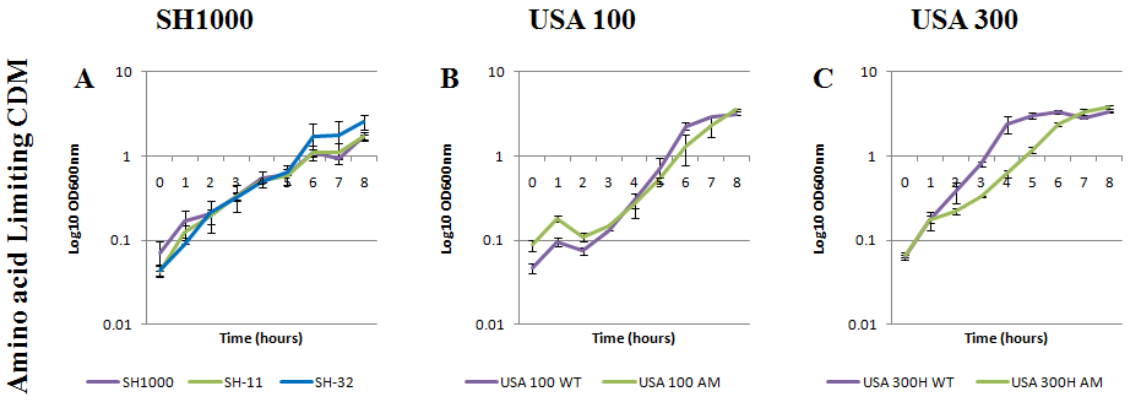

Figure 11. Amino acid-limiting growth curves of the NsβL-resistant mutant strains. (A) SH1000 and its spontaneous mutants; (B) USA 100 and its adaptive mutants; (C) USA 300 Houston and its adaptive mutants. All assays were performed in triplicate.

There were no significant differences for any of the mutants when glucose was the limiting factor (data not shown).

Likewise, there were no differences for the spontaneous mutants or the USA 100 adaptive mutant when phosphate was limited. However, the USA 300 adaptive mutant showed increased growth during late lag and early-exponential phase, and decreased growth during late-exponential and stationary phase (**Fig. 12**).

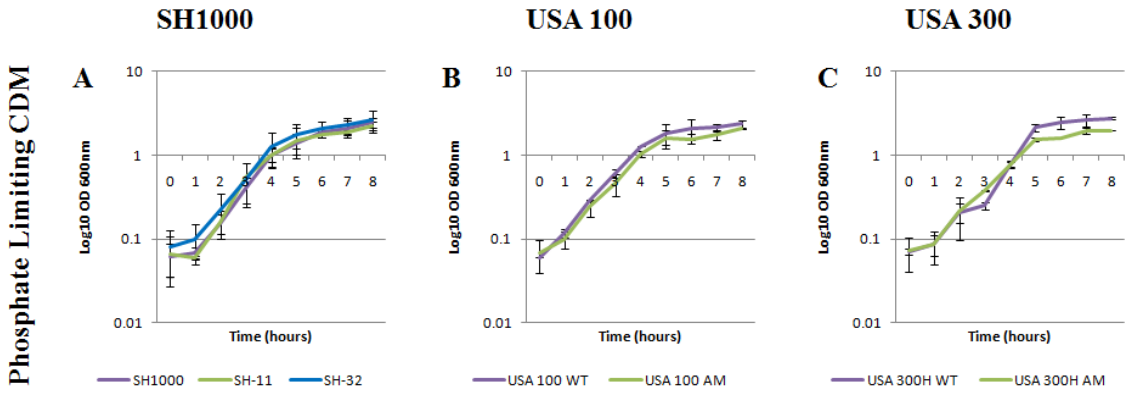

Figure 12. Phosphate-limiting growth curves of the NsβL-resistant mutant strains. (A) SH1000 and its spontaneous mutants; (B) USA 100 and its adaptive mutants; (C) USA 300 Houston and its adaptive mutants. All assays were performed in triplicate.

Metal ion-limiting media was also used to analyze growth over a 36 hour period, although the first 12 hours were not assayed as *S. aureus* has a prolonged lag phase during growth under these conditions. Both spontaneous mutants had decreased levels of growth during exponential phase, with SH-32 growth more significantly reduced than SH-11. There was no change for the USA 100 adaptive mutant, while the USA 300 adaptive mutant had higher growth levels during exponential phase than its parent strain (**Fig. 13**).

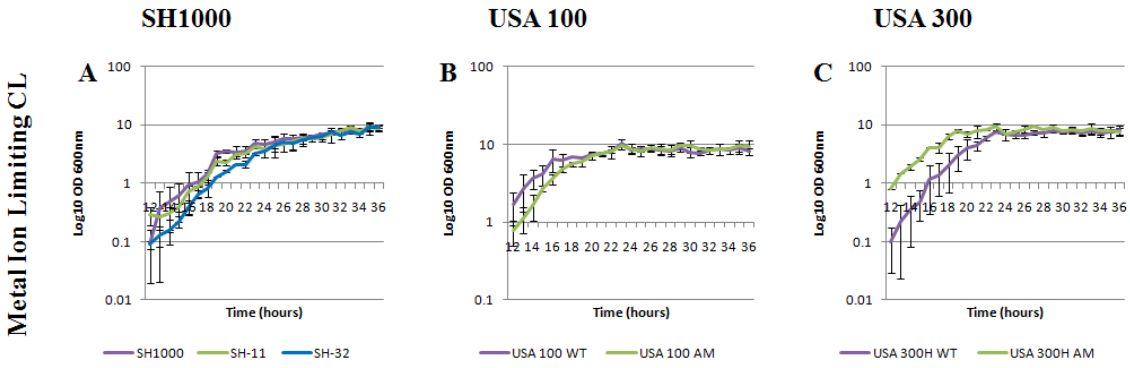

Figure 13. Metal ion-limiting growth curves for the NsβL-resistant mutant strains. (A) SH1000 and its spontaneous mutants; (B) USA 100 and its adaptive mutants; (C) USA 300 Houston and its adaptive mutants. All assays were performed in triplicate.

Assessment of the proteolytic activity of the NsβL-resistant mutant strains. *S. aureus* expresses multiple extracellular proteases as part of its virulence determinant network. To assess this activity in the NsβL-resistant mutants, these strains were incubated both aerobically and anaerobically (**Fig. 14**) on plates containing 2% skim milk. SH1000 naturally has very low levels of proteolytic activity, which did not change with its NsβL-resistant mutants (data not shown). Both the USA 100 and USA 300 adaptive mutants displayed reduced aerobic proteolytic activity compared to their parental strains. Only USA 300 retained proteolytic activity when grown in an anaerobic chamber, which was not displayed by its adaptive mutant.

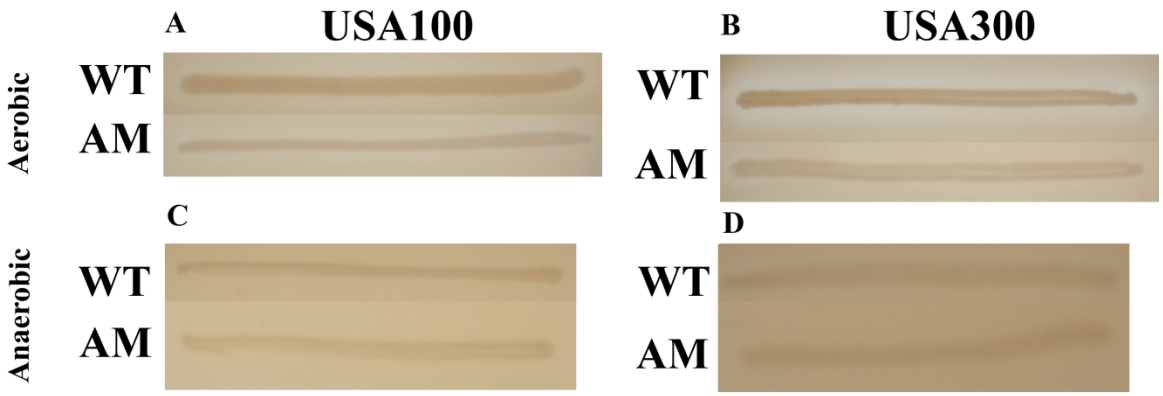

Figure 14. Changes in proteolytic activity of the NsβL-resistant mutants under aerobic (top) and anaerobic (bottom) conditions. TSA containing 2% skim milk was inoculated with the parent strains and their respective mutants. A representative example of three experiments is shown. (A, C) USA 100 WT and its adaptive mutant; (B, D) USA 300 WT and its adaptive mutant.

Investigation of changes in the hemolytic activity of the NsβL-resistant mutant strains. One of the major contributions to *S. aureus* disease comes from its hemolytic activity. To assay these toxins, sheep blood agar was used to compare the hemolytic activity of the parental strains with their respective mutants (**Fig. 15**). The SH1000 spontaneous mutants did not show any apparent change in hemolysis in comparison with the parent (data not shown), while the USA 100 adaptive mutant had reduced activity. Of

significant interest, the USA 300 adaptive mutant lost all hemolytic activity when assayed using blood agar.

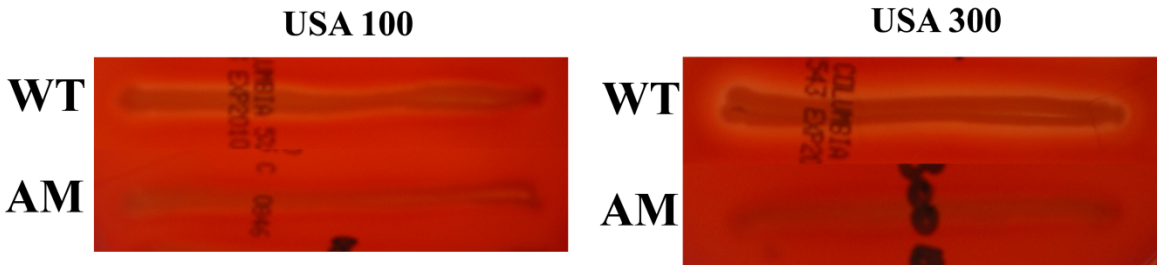

Figure 15. Alterations in hemolysis of the NsβL-resistant mutant strains. Wild-types and their mutants were streaked in triplicate on 5% blood agar. A representative example of three experiments is shown. (A) USA 100 and its adaptive mutant; (B) USA 300 and its adaptive mutant.

Alterations in capsule production by the NsβL-resistant mutants. *S. aureus* has the ability to produce a capsule composed of polysaccharides which aids in defense from phagocytosis, the host's primary defense against bacterial infection. To assay alterations in the production of capsule by the NsβL-resistant mutants, congo red agar (CRA) was inoculated with the wild-types and respective mutant strains (**Fig. 16**). SH1000 and its spontaneous mutants displayed colony morphologies indicative of strong capsule production, i.e. rough, dry, black colonies (data not shown). Conversely, while both the USA 100 and USA 300 wild-types displayed capsule production, their adaptive mutants lost the characteristic black pigmentation altogether, indicating that they were not producing capsules.

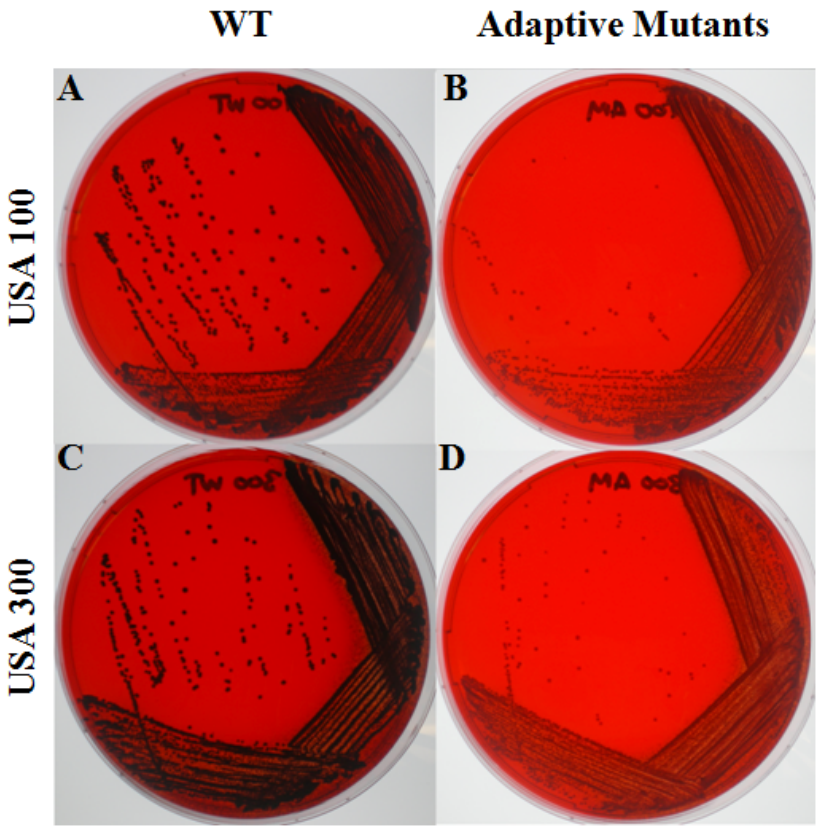

Figure 16. Alterations in capsule production by the NsβL-resistant mutant strains. CRA was inoculated with each strain and examined for colony morphology and capsule production. (A) USA 100 wild type; (B) USA 100 adaptive mutant; (C) USA 300 wild type; (D) USA 300 adaptive mutant.

The effects of resistance to NsβL on virulence determinant production and secretion. *S. aureus* produces a wide variety of toxins and other secreted proteins associated with virulence. In addition, MSCRAMMS and other cell-wall associated proteins are involved in invasion of the host and attachment to various surfaces. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) was used to compare the production of cell-wall associated and secreted proteins produced by the parent and mutant strains. SDS-PAGE of the cell-wall associated proteins (**Fig. 17**) shows that SH-11 appears to produce slightly increased levels of these proteins than either the wild-type or SH-32. Both the USA 100 and USA 300 adaptive mutants produced significantly less

cell-wall associated proteins than their respective parental strains. Particularly notable is a ~45 kDa protein produced by USA 300 wild-type which is significantly diminished in its adaptive mutant.

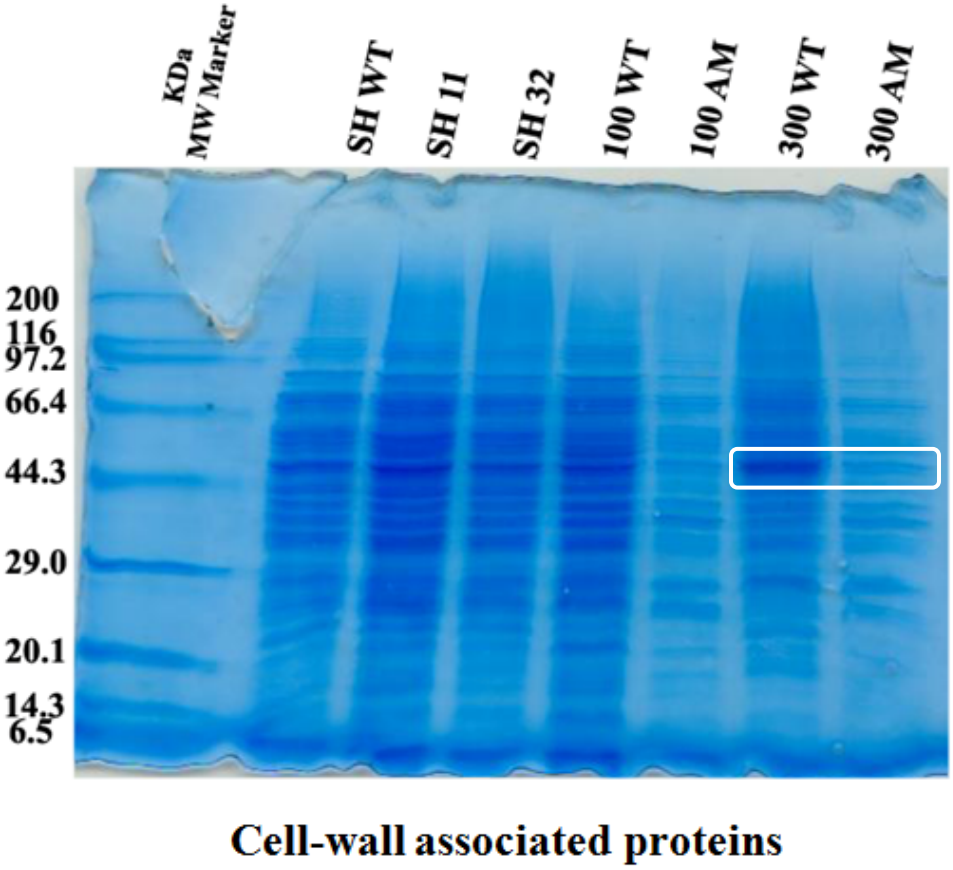

Figure 17. SDS-PAGE of cell-wall associated virulence determinants for wild-types and their NsβL-resistant mutants. The gel shown here is representative of four experiments. The cell-wall associated proteins were extracted from a culture standardized to OD_{600nm} = 50.0. The white box indicates the ~45 kDa protein expressed in the USA 300 WT but not in the adaptive mutant.

SDS-PAGE of secreted proteins (**Fig. 18**) showed similar patterns of expression, with protein levels secreted by SH-11 slightly increased as compared to the wild-type. The increase in expression of an ~80 kDa protein was particularly apparent. The proteins secreted by both adaptive mutant strains were significantly decreased compared to their parental strains, particularly an ~80 kDa protein that was also seen over-expressed in SH-11, a ~50 kDa protein, and a ~35 kDa protein. Interestingly, the levels of two proteins

secreted by both adaptive mutant strains appeared to be less reduced than the rest, seen at ~95 kDa and ~28 kDa.

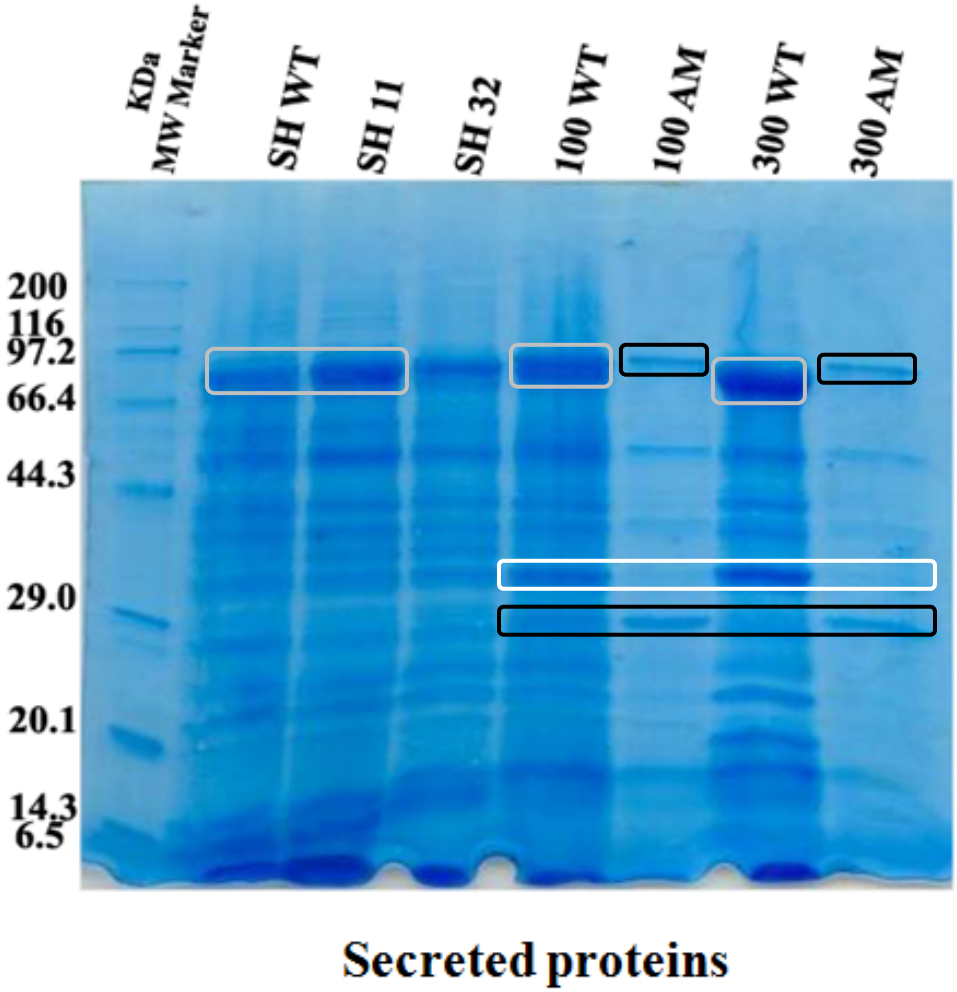

Figure 18. SDS-PAGE of secreted virulence determinants for wild-types and their NsβL-resistant mutants. The gel shown here is representative of four experiments. The secreted proteins were extracted from a culture standardized to the same absorbance at 600nm. The gray boxes indicates the ~80 kDa protein band, the white box indicates the ~35 kDa protein band, and the black boxes indicate the ~28 kDa and ~95 kDa protein bands.

Evaluation of electron transport in the NsβL-resistant mutants. Growth of *S. aureus* in anoxic environments requires the presence of nitrogen, which serves as a terminal electron acceptor. To assess the phenotype of the NsβL-resistant mutants with regards to electron transport, media containing either nitrate or nitrite was inoculated with the wild-

type strains and their respective NsβL-resistant mutants. These plates were incubated in a GasPak chamber to ensure an anaerobic environment. No significant alterations in growth were observed for any of the mutant strains tested (data not shown**)**.

Alterations in the ability of the NsβL-resistant mutants to ferment alternative carbon sources. Following from this, we examined the ability of the NsβL-resistant strains to ferment a variety of carbon sources when grown under anaerobic conditions. Interestingly, *S. aureus* has the ability to use a variety of different sugars as its carbon source in the absence of glucose. As such, purple broth was used, which has a pH indicator that changes the media from purple to yellow when the media becomes acidified as the result of lactate or acetate production during fermentation. No changes in sugar fermentation were seen for dextrose, fructose, galactose, *D*-glucosamine, lactose, mannose, sucrose, trehalose, raffinose, or xylose. The spontaneous mutants SH-11 and SH-32 did not show any changes from their parent, while both the USA 100 and USA 300 adaptive mutants lost the ability to ferment ribose. Further to this, the USA 300 adaptive mutant was also unable to ferment maltose when compared to the parental strain (**Fig. 19**).

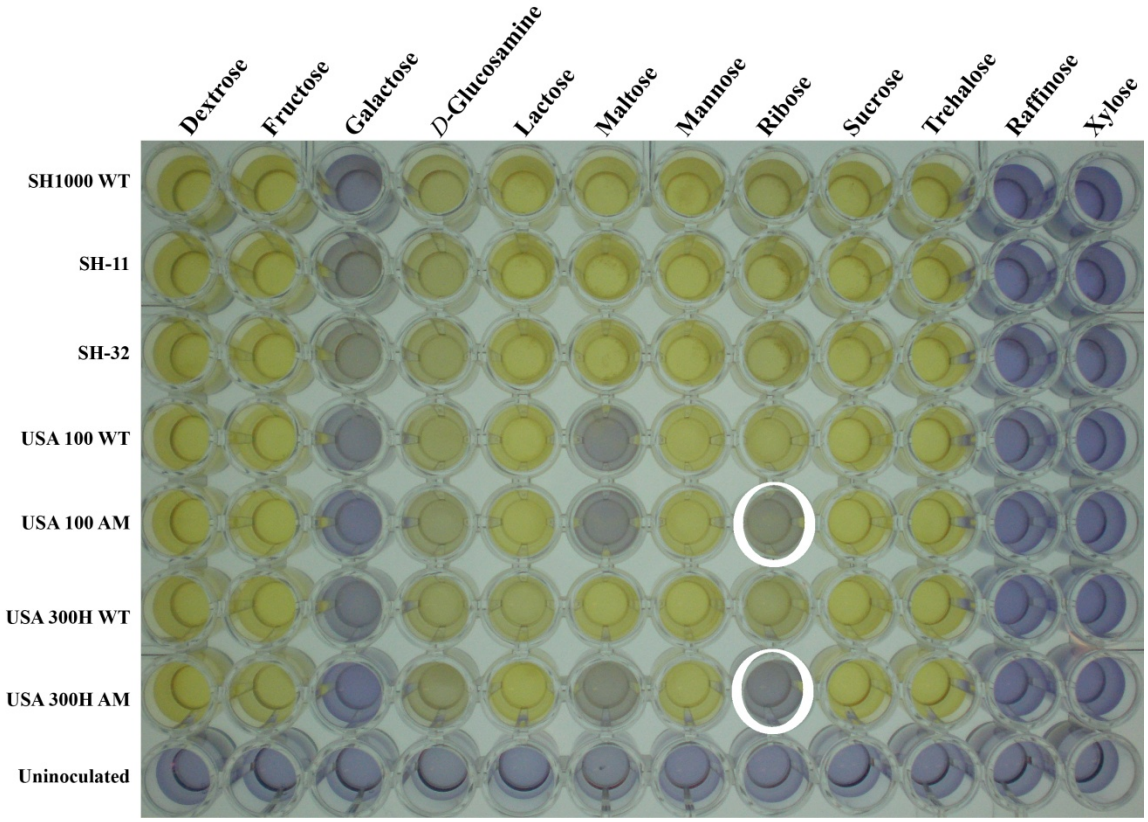

Figure 19. Microbroth dilution assay of alternative sugar fermentation by the NsβL-resistant mutants. A 96-well plate containing purple broth supplemented with a variety of sugars (at 1%) was inoculated with parent and mutant strains and grown overnight to determine if there were any changes in the ability to ferment alternative carbon sources. The plate shown is representative of three experiments.

Alterations of the adaptive and stress resistant capacities of the NsβL-resistant mutants. A chemical library containing diverse acids, bases, detergents, disulfides, alcohols, oxidative agents, and DNA damaging agents was used to test the spontaneous and adaptive mutants for changes in their stress resistance capabilities. This was assessed via disk diffusion assay, however, no compounds resulted in significant changes in the ZOI for any strains tested (data not shown).

Exploration of the effects of existing antibiotics on the NsβL-resistant mutants. Disk diffusions were used to determine changes in ZOI between the parent strains and their resistant mutants for a range of antimicrobial compounds. The antimicrobials tested

included representatives of each major class, including inhibitors of DNA synthesis, RNA synthesis, protein synthesis, fatty acid synthesis, and cell wall synthesis. Only those antimicrobials that resulted in significant changes in the ZOI are shown. SH-11 and USA 100 did not show any significant changes in antimicrobial susceptibility (data not shown), while SH-32 was more resistant to mupirocin and penicillin G (**Fig. 20**; **Table 7**). Interestingly, SH-32 showed signs of heteroresistance to mupirocin, as indicated by the zone of reduced growth around the discrete ZOI.

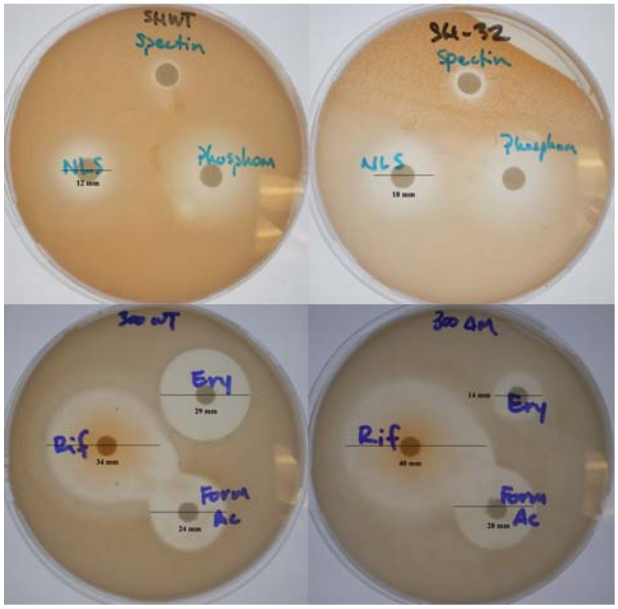

Figure 20. Disk diffusion assay of changes in antimicrobial susceptibility for the SH-32 spontaneous mutant. Mup = Mupirocin; PenG = Penicillin G; Linco = Lincomycin; Kan = Kanamycin

Antimicrobial	Fold Change from WT
Mupirocin	-1.77
Penicillin G	-2.15

Table 7. Fold change for antimicrobial ZOIs of SH1000 and its SH-32 spontaneous NsβL-resistant mutant. Each assay was performed in triplicate.

The USA 300 adaptive mutant showed increased resistance to ampicillin, ciprofloxacin, kanamycin, and erythromycin (**Fig. 21**; **Table 8**).

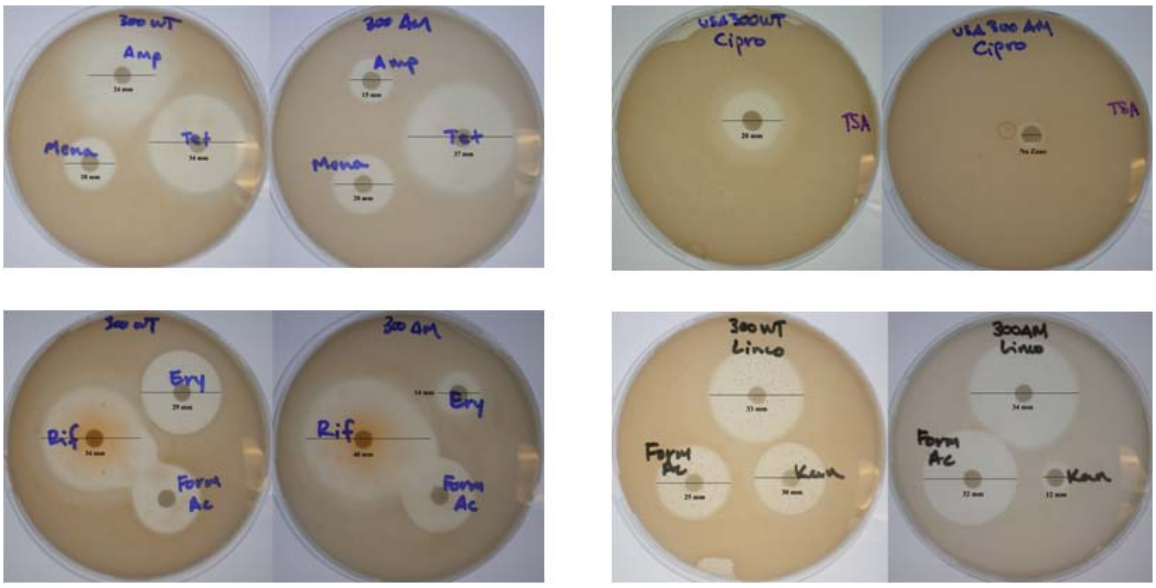

Figure 21. Disk diffusion assay of changes in antimicrobial susceptibility for the USA 300 adaptive mutant. Amp = Ampicillin; Cipro = Ciprofloxacin; Rif = Rifampicin; Ery = Erythromycin.

Antimicrobial	Fold Change
Ampicillin	-1.81
Erythromycin	-1.91
Kanamycin	-2.5
Ciprofloxacin	Mutant had no zone

Table 8. Fold change for antimicrobial ZOIs of USA 300 and its adaptive NsβL-resistant mutant. Each assay was performed in triplicate.

Functional characterization of the stability of the cell envelope of the NsβL-resistant mutants. The integrity of the bacterial cell envelopes for the NsβL-resistant strains was investigated using penicillin-G and Triton X-100 lysis assays (**Fig. 22**). For both penicillin-G and Triton X-100, there was no apparent difference in lysis between SH1000 and its spontaneous mutants. There was also no difference in lysis when USA 100 and its adaptive mutant were treated with Triton X-100. However, the USA 100 adaptive mutant showed a reduced ability to survive prolonged exposure to penicillin-G, while the USA 300 adaptive mutant appeared to be significantly impaired at all timepoints. When

treated with Triton X-100, the USA 300 adaptive mutant showed increased lysis only towards the end of the assay.

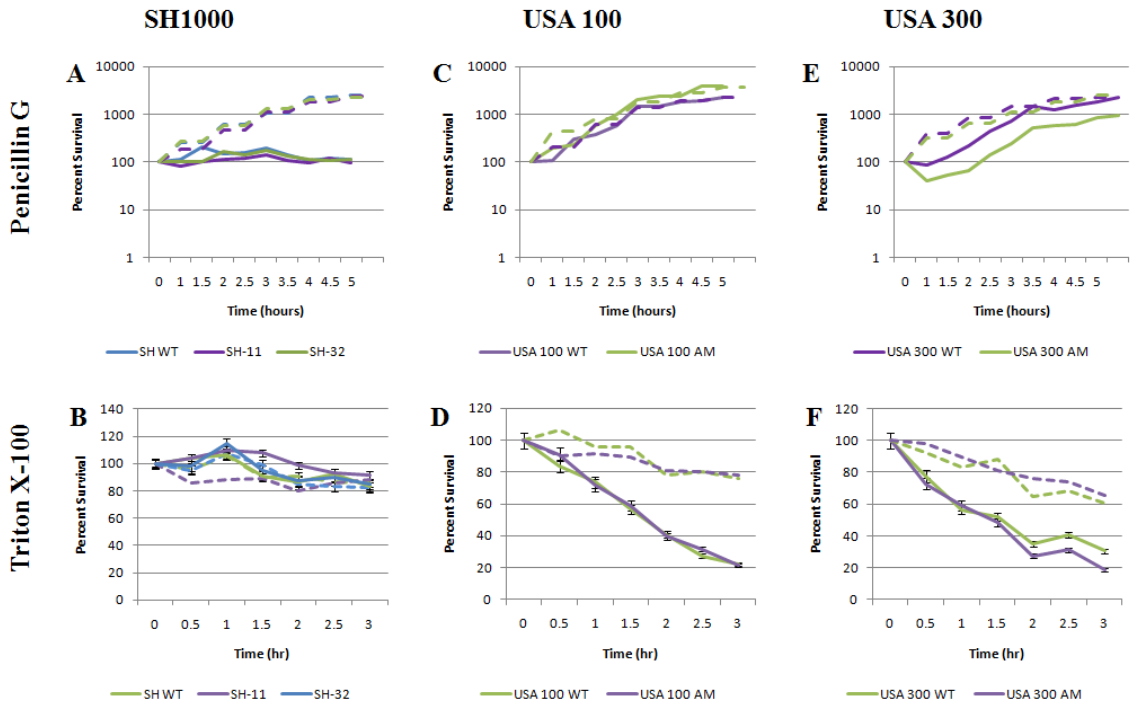

Figure 22. Assays of the stability of the cell envelope of the NsβL-resistant mutants. Penicillin-G lysis (top) was performed over 5 hours in the presence of 0.4 µg/mL penicillin G. Triton X-100 lysis (bottom) was performed over 3 hours in the presence of 0.5% Triton X-100. The graphs show the percent survival of each strain. All assays were performed in triplicate. The dashed lines are untreated controls. (A, B) SH1000 and its spontaneous mutants; (C, D) USA 100 and its adaptive mutant; (E, F) USA 300 Houston and its adaptive mutant.

Sequence analysis of *fabH* in the NsβL-resistant mutants. NsβL has previously been suggested to inhibit FabH activity[92]. One of the many ways *S. aureus* develops resistance to antibiotics is by spontaneously mutating the gene which encodes the target protein(s). Thus, genomic DNA was extracted from each of the mutant and wild-type strains and used to amplify PCR-amplify *fabH* (**Fig. 23**). Sequencing for each strain was attempted, but was unsuccessful, possibly due to problems at the external facility the samples were sent to, or compromised DNA samples (data not shown).

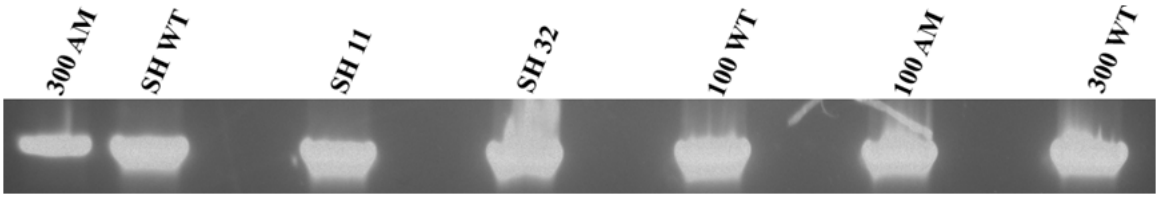

Figure 23. PCR of *fabH* genes from parental strains and their NsβL-resistant mutants.

We were, however, able to obtain sequence data for the *fabH* gene from an additional USA 100 NsβL-resistant mutant previously generated in our laboratory (Burda and Shaw, unpublished observation). The amino acid sequences were determined and compared, and no differences in the FabH sequences were found between the wild-type and resistant mutant (**Fig. 24**).

```
WT      MNVGIKGFGAYAPEKIIDNAYFEQFLDTSDEWISKMTGIKERHWADDDQDTSDLAYEASV
        MNVGIKGFGAYAPEKIIDNAYFEQFLDTSDEWISKMTGIKERHWADDDQDTSDLAYEASV
SM      MNVGIKGFGAYAPEKIIDNAYFEQFLDTSDEWISKMTGIKERHWADDDQDTSDLAYEASV

WT      KAIADAGIQPEDIDMIIVATATGDMPFPTVANMLQERLGTGKVASMDQLAACSGFMYSMI
        KAIADAGIQPEDIDMIIVATATGDMPFPTVANMLQERLGTGKVASMDQLAACSGFMYSMI
SM      KAIADAGIQPEDIDMIIVATATGDMPFPTVANMLQERLGTGKVASMDQLAACSGFMYSMI

WT      TAKQYVQSGDYHNILVVGADKLSKITDLTDRSTAVLFGDGAGAVIIGEVSEGRGIISYEM
        TAKQYVQSGDYHNILVVGADKLSKITDLTDRSTAVLFGDGAGAVIIGEVSEGRGIISYEM
SM      TAKQYVQSGDYHNILVVGADKLSKITDLTDRSTAVLFGDGAGAVIIGEVSEGRGIISYEM

WT      GSDGTGGKHLYLDKDTGKLKMNGREVFKFAVRIMGDASTRVVEKANLTSDDIDLFIPHQA
        GSDGTGGKHLYLDKDTGKLKMNGREVFKFAVRIMGDASTRVVEKANLTSDDIDLFIPHQA
SM      GSDGTGGKHLYLDKDTGKLKMNGREVFKFAVRIMGDASTRVVEKANLTSDDIDLFIPHQA

WT      NIRIMESARERLGISKDKMSVSVNKYGNTSAASIPLSIDQELKNGKLKDDDTIVLVGFGG
        NIRIMESARERLGISKDKMSVSVNKYGNTSAASIPLSIDQELKNGKLKDDDTIVLVGFGG
SM      NIRIMESARERLGISKDKMSVSVNKYGNTSAASIPLSIDQELKNGKLKDDDTIVLVGFGG

WT      GLTWGAMT
        GLTWGAMT
SM      GLTWGAMT
```

Figure 24. FabH amino acid sequence alignment of USA 100 635 wild type (WT) and its NsβL-resistant spontaneous mutant (SM).

Proteomic analysis of the NsβL resistant mutants. As a final and global approach to understand the mechanism of action of NsβL, we undertook both comprehensive and quantitative proteomic analysis of the USA 100 and USA 300 adaptive strains. Differences between the intracellular proteomes of the USA 100 and USA 300 parent strains and their respective adaptive mutants were evaluated at 8 hours (post-exponential phase) and 15 hours (stationary phase) using isobaric tagging for relative and absolute quantitation (iTRAQ) mass spectrometry. For the post-exponential phase cultures, the data for each parental strain and resistant mutant was performed in duplicate, and the average fold cfhange was calculated. At 8 hours, 85 proteins were identified from USA 100 and 66 proteins from USA 300 (see appendix for complete lists). Forty of the proteins identified from the USA 100 adaptive mutant had expression altered by 1.5-fold or greater from the parent strain, many of which were involved in nucleotide synthesis, translation, glycolysis, pyruvate metabolism, and TCA cycle (**Table 9**). However, only four proteins with a change in expression greater than 1.5-fold were identified from the USA 300 adaptive mutant, which included proteins involved in fermentation, cell wall degradation, and energy production (**Table 10**). Of all the proteins identified, 46 were found to have altered expression in both USA 100 and USA 300, including proteins involved in translation, glycolysis, pyruvate metabolism, the TCA cycle, and the oxidative stress response (**Table 11**). At 15 hours, 796 proteins were identified from USA 100 and 791 proteins from USA 300, 56 of which were found to have significantly altered expression in both strains; however, the stationary phase data is purely exploratory, as only one replicate was performed and statistical significance could not be calculated (**Table 12**). It is worth noting that a number of proteins associated with

nucleotide metabolism, transcription, DNA repair, amino acid metabolism, translation, peptidoglycan synthesis, cell division, glycolysis, the TCA cycle, and sugar transport were all significantly decreased in both the USA 100 and USA 300 adaptive mutants.

Pathway	Late Exponential Phase Proteins Identified from USA 100 (40)	Accession Number	Fold Change from Wild-Type
Purine biosynthesis	Inosine-5'-monophosphate dehydrogenase (guaB)	P99106|IMDH_STAAN	-1.5
	Phosphoribosylaminoimidazole carboxylase ATPase subunit (purK)	Q7A695|PURK_STAAN	-2.45
	Phosphoribosylformylglycinamidine synthase 1 (purQ)	P99166|PURQ_STAAN	-2.4
Pyrimidine biosynthesis	Aspartate carbamoyltransferase (pyrB)	P65618|PYRB_STAAN	-2.65
Virulence Determinant Regulation	GTP-sensing transcriptional pleiotropic repressor (codY)	P63844|CODY_STAAN	-2.2
Cysteine metabolism	Cysteine synthase (cysK)	P63871|CYSK_STAAN	-2.05
Nitrogen metabolism	Glutamine synthetase (glnA)	P99095|GLNA_STAAN	-1.5
Electron transport	ATP synthase subunit beta (atpD)	P99112|ATPB_STAAN	-1.7
Energy production	L-lactate dehydrogenase 1 (ldhA)	P65256|LDH1_STAAN	-2.55
	NADH dehydrogenase-like protein SA0802 (SA0802)	Q7A6J4|Y802_STAAN	-2.5
Glycolysis	Enolase (eno)	P99088|ENO_STAAN	-2.15
	Glucose-6-phosphate isomerase (pgi)	P99078|G6PI_STAAN	-1.8
	Pyruvate kinase (pyk)	Q7A559|KPYK_STAAN	-1.6
TCA cycle	Aconitate hydratase (acnA)	P99148|ACON_STAAN	-2.6
	Citrate synthase II (citZ)	Q7A561|Q7A561_STAAN	-2.55
	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex (odhB)	Q7A5N4|ODO2_STAAN	-2.1
	Phosphoglycerate kinase (pgk)	P99135|PGK_STAAN	-1.7
	Probable malate:quinone oxidoreductase 2 (mqo2)	P99115|MQO2_STAAN	-1.55
	Succinyl-CoA ligase [ADP-forming] subunit alpha (sucD)	P99070|SUCD_STAAN	-1.55
Pyruvate metabolism	Dihydrolipoyl dehydrogenase (pdhD)	P99084|DLDH_STAAN	-2.25
	Phosphate acetyltransferase (pta)	P99092|PTA_STAAN	-2.25

	Pyruvate dehydrogenase E1 component subunit beta (pdhB)	P99063|ODPB_STAAN	-2.6
Pentose-Phosphate	6-phosphogluconate dehydrogenase, decarboxylating (gnd)	P63334|6PGD_STAAN	-2.55
Iron storage	Ferritin (ftnA)	Q7A4R2|FTN_STAAN	-3
Stress response	Alkaline shock protein 23 (asp23)	P99157|ASP23_STAAN	-1.55
	Catalase (katA)	Q7A5T2|CATA_STAAN	-1.95
	Chaperone protein (hchA)	P64313|HCHA_STAAN	-1.65
	Putative uncharacterized protein (SA1528)	Q7A553|Q7A553_STAAN	-2.75
	Superoxide dismutase [Mn/Fe] 1 (sodA)	P99098|SODM1_STAAN	-2.05
Protein Synthesis	30S ribosomal protein S1 (rpsA)	Q7A5J0|RS1_STAAN	-2.3
	30S ribosomal protein S10 (rpsJ)	P66334|RS10_STAAN	-2.3
	30S ribosomal protein S9 (rpsI)	P66646|RS9_STAAN	-2.1
	50S ribosomal protein L11 (rplK)	P0A0F2|RL11_STAAN	-1.75
	50S ribosomal protein L13 (rplM)	Q7A473|RL13_STAAN	-1.6
	50S ribosomal protein L18 (rplR)	Q7A467|RL18_STAAN	-1.5
	Seryl-tRNA synthetase (serS)	P99178|SYS_STAAN	-1.4
Unknown	SA2119 protein (SA2119)	Q7A3Z5|Q7A3Z5_STAAN	-1.6
	DNA-binding protein HU (hup)	Q7A5J1|DBH_STAAN	-1.85

Table 9. Intracellular proteins found to have altered expression at 8 hours in the USA 100 adaptive mutant.

Pathway	Late Exponential Phase Proteins Identified from USA 300 (4)	Accession Number	Fold Change from Wild-Type
Fermentation	Alcohol dehydrogenase (adh)	Q2FJ31|ADH_STAA3	-2.3
Energy production	Formate acetyltransferase (pflB)	Q2FK44|PFLB_STAA3	-2
Cell wall degredation	Immunodominant staphylococcal antigen A (isaA)	Q2FDT8|ISAA_STAA3	1.45
Unknown	Putative uncharacterized protein (SAUSA300_2473)	Q2FDX1|Q2FDX1_STAA3	2.5

Table 10. Intracellular proteins found to have altered expression at 8 hours in the USA 300 adaptive mutant.

Pathway	Late Exponential Phase Proteins Identified in Common (46)	Fold Change from Wild-Type	
		USA 100	USA 300
Cell division	Cell division protein ftsZ (ftsZ)	-1.15	0.65
Cysteine metabolism	Cysteine synthase (cysK)	-2.05	-0.75
DNA replication	DNA polymerase III subunit beta (dnaN)	-1.4	0.2
Electron transport	NADH dehydrogenase-like protein	-1.7	-0.15

	(SA0802/SAUSA300_0844)		
Energy production	ATP synthase subunit alpha (atpA)	-0.8	0.85
	ATP synthase subunit beta (atpD)	-2.5	0
	L-lactate dehydrogenase 1 (ldhA/ldh1)	-2.55	-0.25
Folate synthesis	Serine hydroxymethyltransferase (glyA)	-0.6	0.65
Glycolysis	Enolase (eno)	-2.15	-0.5
	Glucose-6-phosphate isomerase (pgi)	-1.8	-0.7
	Glyceraldehyde-3-phosphate dehydrogenase 1 (gapA1)	-1.35	0.1
	Pyruvate kinase (pyk)	-1.6	0.15
Iron storage	Ferritin (ftnA)	-3	-0.2
Nitrogen metabolism	Glutamine synthetase (glnA)	-1.5	-0.2
	NAD-specific glutamate dehydrogenase (gluD/gudB)	-1.6	-0.6
Oxidative stress response	Alkyl hydroperoxide reductase subunit C (ahpC)	-1.25	0.3
	Alkyl hydroperoxide reductase subunit F (ahpF)	-1.55	0.5
	Catalase (katA)	-1.65	-0.25
Pentose-Phosphate	6-phosphogluconate dehydrogenase, decarboxylating (gnd)	-2.55	-0.6
Protein Synthesis	30S ribosomal protein S1 (rpsA)	-1.75	-0.35
	30S ribosomal protein S2 (rpsB)	-0.75	1.05
	30S ribosomal protein S5 (rpsE)	Value missing	0.4
	30S ribosomal protein S9 (rpsI)	-2.1	0.15
	50S ribosomal protein L1 (rplA)	-1.35	0.55
	50S ribosomal protein L13 (rplM)	-1.5	0.55
	50S ribosomal protein L14 (rplN)	-1.05	0.4
	50S ribosomal protein L2 (rplB)	-1.25	0.25
	50S ribosomal protein L3 (rplC)	No values	0.6
	50S ribosomal protein L6 (rplF)	No values	No Values
	Elongation factor G (fusA)	-1.15	0.35
	Elongation factor Tu (tuf)	-1.3	0.65
	Glycyl-tRNA synthetase (glyQS)	-0.95	0.25
Stress response	Alkaline shock protein 23 (asp23)	-1.55	0.3
Purine biosynthesis	Inosine-5'-monophosphate dehydrogenase (guaB)	-1.5	-0.4
Pyruvate metabolism	Dihydrolipoyl dehydrogenase (pdhD/lpdA)	-2.25	-0.25
	D-lactate dehydrogenase (ldhD/ddh)	No values	0.75
	Pyruvate dehydrogenase E1 component subunit alpha (pdhA)	No values	0
	Pyruvate dehydrogenase E1 component subunit beta (pdhB)	-2.25	-0.35
	Formate acetyltransferase (pflB)	Value missing	-2.3
Regulation	GTP-sensing transcriptional pleiotropic repressor (codY)	-2.2	0.1
TCA cycle	Aconitate hydratase (acnA)	-2.55	-1.2
	Phosphoglycerate kinase (pgk)	-2.6	-0.1
	Succinyl-CoA ligase [ADP-forming] subunit alpha (sucD)	-1.7	-0.55

	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex (odhB)	-1.55	-0.45
Transcription	DNA-directed RNA polymerase subunit beta (rpoB)	-0.8	0
	DNA-directed RNA polymerase subunit beta' (rpoC)	-1.2	0.2
Unknown	DNA-binding protein HU (hup)	-1.85	0

Table 11. Intracellular proteins found to have altered expression at 8 hours in both the USA 100 and USA 300 adaptive mutants.

Pathway	Stationary Phase Proteins Identified in Common (129)	Fold Change from Wild-Type	
		USA 100	USA 300
Acetoin catabolism	Acetoin(diacetyl) reductase (butA)	-2.3	-2.6
Amino acid metabolism	Ornithine carbamoyltransferase, catabolic (arcB)	-2.7	-2
Arginine metabolism	Carbamate kinase 1 (arcC1)	-3.3	-2.4
	Carbamoyl-phosphate synthase large chain (carB)	-2.6	-2.4
ATP binding	Cytidylate kinase (cmk)	-2.2	-2.5
ATP synthesis	ATP synthase gamma chain (atpG)	-2.8	-1.9
	ATP synthase subunit alpha (atpA)	-2.4	-2.5
	ATP synthase subunit b (atpF)	-2.8	-2.4
	ATP synthase subunit beta (atpD)	-2.2	-2.1
	ATP synthase subunit delta (atpH)	-3.5	-2.6
Cell division	Cell division protein (ftsA)	-2.1	-1.6
	Septation ring formation regulator (ezrA)	-1.7	-1.5
	GTP-binding protein era homolog (era)	-1.9	-1.6
Cell redox homeostasis	Alkyl hydroperoxide reductase subunit C (ahpC)	-1.5	-1.5
Cell wall degredation; peptidoglycan biosynthesis; cell shape	D-alanine--D-alanine ligase (ddl)	-1.8	-1.6
DNA repair	ATP-dependent DNA helicase (pcrA)	-2.1	-2
	Protein recA (recA)	-1.7	-1.7
DNA replication	DNA gyrase subunit B (gyrB)	-1.5	-1.7
	DNA polymerase III subunit beta (dnaN)	-1.9	-1.8
	Ribonucleoside-diphosphate reductase (nrdE)	-1.8	-2.2
	Single-stranded DNA-binding protein (ssb)	-1.6	-1.8
DNA replication; stress response	Chaperone protein (dnaJ)	-1.7	-2.8
Electron transport	NADH dehydrogenase-like protein SA0802 (SA0802)	-2.6	-2
	Probable quinol oxidase subunit 2 (qoxA)	-2.4	-3.2
Fatty acid biosynthesis	Trans-2-enoyl-ACP reductase (fabI)	-2.1	-2
Folic acid metabolism	Formate--tetrahydrofolate ligase (fhs)	-2.2	-1.9
Formate metabolism	Putative formate dehydrogenase (SA2102)	-1.6	-1.5
Glutamine metabolism	Carbamoyl-phosphate synthase small chain (carA)	-2.3	-1.5
Glycerol	Aerobic glycerol-3-phosphate dehydrogenase (glpD)	-2.2	-1.7

metabolism			
Glycolysis	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (gpmA)	-2.3	-2.1
	Fructose-bisphosphate aldolase class 1 (fda)	-1.7	-1.6
	Glyceraldehyde-3-phosphate dehydrogenase 2 (gapA2)	-1.5	-2.9
	Pyruvate kinase (pyk)	-1.9	-1.6
	L-lactate dehydrogenase 1 (ldhA)	-3	-1.6
	L-lactate dehydrogenase 2 (ldhB)	-2.7	-2.5
Histidine metabolism	Urocanate hydratase (hutU)	-2.1	-1.8
Lipoate biosynthesis	Lipoyl synthase (lipA)	-2	-3.1
Metabolism	Putative dipeptidase SA1572 (SA1572)	-1.9	-1.5
	Pyridoxal biosynthesis lyase (pdxS)	-1.8	-2.9
Peptidoglycan biosynthesis	Aminoacyltransferase femB (femB)	-2.1	-3.1
	D-alanine--D-alanine ligase (ddl)	-1.8	-1.6
	Penicillin binding protein 2 prime (mecA)	-2.1	-2.1
	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (murF)	-1.5	-1.7
MSCRAMMs	Elastin-binding protein (ebpS)	-1.7	-2
	Extracellular matrix protein-binding protein (emp)	-2	-1.8
Nucleoside transport	Pyrimidine nucleoside transport protein (nupC)	-2	-2.2
Nucleotide biosynthesis	Ribose-phosphate pyrophosphokinase (prs)	-2.8	-1.9
Organic acid metabolism	Acetate kinase (ackA)	-1.9	-1.6
Phospholipid biosynthesis	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (gpsA)	-2.3	-2.1
Porphyrin biosynthesis	Glutamate-1-semialdehyde 2,1-aminomutase 1 (hemL1)	-2.9	-1.9
	Glutamate-1-semialdehyde 2,1-aminomutase 2 (hemL2)	-1.8	-3.3
Proline biosynthesis	1-pyrroline-5-carboxylate dehydrogenase (rocA)	-2.1	-1.7
	Ornithine aminotransferase 2 (rocD2)	-2.9	-1.7
	Pyrroline-5-carboxylate reductase (proC)	-1.6	-1.7
Protein folding	ATP-dependent Clp protease ATP-binding subunit (clpX)	-2.2	-1.7
	Putative peptidyl-prolyl cis-trans isomerase (SA0815)	-1.5	-1.7
Protein transport	Protein translocase subunit secA 1 (secA1)	-2.4	-2.3
	Protein-export membrane protein (secF)	-2.5	-2.8
Purine biosynthesis	Adenylosuccinate synthetase (purA)	-1.6	-1.7
	Amidophosphoribosyltransferase (purF)	-2.3	-2.5
	Bifunctional purine biosynthesis protein purH (purH)	-2.9	-2.3
	Phosphoribosylamine--glycine ligase (purD)	-3.1	-2.9
	Phosphoribosylaminoimidazole carboxylase ATPase subunit (purK)	-2.9	-2.4
	Phosphoribosylaminoimidazole-succinocarboxamide synthase (purC)	-3.5	-2.7
	Phosphoribosylformylglycinamidine synthase 1 (purQ)	-2.6	-3.1
	Phosphoribosylformylglycinamidine synthase 2 (purL)	-3	-3.4
Purine ribonucleoside salvage	Hypoxanthine-guanine phosphoribosyltransferase (hpt)	-1.8	-1.9
	Xanthine phosphoribosyltransferase (xpt)	-2.1	-2.1
Pyrimidine	Pyrimidine-nucleoside phosphorylase (pdp)	-2.9	-1.5

metabolism	Uracil phosphoribosyltransferase (upp)	-1.5	-3.4
	Uridine kinase (udk)	-2.1	-3.2
Pyruvate biosynthesis	Pyruvate dehydrogenase E1 component subunit beta (pdhB)	-1.8	-1.5
RNA degredation	Ribonuclease J 2 (SA1118)	-1.8	-2.7
Stress response	10 kDa chaperonin (groS)	-1.6	-1.5
	ATP-dependent protease ATPase subunit (hslU)	-2	-3.2
	GTPase obg (obg)	-2.6	-2
Stringent response	GTP pyrophosphokinase (relA)	-2.4	-1.6
Sugar metabolism	Acetyl-CoA synthetase (acsA)	-1.9	-1.7
Sugar transport	PTS system EIIBC component (SA0186)	-1.8	-1.5
	PTS system glucose-specific EIICBA component (ptsG)	-3	-3.6
	PTS system glucoside-specific EIICBA component (glcB)	-3.2	-1.6
TCA cycle	Citrate synthase II (citZ)	-2	-1.6
	Isocitrate dehydrogenase [NADP] (icd)	-1.9	-1.9
	Succinate dehydrogenase flavoprotein subunit (sdhA)	-2.2	-1.8
	Succinate dehydrogenase iron-sulfur protein subunit (sdhB)	-1.9	-2
	Succinyl-CoA ligase [ADP-forming] subunit alpha (sucD)	-1.8	-1.6
	Succinyl-CoA ligase [ADP-forming] subunit beta (sucC)	-1.5	-1.5
Transcription	DNA-directed RNA polymerase subunit beta (rpoB)	-1.6	-1.5
	DNA-directed RNA polymerase subunit beta' (rpoC)	-2	-1.5
	Probable DNA-directed RNA polymerase subunit delta (rpoE)	-1.9	-1.6
Transcription regulation	Serine-protein kinase (rsbW)	-2.2	-2.3
	Bifunctional protein (pyrR)	-3.2	-2.4
Translation	Asparaginyl-tRNA synthetase (asnS)	-2.5	-1.9
	Elongation factor Tu (tuf)	-1.8	-1.5
	Methionyl-tRNA formyltransferase (fmt)	-1.9	-2.3
	Prolyl-tRNA synthetase (proS)	-1.9	-1.7
	Seryl-tRNA synthetase (serS)	-3.3	-1.5
	Threonyl-tRNA synthetase (thrS)	-2.2	-1.5
	Translation initiation factor IF-2 (infB)	-2.1	-1.9
	30S ribosomal protein S11 (rpsK)	-2.1	-1.8
	30S ribosomal protein S12 (rpsL)	-1.9	-1.7
	30S ribosomal protein S13 (rpsM)	-1.9	-1.6
	30S ribosomal protein S14 type Z (rpsZ)	-2	-1.8
	30S ribosomal protein S3 (rpsC)	-1.5	-2.1
	30S ribosomal protein S4 (rpsD)	-1.5	-1.6
	30S ribosomal protein S5 (rpsE)	-2.1	-1.5
	30S ribosomal protein S6 (rpsF)	-1.8	-1.6
	50S ribosomal protein L1 (rplA)	-2.2	-2
	50S ribosomal protein L10 (rplJ)	-1.7	-1.6
	50S ribosomal protein L13 (rplM)	-2.3	-1.6
	50S ribosomal protein L14 (rplN)	-2.6	-1.6
	50S ribosomal protein L19 (rplS)	-2.4	-1.8
	50S ribosomal protein L2 (rplB)	-1.9	-1.7
	50S ribosomal protein L20 (rplT)	-2.8	-2.1
	50S ribosomal protein L3 (rplC)	-1.5	-1.9
	50S ribosomal protein L4 (rplD)	-2.2	-1.9

	50S ribosomal protein L5 (rplE)	-2.7	-2.5
tRNA modification	(Dimethylallyl)adenosine tRNA methylthiotransferase (miaB)	-1.5	-1.5
	tRNA modification GTPase (mnmE)	-1.7	-2.2
Virulence	Conserved virulence factor B (cvfB)	-1.5	-1.7
Unknown	DegV domain-containing protein (SA1258)	-2.3	-1.9
	GTP-binding protein (engA)	-2.5	-1.8
	PhoH protein (phoH)	-1.9	-1.5
	Putative phosphotransferase (SA1392)	-2	-1.9
	Uncharacterized lipoprotein (SA2158)	-3	-1.5
	UPF0051 protein (SA0778)	-1.9	-1.8
	UPF0133 protein (SA0437)	-1.5	-1.5
	UPF0365 protein SA1402 (SA1402)	-1.7	-2
	UPF0477 protein (SA0873)	-1.9	-1.9
	UPF0478 protein SA1560 (SA1560)	-1.9	-2

Table 12. Intracellular proteins found to have altered expression at 15 hours in both the USA 100 and USA 300 adaptive mutants.

DISCUSSION

Antimicrobial resistance has been an escalating problem since the advent of clinical antimicrobial use. Every new antibiotic that has been released, including completely synthetic antimicrobials, has rapidly encountered resistance in one form or another[19, 43, 69, 75, 102]. The cost of developing antibiotics is high, especially considering their short lifespan; and is not considered lucrative by pharmaceutical companies. For this reason, the number of new therapies has dwindled, while the number of effective therapeutics continues to decrease. The research presented here investigates the mode of action of a novel β-lactam antimicrobial, with potent activity against MRSA by analyzing laboratory-generated resistant mutants.

A number of diverse laboratory and clinical *S. aureus* isolates were used in this study because the characteristics of pathogenesis and antimicrobial susceptibility can differ widely depending on the strain. Importantly, the NsβL MIC was found to be comparable across all strains tested, so the mode of action of this drug does not appear to be affected by existing, intrinsic resistance factors. Previous studies have suggested that NsβL may target 3-oxoacyl-acyl carrier protein synthase (ACP) III (FabH) either directly or indirectly[92], so we set forth to determine if the addition of fatty acids to the culture media would have an effect on the NsβL MICs.

The results of our fatty acid assays with NsβL indicate that fatty acid biosynthesis may not be the sole or primary target of this drug. This is apparent when the effects of fatty acids on NsβL activity are compared to their effects on triclosan and vancomycin activity. The MIC of vancomycin, a cell wall synthesis inhibitor, was reduced by Tween 80. The effect of Tween 80 on the MIC of NsβL was, however, not significant. The MIC of triclosan, an inhibitor of enoyl-ACP reductase (FabI), which catalyzes the final step of fatty acid synthesis, was significantly affected by the presence of Tween 80, being increased by at least 20-fold for all strains tested, from 0.125 μg/mL to ≥ 6.25 μg/mL. It is noteworthy that this drastic increase in MIC does not agree with that published by Balemans, et. al[6]. They saw that the MIC of triclosan increased from 0.125 μg/mL to 2 μg/mL in the presence of the same concentration of Tween 80 as used in our study, and attributed this to the plasma binding properties of triclosan. They also showed that other known fatty acid synthesis inhibitors behaved similarly[6]. However, Altenbern showed that cerulenin, an inhibitor of 3-oxoacyl-ACP synthase I/II (FabB/F), which catalyzes the second condensation step of fatty acid synthesis, lost efficacy in the presence of both saturated and unsaturated fatty acids[2]. This was confirmed by Brinster, et. al, who used *Streptococcus agalactiae* as their initial model[17], and *S. aureus* in response to the criticism from Balemans, et. al.[16], which is again confirmed by our work. Because NsβL does not follow the rescue pattern established by triclosan and other fatty acid synthesis inhibitors, an enzyme of the fatty acid synthesis pathway may not be its primary target.

Biofilm-mediated infections often lead to chronic illness due to persistence, and difficulty in treating biofilm-mediated conditions. Currently, a prophylactic view towards

preventing colonization is taken, but there are many limitations, particularly considering only catheter-associated biofilms are targeted by this method. Our study compared the effects of vancomycin, triclosan, and tetracycline to NsβL on biofilms and found that the ability of NsβL to kill established biofilms exceeded that of the other antimicrobials tested, as measured by percent reduction. There are a number of factors that affect the activity of an antimicrobial on the target biofilm, such as the rate of diffusion of the drug through the biofilm[61] and the ability of the drug to kill stationary phase bacteria[74]. NsβL reduced biofilm formation by 43%, which was the greatest observed decrease. Tetracycline was shown in one *in vitro* experiment to completely reduce metabolic activity in an *S. aureus* biofilm[36] and to have high levels of killing of *S. epidermidis* biofilms[74]; we showed here that tetracycline was effective at reducing biofilms by 29%. Both vancomycin and triclosan were ineffective at killing biofilms, which has been demonstrated previously in *S. aureus*[32], *S. epidermidis*[74], and *Salmonella typhimurium*[99] to be due to restricted diffusion through the biofilm. The biofilm-killing activity of NsβL may be due to high levels of diffusion through the biofilm matrix, an enhanced ability to kill stationary phase cells, or a combination of both of these factors.

It is important, when dealing with antimicrobial agents, to have a sense of the rate at which clinical isolates spontaneously become resistant to the drug. This is particularly important when determining the dose to administer to patients. The spontaneous mutation rate for SH1000, a non-resistant laboratory strain, was 5.2×10^{-9} at 7x the NsβL MIC. Interestingly, resistance occurred more frequently at 2×10^{-8} when a nitrosoguanidine (NTG) mutant library of SH1000 was exposed to the same NsβL

concentration. With that said, these latter isolates had NsβL MICs no greater than 10 μg/mL, whereas the spontaneous, untreated SH1000 mutants had NsβL MICs as high as 50 μg/mL. The spontaneous mutation rate of NsβL was found to be comparable to a number of clinically relevant antimicrobials having a wide range of modes of action (**Table 13**). Rifampicin, for example, is used only as a combination therapy due to its high rate of spontaneous mutagenesis resulting in resistance[72]. NsβL had a spontaneous mutation rate 19- to 20-fold lower than rifampicin, indicating that it could conceivably be used in single therapy.

Antimicrobial	Spontaneous Mutation Rate at 8x MIC	References
Ceftobiprole	$0.9 \times 10^{-10} – 5.3 \times 10^{-10}$	13
Ciprofloxacin	3.2×10^{-10}	85
Daptomycin	$0.8 \times 10^{-10} – 9.1 \times 10^{-11}$	13, 55
Levofloxacin	6.4×10^{-10}	85
Linezolid	$1.3 \times 10^{-9} – 8.7 \times 10^{-10}$	13
Minocycline	$6.7 \times 10^{-9} – 9.5 \times 10^{-10}$	13
Mupirocin	$1.5 \times 10^{-8} – 9.5 \times 10^{-10}$	13
NsβL (SH1000) †	5.2×10^{-9}	This study
NsβL (MNNG-treated SH1000) †	2×10^{-8}	This study
Quinupristin/Dalfopristin	$3.3 \times 10^{-9} – 8.7 \times 10^{-10}$	13
Rifampicin‡	$10^{-7} – 10^{-8}$	72
Teicoplanin	$1.6 \times 10^{-8} – 7.1 \times 10^{-11}$	55
Telavancin	$1 \times 10^{-11} – 5 \times 10^{-11}$	55

Table 13. Spontaneous mutation rates for various antimicrobials. The single-step spontaneous mutation rates for various clinically relevant antimicrobials are reported in the literature and compiled here for comparison to NsβL. † NsβL spontaneous mutagenesis was performed at 7x MIC. ‡ Rifampicin spontaneous mutagenesis was performed at 10x MIC.

The spontaneous and adaptive mutants generated were characterized in order to provide insight into their mechanism(s) of resistance to NsβL. The rationale for this is that we may be able to extrapolate the mode of action of NsβL, by examining the phenotypic changes of the mutants. Based on previous analysis of the drug[92], we would expect to see

changes in those processes involving coenzyme-A (CoA), such as glycolysis, the citric acid cycle (TCA), pyruvate metabolism, and, particularly, fatty acid biosynthesis. Because changes in these pathways would have widespread consequences, we used a global approach to determine phenotypic changes in the NsβL-resistant mutants.

The production of virulence factors by *S. aureus* is a complex and highly regulated process involving multiple regulatory systems which control growth phase-dependent virulence factor production[81]. No changes were found in virulence factor production for either of the SH1000 spontaneous mutants as determined by growth on blood or milk plates. Conversely, it is interesting to note that SDS-PAGE analysis of SH-11 appears to show an increase in production of cell-wall associated and secreted proteins. This may simply be an incongruity in the SDS-PAGE, rather than a true phenotypic change, or it may be that SH-11 is producing other virulence factors that were not tested for. On the other hand, virulence determinant production in both the USA 100 and USA 300 adaptive mutants was dramatically reduced, as shown by a reduction or loss of proteolytic activity, hemolysis, capsule production, and cell-wall and secreted protein production. The genes encoding proteases, hemolysins, exotoxins, and capsular polysaccharides are all positively regulated by the central virulence regulator, *agr* (accessory gene regulator)[81], indicating that both the USA 100 and USA 300 adaptive mutants may have developed *agr* mutations. Because staphylococcal virulence regulation is so convoluted, there may be additional changes in the adaptive mutants that resulted in the observed phenotype, such as repression of, or changes in, the staphylococcal accessory regulator A (SarA), an activator of *agr*[12]. It is also possible that there is repression of, or changes in, SaeRS,

which increases transcription of hemolysins and capsule genes[68]. Finally, there may be an increase in transcription of the repressor of toxin (Rot), which inhibits transcription of multiple protease and hemolysin genes[48]. Interestingly, deletion of s*arA* was shown to result in increased susceptibility to ciprofloxacin, rifampicin, and vancomycin[83] and deletion of *sarA* and *agr* together resulted in increased susceptibility to oxacillin, cefoxitin, and imipenem[38]. To date, changes in *sarA* or *agr* have not been associated with increased antimicrobial resistance. These and other issues will be addressed in more detail in the proteomics section.

Amino acid limitation leads to activation of the stringent response in *S. aureus*, mediated by the synthesis of polyphosphorylated guanosine nucleotides ((p)ppGpp) by *rsh* (RelA/SpoT homolog)[40]. (p)ppGpp induces overexpression of genes involved in amino acid synthesis and repression of ribosomal and tRNA genes, allowing the bacteria to survive under less than optimal conditions. Mutants defective in *rsh* were found to be more susceptible to mupirocin, and not changed in susceptibility to vancomycin and ciprofloxacin[22, 40]. A clinical isolate with a persistently active stringent response was also found to have no changes in susceptibility to vancomycin, teicoplanin, gentamycin, linezolid, daptomycin, tigecycline, rifampicin, or ciprofloxacin[39]. While neither spontaneous mutant showed changes in growth under amino acid limiting conditions, both adaptive mutants showed changes. The USA 100 adaptive mutant had increased growth levels during lag and early-exponential phase, but decreased levels of growth during late- and post-exponential phase. The USA 300 adaptive mutant had significantly reduced levels of growth during exponential phase as compared to its parent. While

glucose limitation is also known to induce the stringent response[40], none of the strains tested showed changes in growth in glucose limiting media. It has also been suggested that a fully functioning TCA cycle is necessary for effective amino acid catabolism[96], which will be further discussed in the proteomics section. We know from growth curves in tryptic soy broth (TSB) that both adaptive mutants have reduced growth levels during exponential phase, a possible indicator of defects in energy production. Furthermore, SarA, proposed above to be repressed, is known to positively regulate expression of amino acid transport and metabolism proteins[31]; thus, if the adaptive mutants have defects in regulation by SarA, they will have reduced viability under amino acid limiting conditions. Taken together, along with the increased resistance of SH-32 and the USA 300 adaptive mutant to a number of antimicrobials (discussed later), this may indicate that the adaptive mutants are defective in transport of extracellular amino acids, rather than in their overall response to nutrient limitation as regulated by (p)ppGpp or SarA. Such a deficiency in amino acid utilization may lead to weaker peptidoglycan cross-links, resulting in changes in susceptibility to cell wall-active antimicrobials and autolytic activity[97], possibly implying that NsβL has an effect on the integrity of the cell wall.

Reduced survivability in response to phosphate limitation has been attributed to a number of factors. Lithgow et. al. have described the role of cysteine synthase[65] and FtsH[66] in recovery from amino acid- and phosphate limiting-conditions as due to defects in protein synthesis during starvation. Cysteine synthase is responsible for *S. aureus'* resistance to tellurite, oxidative stress, and disulfides, and is proposed to be important as part of the thiol redox balance in *S. aureus*[65], while FtsH has chaperone-like activities and mediates

resistance to methyl viologen and tellurite[66]. This is of particular interest concerning NsβL, as Revell, et. al. have proposed that this drug may alter the thiol redox balance by reducing CoA, which would prevent it performing its role in this buffer system[92]. The USA 300 adaptive mutant showed reduced growth levels in amino acid- and phosphate-limiting conditions, and the USA 100 adaptive mutant had reduced growth levels during late exponential and stationary phase in amino acid-limiting conditions, suggesting that cysteine synthase and/or FtsH activity may have been reduced as a result of gaining resistance to NsβL.

The loss of the ability to ferment ribose, as seen with both the USA 100 and USA 300 adaptive mutants, has been associated with an increase in fitness under nutrient limiting conditions in *Escherichia coli*[21]. This may indicate that gaining resistance to NsβL results in insufficient metabolism or utilization of nutrients, and that the loss of ribose fermentation ameliorates this defect.

The NsβL-resistant mutants were subjected to metal ion-limiting conditions by growing them in CL medium, which contains only magnesium as a metal ion source. The spontaneous mutant SH-32 was shown to have decreased fitness during exponential phase under these conditions. The binding and uptake of magnesium from the environment has been shown to be related to the composition of teichoic acids in the bacterial cell wall. Specifically, increased D-alanine content of teichoic acids in *Bacillus subtilis*, *Lactobacillus buchneri*, and *S. aureus* resulted in a reduced ability to bind magnesium ions[3, 59, 80]. Additionally, changes in the D-alanine content of the cell walls

has been associated with increased resistance to β-lactam antimicrobials[80, 82], which is further addressed below.

The oxidative stress response in *S. aureus* is highly regulated and dependent on the availability of iron, manganese (Mn^{2+}) and zinc. Uptake of Mn^{2+} is regulated by MntR, which induces expression of superoxide dismutase (SodA and SodM)[52]. Recently, it has been shown that SH1000 defective in *sarA* had increased superoxide dismutase activity in an Mn^{2+}-independent manner[7]. Based on the increased levels of exponential phase growth in the USA 300 adaptive mutant, and the obvious lack of Mn^{2+} ions, it may be that its oxidative stress response is increased due to defects in regulation by SarA. As mentioned previously, SarA deficiencies have been linked to increased susceptibility to a number of antimicrobials[38, 83]. Additionally, ciprofloxacin and chloramphenicol have been known to induce the oxidative stress response of *S. aureus*, resulting in increased production of superoxide dismuatse[1, 9]. This is particularly relevant, as the USA 300 adaptive mutant showed a complete loss of susceptibility to ciprofloxacin, and indicates that NsβL may induce a similar response in this strain.

Changes in the integrity of the cell wall can lead to increased autolysis and susceptibility to cell wall-synthesis inhibiting antimicrobials. While the spontaneous mutants did not exhibit changes in autolysis, SH-32 became 2-fold more resistant to penicillin G than its parent. The mechanism of penicillin G involves inhibiting the cross-linking of peptidoglycan, causing osmotic stress and cell lysis. As previously mentioned, penicillin G resistance can be correlated to increased D-alanine content of the cell wall[82]. It is

interesting to note that no changes in autolysis were observed in this strain, which is often associated with cell wall synthesis-inhibitor resistance. SH-32 also gained heteroresistance to mupirocin, which has primarily been associated with the inhibition of isoleucine-tRNA synthetase, but also with inhibiting cell wall synthesis[46]. This heteroresistance may be similar to that seen with heteroresistance to vancomycin, where only a small subset of the bacterial population is resistant[44], indicating that the mutation induced by resistance to NsβL does not confer complete protection from mupirocin in SH-32.

While the USA 100 adaptive mutant did not show any changes in antimicrobial susceptibility, the USA 300 adaptive mutant gained resistance to kanamycin, ampicillin, erythromycin, and ciprofloxacin. A study using *S. aureus* strain COL showed that prolonged exposure to oxacillin resulted in increased resistance to erythromycin, kanamycin, and ciprofloxacin, among others, due to increased efflux pump activity[70]. Considering that this efflux pump activity arose in COL after a similar antimicrobial treatment as used in our study, and that they both had similar antimicrobial resistance profiles, it is possible that the increased resistance of the USA 300 adaptive mutant to NsβL may be due to efflux of these antimicrobials out of the cells.

As mentioned before, previous studies have suggested that NsβL may target FabH, the initial enzyme involved in fatty acid biosynthesis[92]. With this in mind, the *fabH* gene of a USA 100 spontaneous mutant was sequenced, but found to have no differences from its parent, implying that altering FabH did not induce a benefit leading to NsβL-resistance.

Consequently, the sequenced gene was compared to *fabH* of the COL strain and found to have differences in three distinct amino acids, L40V, D151E, and I276L. Additionally, the USA 100 FabH sequence was found to have the same amino acid differences when compared to Newman, USA 300 Houston, and USA 400 MW2, but was identical to USA 100 Mu50 and USA 200 MRSA252. Comparison of the predicted secondary structures of the amino acid sequences of COL and USA 100 635 using QuickPhyre analysis did not reveal any structural differences in FabH; thus, the structure of FabH likely does not have an effect on the response of these strains to NsβL (see appendix for results).

Comparative proteomic analysis of the USA 100 and USA 300 wild-type strains, and their respective adaptive mutants was performed at 8 hours (post-exponential phase) in duplicate and a pilot run at 15 hours (stationary phase) in order to further elucidate the mechanism(s) by which these isolates gained resistance to NsβL. A change in protein expression of 1.5-fold or more was considered to be significant.

During post-exponential phase, the USA 100 adaptive mutant was found to have reduced expression of numerous proteins involved in nucleotide synthesis, glycolysis, pyruvate metabolism, the TCA cycle, amino acid synthesis, protein synthesis, and stress responses. A specific protein from the TCA cycle, aconitate hydratase, was reduced by 2.6 fold. Aconitate hydratase has been shown by Somerville, et. al. to be required for amino acid catabolism, specifically for synthesis of arginine, leucine, proline, and histidine[96], and this mutant had reduced growth levels under amino acid-limiting conditions. This protein was also expressed 2.2-fold less during stationary phase. Interestingly, cysteine synthase

(CysK) expression was reduced by 2.05-fold during post-exponential and 1.9-fold during stationary phase. In addition to being involved in the synthesis of cysteine, CysK has also been associated with stress response to H_2O_2, acidic pH, tellurite, diamide (Fig. 25), and limited amino acids and phosphate[65]. Revell, et. al. have proposed that NsβL may act as a sulfenylating agent towards CoA, leading to its inactivation[92], similar to the thiol-oxidating activity of diamide. Specific proteins affected during post-exponential phase that utilize CoA in one form or another are citrate synthase II (2.5-fold reduction), the 2-oxoglutarate dehydrogenase complex (2.1-fold reduction), and phosphate acetyltransferase (2.25-fold reduction). During stationary phase, the expression of multiple proteins with acetyl-CoA as their final product were significantly reduced, including alcohol-acetaldehyde dehydrogenase (1.7-fold reduction), acetyl-CoA synthetase (1.9-fold reduction), format acetyltransferase (2.4-fold reduction), and pyruvate dehydrogenase (3-fold reduction). Notably, while acetyl-CoA is required for initiation of fatty acid synthesis by FabH, no changes in expression of this enzyme were detected at any time point tested. However, AccA, FabF, FabI, and FabZ were all found to have expression reduced between 1.8- and 2.2-fold during stationary phase.

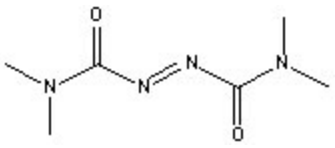

Figure 25. Diamide.

Analysis of the USA 300 adaptive mutant at 8 hours resulted in only four proteins with a significant change from the parent; however, analysis at 15 hours resulted in 11 proteins upregulated and 260 downregulated proteins changed by 1.5-fold or more. Proteins involved in glycolysis, the TCA cycle, and pyruvate metabolism were found to be decreased during stationary phase, but, unexpectedly, proteins involved in fatty acid

synthesis were not identified as significantly altered. Unlike the USA 100 adaptive mutant or other timepoints tested, the USA 300 adaptive mutant showed a number of proteins overexpressed during stationary phase. Both forms of superoxide dismutase (SodA and SodM) were upregulated 1.6- and 2.2-fold, respectively, possibly due to deficiencies in regulation by SarA, as discussed previously. Most interesting in this mutant were the changes in its global regulators. CodY and σ^B were detected, but not significantly changed, while Agr (3.8 fold reduction), SarR (2.6-fold reduction), and SaeS (2.2-fold reduction) were all significantly reduced. These regulators were previously discussed in reference to the marked decrease in virulence factors detected in this mutant strain. SarR is a repressor of SarA[81], expression of which was found to be increased by only 0.6-fold, which may mean that there is another factor involved in regulation of *agr*. The repressor of *sarR* (*rsr*) was recently described as reducing transcription of both *sarR* and *agr*[100]. This supports the hypothesis that *agr* was downregulated in this mutant, and that SarA was not playing a significant role in virulence factor determination or antimicrobial susceptibility.

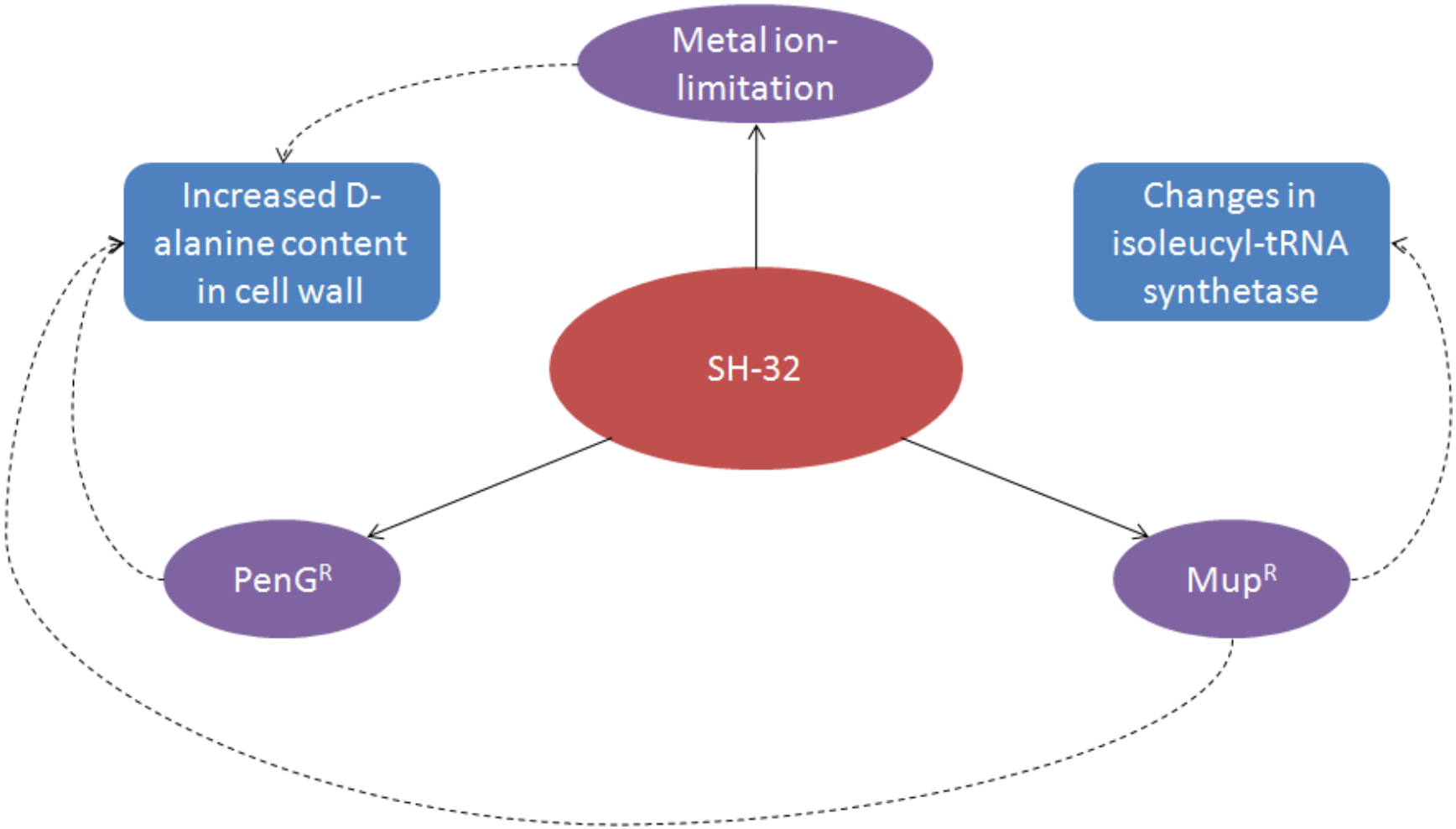

Figure 26. Phenotypic changes observed in SH-32 spontaneous mutant and proposed mechanisms of those changes. Purple indicates the observed phenotypic change. Arrows with dotted lines pointing to blue indicates the proposed mechanism.

While few changes were observed in the spontaneous mutants used in this study, a key point can be gleaned from analysis of SH-32. Based on the increased resistance to penicillin G and the decreased growth in metal ion limiting conditions, resistance to NsβL may have induced changes in the D-alanine content of the cell wall. It is possible that this is the mechanism by which heteroresistance to mupirocin was caused, and that the primary target, isoleucyl-tRNA synthetase, was not affected by resistance to NsβL.

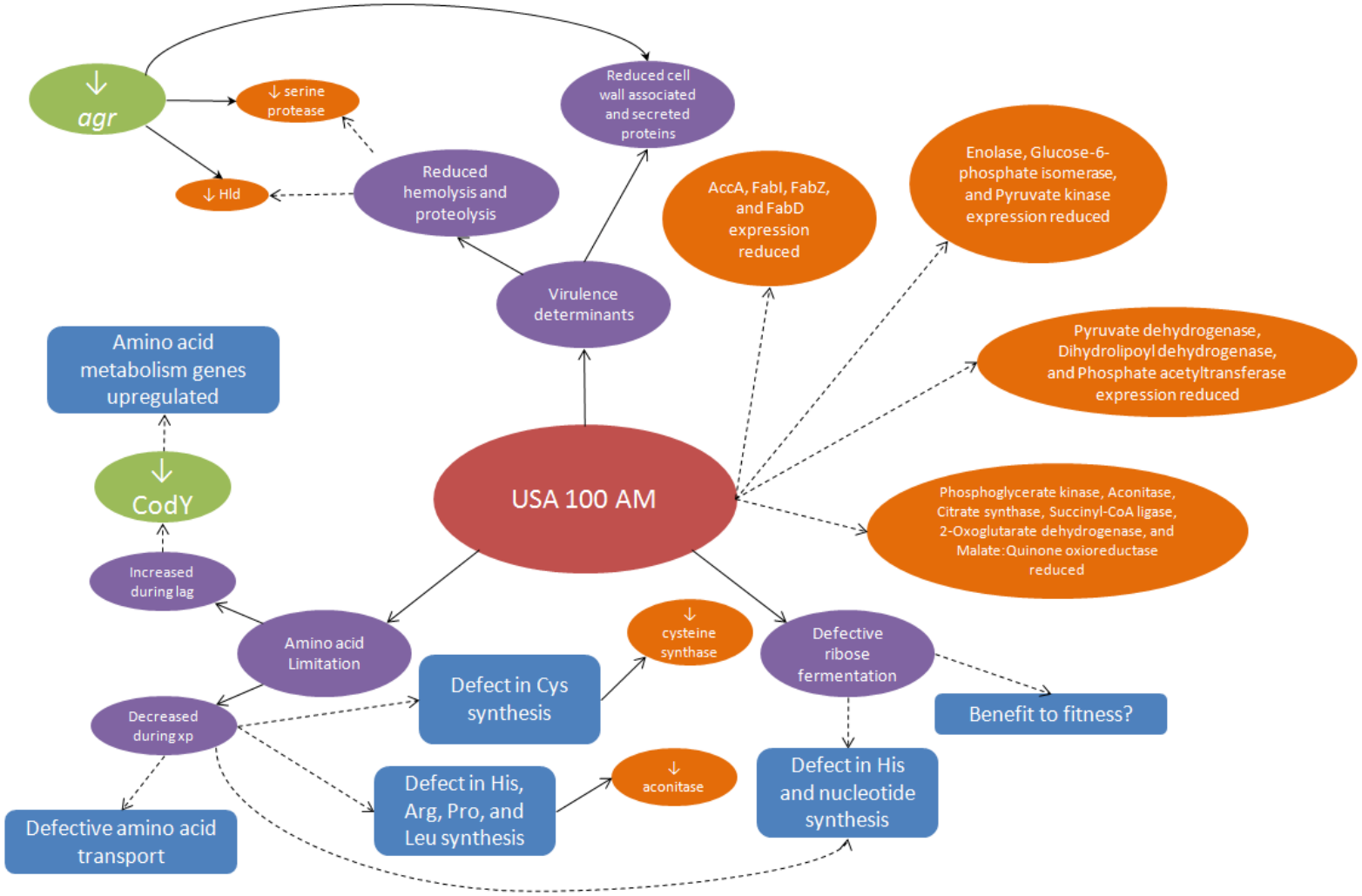

Figure 27. Phenotypic changes observed in USA 100 adaptive mutant (AM) and proposed mechanisms of those changes. Purple indicates the observed phenotypic change. Arrows with dotted lines pointing to blue indicates the proposed mechanism. Both green and orange indicate proteins observed by proteomic analysis.

Analysis of the comparative proteomics results for the USA 100 adaptive mutant was most insightful and indicates that those pathways reliant on CoA were significantly downregulated. While expression of FabH was not specifically reduced, the majority of proteins involved in fatty acid synthesis were found to be significantly reduced, as were glycolysis, pyruvate metabolism, and TCA cycle enzymes. This supports the conclusions made in previous studies that NsβL has an effect on CoA[92].

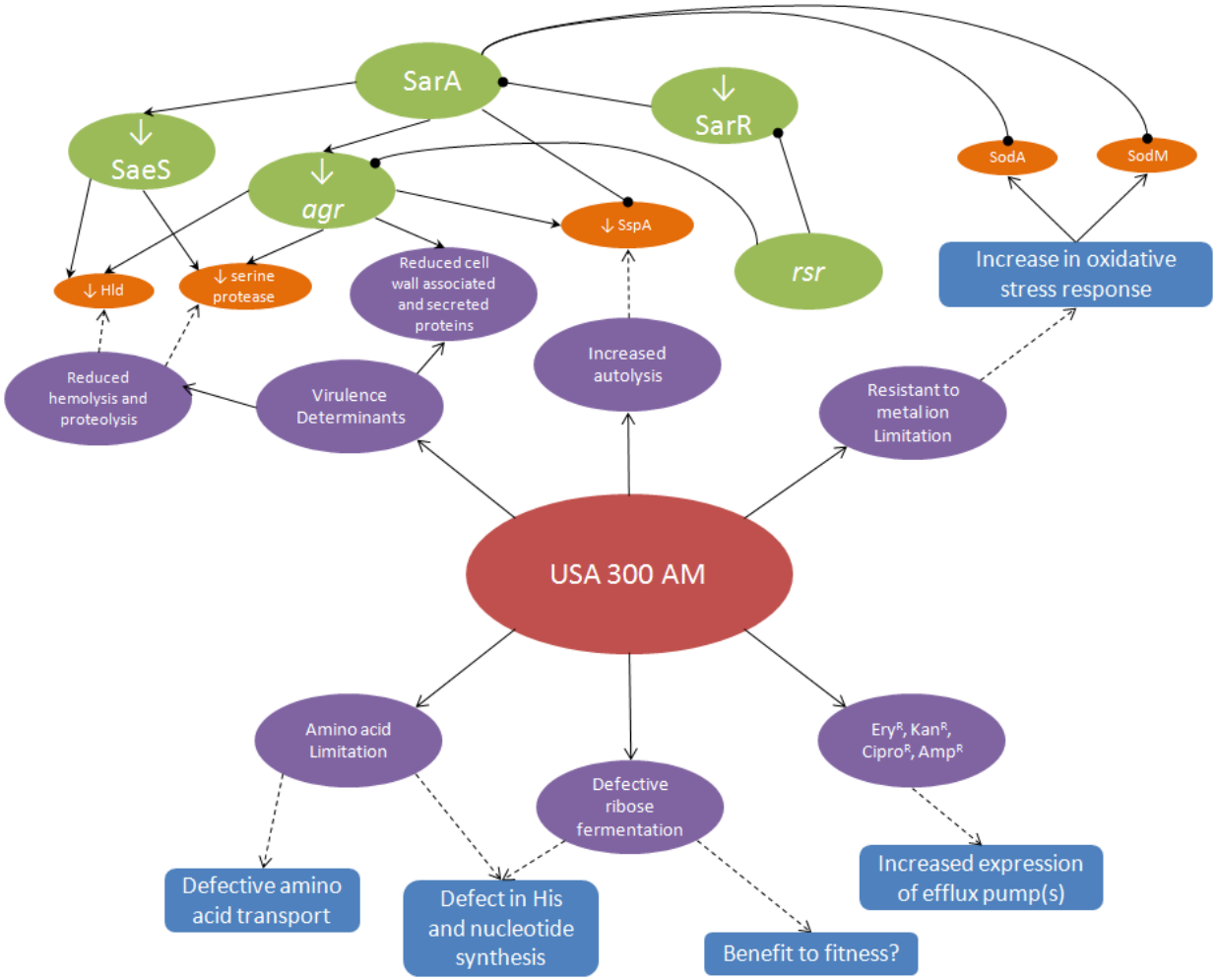

Figure 28. Phenotypic changes observed in USA 300 adaptive mutant and proposed mechanisms of those changes. Purple indicates the observed phenotypic change. Arrows with dotted lines pointing to blue indicates the proposed mechanism. Both green and orange indicate proteins observed by proteomic analysis. Green indicates regulators known to affect the indicated phenotype. Both green and orange indicate proteins observed by proteomic analysis, except for SarA and rsr. Lines with a blunt end indicate downregulation of that protein or gene.

The USA 300 adaptive mutant appears to have developed a number of alterations in its regulatory pathways. SarR expression was found to be reduced, while SarA expression was unaltered. Agr expression was also reduced, resulting in abridged expression of various virulence factors. Loss of *agr* and SarA activity has been shown to cause increased susceptibility to antimicrobials[38, 83]; however, the USA 300 adaptive mutant displayed increased antimicrobial resistance in the disk diffusion assays. These regulatory changes may be secondary to the expression of a multi-drug efflux pump[70], conferring resistance to kanamycin, ampicillin, erythromycin, ciprofloxacin, and, ultimately, NsβL.

FUTURE DIRECTIONS

There are a number of experiments that could be performed to clarify the precise mechanisms of resistance exhibited by the spontaneous and adaptive mutants. First and foremost, further analysis of the intracellular proteome would allow for statistically significant data. SH-11 and SH-32 could also be evaluated by the same process, particularly as phenotypic analysis did not show dramatic changes. It would also be beneficial to perform whole-genome sequencing of the NsβL-resistant mutants, to further pinpoint genetic changes leading to resistance. This would be further confirmed by introducing similar changes into a clean wild-type strain and observing if there were the expected changes in resistance to NsβL. A straightforward experiment that could be performed is measurement of the efflux activity of the USA 300 adaptive mutant towards NsβL, which would confirm if this was its primary mode of resistance, as hypothesized. Complementation of any clean *S. aureus* strain with a coaABCDE overexpression vector could help determine if NsβL actually targets CoA by monitoring growth for changes in the NsβL MIC as compared to the wild-type strain.

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APPENDICES

Appendix A. Chemically-defined media.

L-glutamic acid	4.44 gL^{-1}	**L-histidine**	0.88 gL^{-1}
L-aspartic acid	4.44 gL^{-1}	**L-valine**	0.88 gL^{-1}
L-proline	4.44 gL^{-1}	**L-arginine**	0.66 gL^{-1}
Glycine	4.44 gL^{-1}	**L-cysteine**	0.44 gL^{-1}
L-threonine	4.44 gL^{-1}	**L-phenylalanine**	0.38 gL^{-1}
L-serine	4.44 gL^{-1}	**L-tyrosine**	0.34 gL^{-1}
L-alanine	4.44 gL^{-1}	**L-methionine**	0.34 gL^{-1}
L-lysine HCl	1.12 gL^{-1}	**L-tryptophan**	0.12 gL^{-1}
L-isoleucine	1.12 gL^{-1}		

Table A1. CL1. Autoclave and store at -20°C.

Na_2HPO_4	70 gL^{-1}
KH_2PO_4	30 gL^{-1}

Table A2. CL2. Autoclave and store at 4°C.

Adenine sulfate	2 gL^{-1}
Guanine HCl	2 gL^{-1}

Table A3. CL3. Make up in 0.1M HCl. Autoclave and store at 4°C.

Pyridoxal	0.4 gL^{-1}	**Nicotinic acid**	0.2 gL^{-1}
Pyridoxamine HCl	0.4 gL^{-1}	**Thiamine HCl**	0.2 gL^{-1}
D-pantothenic acid	0.2 gL^{-1}	**Biotin**	0.01 gL^{-1}
Riboflavin	0.2 gL^{-1}		

Table A4. CL4. Add 10g Chelex-100 and stir for 4 hours before filter sterilizing. Store at 4°C.

L-aspartic acid	2.14 gL^{-1}	**L-methionine**	1.43 gL^{-1}
L-alanine	1.43 gL^{-1}	**L-phenylalanine**	1.43 gL^{-1}
L-arginine	1.43 gL^{-1}	**L-proline**	2.14 gL^{-1}
L-cysteine	0.714 gL^{-1}	**L-serine**	1.43 gL^{-1}
Glycine	1.43 gL^{-1}	**L-threonine**	2.14 gL^{-1}
L-glutamic acid	2.14 gL^{-1}	**L-tryptophan**	1.43 gL^{-1}
L-histidine	1.43 gL^{-1}	**L-tyrosine**	1.43 gL^{-1}
L-isoleucine	2.14 gL^{-1}	**L-valine**	2.14 gL^{-1}
L-lysine HCl	1.43 gL^{-1}	**Na_2HPO_4**	50 gL^{-1}
L-leucine	2.14 gL^{-1}	**KH_2PO_4**	21.43 gL^{-1}

Table A5. CDM1. Autoclave and store at -20°C.

Biotin	0.001 gL^{-1}	**Riboflavin**	0.02 gL^{-1}
D-panthothenic acid	0.02 gL^{-1}	**Nicotinic acid**	0.02 gL^{-1}
Pyridoxal	0.04 gL^{-1}	**Thiamine HCl**	0.02 gL^{-1}
Pyridoxamine HCl	0.04 gL^{-1}		

Table A6. CDM2. Filter sterilize and store at 4°C.

Adenine sulfate	0.4 gL^{-1}
Guanine HCl	0.4 gL^{-1}

Table A7. CDM3. Make up in 0.1M HCl. Autoclave and store at 4°C.

$CaCl_2 \cdot 6H_2O$	10 gL^{-1}
$MnSO_4$	5 gL^{-1}
$FeNH_4(SO_4)_2 \cdot 12H_2O$	6 gL^{-1}

Table A8. CDM4. Make up in 0.1M HCl. Autoclave and store at room temperature.

Glucose	100 gL^{-1}
$MgSO_4 \cdot 7H_2O$	5g

Table A9. CDM 5. Autoclave and store at room temperature.

Appendix B. Complete proteomics data.

#	Identified Proteins (85)	Accession Number	Fold Change from WT		Average Fold Change
37	SA0295 protein OS=Staphylococcus aureus (strain N315) GN=SA0295 PE=4 SV=1	Q7A7Q2|Q7A7Q2_STAAN	-4.2	Value Missing	**-4.2**
40	Ferritin OS=Staphylococcus aureus (strain N315) GN=ftnA PE=1 SV=1	Q7A4R2|FTN_STAAN	-2.9	-3.1	**-3**
64	Chaperone protein hchA OS=Staphylococcus aureus (strain N315) GN=hchA PE=1 SV=1	P64313|HCHA_STAAN	-2.9	-2.6	**-2.75**
65	Aspartate carbamoyltransferase OS=Staphylococcus aureus (strain N315) GN=pyrB PE=1 SV=1	P65618|PYRB_STAAN	-2.5	-2.8	**-2.65**
47	Phosphate acetyltransferase OS=Staphylococcus aureus (strain N315) GN=pta PE=1 SV=1	P99092|PTA_STAAN	-2.7	-2.5	**-2.6**
73	Phosphoglycerate kinase OS=Staphylococcus aureus (strain N315) GN=pgk PE=1 SV=1	P99135|PGK_STAAN	-2.6	-2.6	**-2.6**
8	L-lactate dehydrogenase 1 OS=Staphylococcus aureus (strain N315) GN=ldhA PE=1 SV=1	P65256|LDH1_STAAN	-2.5	-2.6	**-2.55**
20	Aconitate hydratase OS=Staphylococcus aureus (strain N315) GN=acnA PE=1 SV=1	P99148|ACON_STAAN	-2.7	-2.4	**-2.55**
29	6-phosphogluconate dehydrogenase, decarboxylating OS=Staphylococcus aureus (strain N315) GN=gnd PE=1 SV=1	P63334|6PGD_STAAN	-2.6	-2.5	**-2.55**
23	ATP synthase subunit beta OS=Staphylococcus aureus (strain N315) GN=atpD PE=1 SV=1	P99112|ATPB_STAAN	-2.6	-2.4	**-2.5**
32	Phosphoribosylformylglycinamidine synthase 1 OS=Staphylococcus aureus (strain N315) GN=purQ PE=1 SV=1	P99166|PURQ_STAAN	-2.3	-2.6	**-2.45**
79	Phosphoribosylaminoimidazole carboxylase ATPase subunit OS=Staphylococcus aureus (strain N315) GN=purK PE=1 SV=1	Q7A695|PURK_STAAN	-2.3	-2.5	**-2.4**
52	50S ribosomal protein L18 OS=Staphylococcus aureus (strain N315) GN=rplR PE=1 SV=1	Q7A467|RL18_STAAN	-2.3	-2.3	**-2.3**
74	Seryl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=serS PE=1 SV=1	P99178|SYS_STAAN	-2.3	-2.3	**-2.3**
4	Dihydrolipoyl dehydrogenase OS=Staphylococcus aureus (strain N315) GN=pdhD PE=1 SV=1	P99084|DLDH_STAAN	-2.2	-2.3	**-2.25**
5	Pyruvate dehydrogenase E1 component subunit beta OS=Staphylococcus aureus (strain N315) GN=pdhB PE=1 SV=1	P99063|ODPB_STAAN	-2.1	-2.4	**-2.25**
61	GTP-sensing transcriptional pleiotropic repressor codY OS=Staphylococcus aureus (strain N315) GN=codY PE=1 SV=1	P63844|CODY_STAAN	-2.2	-2.2	**-2.2**
15	Enolase OS=Staphylococcus aureus (strain N315) GN=eno PE=1 SV=1	P99088|ENO_STAAN	-2	-2.3	**-2.15**
25	30S ribosomal protein S9 OS=Staphylococcus aureus (strain N315) GN=rpsI PE=1 SV=1	P66646|RS9_STAAN	-2	-2.2	**-2.1**

76	Citrate synthase II OS=Staphylococcus aureus (strain N315) GN=citZ PE=1 SV=1	Q7A561|Q7A561_STAAN	-2.2	-2	**-2.1**
62	Cysteine synthase OS=Staphylococcus aureus (strain N315) GN=cysK PE=1 SV=1	P63871|CYSK_STAAN	-2.1	-2	**-2.05**
75	Putative uncharacterized protein SA1528 OS=Staphylococcus aureus (strain N315) GN=SA1528 PE=4 SV=1	Q7A553|Q7A553_STAAN	-2.1	-2	**-2.05**
70	Superoxide dismutase [Mn/Fe] 1 OS=Staphylococcus aureus (strain N315) GN=sodA PE=1 SV=1	P99098|SODM1_STAAN	-1.8	-2.1	**-1.95**
45	DNA-binding protein HU OS=Staphylococcus aureus (strain N315) GN=hup PE=1 SV=1	Q7A5J1|DBH_STAAN	-1.8	-1.9	**-1.85**
24	Glucose-6-phosphate isomerase OS=Staphylococcus aureus (strain N315) GN=pgi PE=1 SV=1	P99078|G6PI_STAAN	-1.7	-1.9	**-1.8**
28	30S ribosomal protein S1 OS=Staphylococcus aureus (strain N315) GN=rpsA PE=1 SV=1	Q7A5J0|RS1_STAAN	-1.7	-1.8	**-1.75**
18	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Staphylococcus aureus (strain N315) GN=sucD PE=1 SV=1	P99070|SUCD_STAAN	-1.8	-1.6	**-1.7**
82	NADH dehydrogenase-like protein SA0802 OS=Staphylococcus aureus (strain N315) GN=SA0802 PE=1 SV=1	Q7A6J4|Y802_STAAN	-1.7	-1.7	**-1.7**
17	Catalase OS=Staphylococcus aureus (strain N315) GN=katA PE=1 SV=2	Q7A5T2|CATA_STAAN	-1.4	-1.9	**-1.65**
35	Pyruvate kinase OS=Staphylococcus aureus (strain N315) GN=pyk PE=1 SV=1	Q7A559|KPYK_STAAN	-1.6	-1.6	**-1.6**
43	SA2119 protein OS=Staphylococcus aureus (strain N315) GN=SA2119 PE=1 SV=1	Q7A3Z5|Q7A3Z5_STAAN	-1.6	-1.6	**-1.6**
66	30S ribosomal protein S10 OS=Staphylococcus aureus (strain N315) GN=rpsJ PE=1 SV=1	P66334|RS10_STAAN	-1.5	-1.7	**-1.6**
81	NAD-specific glutamate dehydrogenase OS=Staphylococcus aureus (strain N315) GN=gluD PE=1 SV=1	Q7A6H8|DHE2_STAAN	-1.8	-1.4	**-1.6**
6	Probable malate:quinone oxidoreductase 2 OS=Staphylococcus aureus (strain N315) GN=mqo2 PE=1 SV=1	P99115|MQO2_STAAN	-1.6	-1.5	**-1.55**
9	Alkaline shock protein 23 OS=Staphylococcus aureus (strain N315) GN=asp23 PE=1 SV=1	P99157|ASP23_STAAN	-1.5	-1.6	**-1.55**
57	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Staphylococcus aureus (strain N315) GN=odhB PE=1 SV=1	Q7A5N4|ODO2_STAAN	-1.6	-1.5	**-1.55**
50	Alkyl hydroperoxide reductase subunit F OS=Staphylococcus aureus (strain N315) GN=ahpF PE=1 SV=1	P99118|AHPF_STAAN	-1.7	-1.4	**-1.55**
10	Inosine-5'-monophosphate dehydrogenase OS=Staphylococcus aureus (strain N315) GN=guaB PE=1 SV=1	P99106|IMDH_STAAN	-1.5	-1.5	**-1.5**
19	Glutamine synthetase OS=Staphylococcus aureus (strain N315) GN=glnA PE=1 SV=1	P99095|GLNA_STAAN	-1.5	-1.5	**-1.5**
21	50S ribosomal protein L13 OS=Staphylococcus aureus (strain N315) GN=rplM PE=1 SV=1	Q7A473|RL13_STAAN	-1.4	-1.6	**-1.5**

34	Q7A3N7|RANDOM_Q7A3N7_STAAN-R	Q7A3N7|RANDOM_Q7A3N7_STAAN-R (+2)	-1.4	-1.4	**-1.4**
48	DNA polymerase III subunit beta OS=Staphylococcus aureus (strain N315) GN=dnaN PE=1 SV=1	P99103|DPO3B_STAAN	-1.4	-1.4	**-1.4**
58	NADPH-dependent oxidoreductase OS=Staphylococcus aureus (strain N315) GN=nfrA PE=3 SV=1	Q7A7J0|RANDOM_NFRA_STAAN-R	-1.4	-1.4	**-1.4**
59	50S ribosomal protein L11 OS=Staphylococcus aureus (strain N315) GN=rplK PE=1 SV=2	P0A0F2|RL11_STAAN	-1.3	-1.5	**-1.4**
2	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Staphylococcus aureus (strain N315) GN=gapA1 PE=1 SV=1	P99136|G3P1_STAAN	-1.4	-1.3	**-1.35**
13	50S ribosomal protein L1 OS=Staphylococcus aureus (strain N315) GN=rplA PE=1 SV=1	Q99W68|RL1_STAAN	-1.3	-1.4	**-1.35**
1	Elongation factor Tu OS=Staphylococcus aureus (strain N315) GN=tuf PE=1 SV=1	P99152|EFTU_STAAN	-1.3	-1.3	**-1.3**
22	50S ribosomal protein L22 OS=Staphylococcus aureus (strain N315) GN=rplV PE=1 SV=1	Q7A460|RL22_STAAN	-1.4	-1.2	**-1.3**
53	Adenylosuccinate lyase OS=Staphylococcus aureus (strain N315) GN=purB PE=1 SV=1	Q7A4Q3|PUR8_STAAN	-1.2	-1.4	**-1.3**
7	Alkyl hydroperoxide reductase subunit C OS=Staphylococcus aureus (strain N315) GN=ahpC PE=1 SV=1	P99074|AHPC_STAAN	-1.3	-1.2	**-1.25**
11	50S ribosomal protein L2 OS=Staphylococcus aureus (strain N315) GN=rplB PE=1 SV=1	P60432|RL2_STAAN	-1.2	-1.3	**-1.25**
69	D-alanine aminotransferase OS=Staphylococcus aureus (strain N315) GN=dat PE=1 SV=1	P99090|DAAA_STAAN	-1.3	-1.2	**-1.25**
42	DNA-directed RNA polymerase subunit beta' OS=Staphylococcus aureus (strain N315) GN=rpoC PE=1 SV=1	P60285|RPOC_STAAN	-1.3	-1.1	**-1.2**
77	SA1224 protein OS=Staphylococcus aureus (strain N315) GN=SA1224 PE=4 SV=1	Q7A5Q0|Q7A5Q0_STAAN	-1.2	-1.2	**-1.2**
3	Elongation factor G OS=Staphylococcus aureus (strain N315) GN=fusA PE=1 SV=2	P68789|EFG_STAAN	-1.2	-1.1	**-1.15**
12	Cell division protein ftsZ OS=Staphylococcus aureus (strain N315) GN=ftsZ PE=1 SV=1	P99108|FTSZ_STAAN	-1.1	-1.2	**-1.15**
36	50S ribosomal protein L21 OS=Staphylococcus aureus (strain N315) GN=rplU PE=1 SV=1	Q7A583|RL21_STAAN	-1	-1.1	**-1.05**
51	50S ribosomal protein L14 OS=Staphylococcus aureus (strain N315) GN=rplN PE=1 SV=1	Q7A463|RL14_STAAN	-1	-1.1	**-1.05**
72	Glycyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=glyQS PE=1 SV=1	P99129|SYG_STAAN	-0.9	-1	**-0.95**
33	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Staphylococcus aureus (strain N315) GN=gatB PE=1 SV=1	P99169|GATB_STAAN	-1	-0.8	**-0.9**
49	ATP synthase subunit alpha OS=Staphylococcus aureus (strain N315) GN=atpA PE=1 SV=1	P99111|ATPA_STAAN	-0.8	-0.8	**-0.8**

56	DNA-directed RNA polymerase subunit beta OS=Staphylococcus aureus (strain N315) GN=rpoB PE=1 SV=1	P60278|RPOB_STAAN	-0.8	-0.8	**-0.8**
16	30S ribosomal protein S2 OS=Staphylococcus aureus (strain N315) GN=rpsB PE=1 SV=1	P66544|RS2_STAAN	-0.8	-0.7	**-0.75**
30	50S ribosomal protein L19 OS=Staphylococcus aureus (strain N315) GN=rplS PE=1 SV=1	P66083|RL19_STAAN	-0.7	-0.7	**-0.7**
60	Cell division protein ftsA OS=Staphylococcus aureus (strain N315) GN=ftsA PE=1 SV=1	P63765|FTSA_STAAN	-0.6	-0.8	**-0.7**
14	Serine hydroxymethyltransferase OS=Staphylococcus aureus (strain N315) GN=glyA PE=1 SV=1	P99091|GLYA_STAAN	-0.7	-0.5	**-0.6**
26	Bifunctional autolysin OS=Staphylococcus aureus (strain N315) GN=atl PE=1 SV=1	Q99V41|ATL_STAAN	-0.4	-0.4	**-0.4**
27	Uncharacterized protein SA0829 OS=Staphylococcus aureus (strain N315) GN=SA0829 PE=1 SV=1	Q7A6H3|Y829_STAAN	No Values	**No Values**	
31	D-lactate dehydrogenase OS=Staphylococcus aureus (strain N315) GN=ldhD PE=1 SV=1	P99116|LDHD_STAAN	No Values	**No Values**	
38	Q7A7W3|Q7A7W3_STAAN	Q7A7W3|Q7A7W3_STAAN	Value Missing	**Value Missing**	
39	ATP-dependent Clp protease ATP-binding subunit clpL OS=Staphylococcus aureus (strain N315) GN=clpL PE=1 SV=1	Q7A3F4|CLPL_STAAN	No Values	**No Values**	
41	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Staphylococcus aureus (strain N315) GN=purC PE=1 SV=1	P99064|PUR7_STAAN	No Values	**No Values**	
44	50S ribosomal protein L3 OS=Staphylococcus aureus (strain N315) GN=rplC PE=1 SV=1	P60449|RL3_STAAN	No Values	**No Values**	
46	50S ribosomal protein L6 OS=Staphylococcus aureus (strain N315) GN=rplF PE=1 SV=1	Q7A466|RL6_STAAN	No Values	**No Values**	
54	Aerobic glycerol-3-phosphate dehydrogenase OS=Staphylococcus aureus (strain N315) GN=glpD PE=1 SV=2	Q7A5V7|GLPD_STAAN	No Values	**No Values**	
55	2-oxoglutarate dehydrogenase E1 component OS=Staphylococcus aureus (strain N315) GN=odhA PE=1 SV=1	Q99U74|ODO1_STAAN	No Values	**No Values**	
63	(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase OS=Staphylococcus aureus (strain N315) GN=fabZ PE=3 SV=1	P64108|FABZ_STAAN	No Values	**No Values**	
67	30S ribosomal protein S5 OS=Staphylococcus aureus (strain N315) GN=rpsE PE=1 SV=1	P66579|RS5_STAAN	Value Missing	**Value Missing**	
68	1-pyrroline-5-carboxylate dehydrogenase OS=Staphylococcus aureus (strain N315) GN=rocA PE=1 SV=1	P99076|ROCA_STAAN	No Values	**No Values**	
71	P99119|LDH2_STAAN	P99119|LDH2_STAAN	No Values	**No Values**	
78	Ribonuclease J 2 OS=Staphylococcus aureus (strain N315) GN=SA1118 PE=1 SV=1	Q7A5X6|RNJ2_STAAN	No Values	**No Values**	
80	Naphthoate synthase OS=Staphylococcus aureus (strain N315) GN=menB PE=1 SV=1	Q7A6A9|MENB_STAAN	No Values	**No Values**	

83	Formate acetyltransferase OS=Staphylococcus aureus (strain N315) GN=pflB PE=1 SV=1	Q7A7X6|PFLB_STAAN	Value Missing	**Value Missing**
84	Pyruvate dehydrogenase E1 component subunit alpha OS=Staphylococcus aureus (strain N315) GN=pdhA PE=1 SV=1	Q820A6|ODPA_STAAN	No Values	**No Values**
85	ATP-dependent Clp protease ATP-binding subunit clpC OS=Staphylococcus aureus (strain N315) GN=clpC PE=1 SV=1	Q7A797|RANDOM_CLPC_STAAN-R	Value Missing	**Value Missing**

Table A10. Complete list of intracellular proteins identified from the USA 100 adaptive mutant at 8 hours.

#	Identified Proteins (66)	Accession Number	Fold Change from WT		Average Fold Change
54	Formate acetyltransferase OS=Staphylococcus aureus (strain USA300) GN=pflB PE=3 SV=1	Q2FK44|PFLB_STAA3	-2	-2.6	**-2.3**
18	Alcohol dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=adh PE=3 SV=1	Q2FJ31|ADH_STAA3	-2.1	-1.9	**-2**
24	Aconitate hydratase OS=Staphylococcus aureus (strain USA300) GN=acnA PE=4 SV=1	Q2FH85|Q2FH85_STAA3	-1.3	-1.1	**-1.2**
9	Formate--tetrahydrofolate ligase OS=Staphylococcus aureus (strain USA300) GN=fhs PE=3 SV=1	Q2FG06|FTHS_STAA3	-1.2	-1.1	**-1.15**
36	Putative universal stress protein SAUSA300_1656 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1656 PE=3 SV=1	Q2FG28|Y1656_STAA3	-1.2	-1.1	**-1.15**
65	Pyruvate carboxylase OS=Staphylococcus aureus (strain USA300) GN=pyc PE=4 SV=1	Q2FHW6|Q2FHW6_STAA3	-1	-0.8	**-0.9**
52	Cysteine synthase OS=Staphylococcus aureus (strain USA300) GN=cysK PE=3 SV=1	Q2FJC8|Q2FJC8_STAA3	-0.9	-0.6	**-0.75**
42	Glucose-6-phosphate isomerase OS=Staphylococcus aureus (strain USA300) GN=pgi PE=3 SV=1	Q2FIB3|G6PI_STAA3	-0.7	-0.7	**-0.7**
56	Phosphoenolpyruvate carboxykinase [ATP] OS=Staphylococcus aureus (strain USA300) GN=pckA PE=3 SV=1	Q2FFV5|PCKA_STAA3	-0.9	-0.5	**-0.7**
40	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Staphylococcus aureus (strain USA300) GN=sucC PE=3 SV=1	Q2FHJ3|SUCC_STAA3	-0.7	-0.6	**-0.65**
50	6-phosphogluconate dehydrogenase, decarboxylating OS=Staphylococcus aureus (strain USA300) GN=gnd PE=3 SV=1	Q2FGM3|Q2FGM3_STAA3	-0.7	-0.5	**-0.6**
62	NAD-specific glutamate dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=gudB PE=3 SV=1	Q2FIB7|Q2FIB7_STAA3	-0.7	-0.5	**-0.6**
32	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Staphylococcus aureus (strain USA300) GN=sucD PE=3 SV=1	Q2FHJ2|Q2FHJ2_STAA3	-0.6	-0.5	**-0.55**
8	Enolase OS=Staphylococcus aureus (strain USA300) GN=eno PE=3 SV=1	Q2FIL7|ENO_STAA3	-0.6	-0.4	**-0.5**
51	Dihydrolipoamide acetyltransferase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0995 PE=3 SV=1	Q2FHY5|Q2FHY5_STAA3	0.2	-1.1	**-0.45**

26	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Staphylococcus aureus (strain USA300) GN=odhB PE=3 SV=1	Q2FH26|ODO2_STAA3	-0.6	-0.3	**-0.45**
6	Inosine-5'-monophosphate dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=guaB PE=3 SV=1	Q2FJM6|IMDH_STAA3	-0.5	-0.3	**-0.4**
5	Pyruvate dehydrogenase E1 component, beta subunit OS=Staphylococcus aureus (strain USA300) GN=pdhB PE=4 SV=1	Q2FHY6|Q2FHY6_STAA3	-0.4	-0.3	**-0.35**
43	30S ribosomal protein S1 OS=Staphylococcus aureus (strain USA300) GN=rpsA PE=4 SV=1	Q2FGW6|Q2FGW6_STAA3	-0.4	-0.3	**-0.35**
3	Dihydrolipoyl dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=lpdA PE=3 SV=1	Q2FHY4|Q2FHY4_STAA3	-0.3	-0.2	**-0.25**
14	L-lactate dehydrogenase 1 OS=Staphylococcus aureus (strain USA300) GN=ldh1 PE=3 SV=2	Q2FK29|LDH1_STAA3	-0.3	-0.2	**-0.25**
23	Catalase OS=Staphylococcus aureus (strain USA300) GN=katA PE=3 SV=1	Q2FH99|CATA_STAA3	-0.3	-0.2	**-0.25**
16	Malate:quinone-oxidoreductase OS=Staphylococcus aureus (strain USA300) GN=mqo PE=3 SV=1	Q2FDQ3|Q2FDQ3_STAA3	-0.3	-0.1	**-0.2**
25	Glutamine synthetase OS=Staphylococcus aureus (strain USA300) GN=glnA PE=3 SV=1	Q2FHD0|Q2FHD0_STAA3	-0.3	-0.1	**-0.2**
30	Ferritin OS=Staphylococcus aureus (strain USA300) GN=ftnA PE=3 SV=1	Q2FFK2|FTN_STAA3	-0.3	-0.1	**-0.2**
47	NADH dehydrogenase-like protein SAUSA300_0844 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0844 PE=3 SV=1	Q2FID4|Y844_STAA3	-0.3	0	**-0.15**
13	Phosphoglycerate kinase OS=Staphylococcus aureus (strain USA300) GN=pgk PE=3 SV=1	Q2FIM0|PGK_STAA3	-0.2	0	**-0.1**
46	Bifunctional protein folD OS=Staphylococcus aureus (strain USA300) GN=folD PE=3 SV=1	Q2FI15|FOLD_STAA3	-0.2	0	**-0.1**
66	Isocitrate dehydrogenase [NADP] OS=Staphylococcus aureus (strain USA300) GN=icd PE=3 SV=1	Q2FG43|Q2FG43_STAA3	-0.1	0	**-0.05**
39	ATP synthase subunit beta OS=Staphylococcus aureus (strain USA300) GN=atpD PE=3 SV=1	Q2FF24|ATPB_STAA3	0	0	**0**
20	Pyruvate dehydrogenase E1 component, alpha subunit OS=Staphylococcus aureus (strain USA300) GN=pdhA PE=4 SV=1	Q2FHY7|Q2FHY7_STAA3	-0.1	0.1	**0**
33	DNA-binding protein HU OS=Staphylococcus aureus (strain USA300) GN=hup PE=3 SV=1	Q2FGW9|Q2FGW9_STAA3	-0.1	0.1	**0**
34	DNA-directed RNA polymerase subunit beta OS=Staphylococcus aureus (strain USA300) GN=rpoB PE=3 SV=2	Q2FJ98|RPOB_STAA3	-0.1	0.1	**0**
64	Phosphoenolpyruvate-protein phosphotransferase OS=Staphylococcus aureus (strain USA300) GN=ptsI PE=3 SV=1	Q2FHZ6|Q2FHZ6_STAA3	-0.1	0.3	**0.1**
4	Glyceraldehyde-3-phosphate dehydrogenase, type I OS=Staphylococcus aureus (strain USA300) GN=gap PE=3 SV=1	Q2FIM1|Q2FIM1_STAA3	0	0.2	**0.1**
38	GTP-sensing transcriptional pleiotropic repressor codY OS=Staphylococcus aureus (strain USA300) GN=codY PE=3 SV=1	Q2FHI3|CODY_STAA3	0	0.2	**0.1**

12	Pyruvate kinase OS=Staphylococcus aureus (strain USA300) GN=pyk PE=3 SV=1	Q2FG40|KPYK_STAA3	0.1	0.2	**0.15**
63	30S ribosomal protein S9 OS=Staphylococcus aureus (strain USA300) GN=rpsI PE=3 SV=1	Q2FES2|RS9_STAA3	0.1	0.2	**0.15**
11	DNA-directed RNA polymerase subunit beta' OS=Staphylococcus aureus (strain USA300) GN=rpoC PE=3 SV=2	Q2FJ97|RPOC_STAA3	0.1	0.3	**0.2**
60	DNA polymerase III, beta subunit OS=Staphylococcus aureus (strain USA300) GN=dnaN PE=3 SV=1	Q2FKQ4|Q2FKQ4_STAA3	0.1	0.3	**0.2**
28	50S ribosomal protein L2 OS=Staphylococcus aureus (strain USA300) GN=rplB PE=3 SV=1	Q2FEP2|RL2_STAA3	0.3	0.2	**0.25**
37	Glycyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=glyQS PE=3 SV=1	Q2FGF8|SYG_STAA3	0.2	0.3	**0.25**
22	Alkyl hydroperoxide reductase subunit C OS=Staphylococcus aureus (strain USA300) GN=ahpC PE=3 SV=1	Q2FJN4|AHPC_STAA3	0.3	0.3	**0.3**
7	Alkaline shock protein 23 OS=Staphylococcus aureus (strain USA300) GN=asp23 PE=3 SV=1	Q2FEV0|ASP23_STAA3	0.2	0.4	**0.3**
2	Elongation factor G OS=Staphylococcus aureus (strain USA300) GN=fusA PE=3 SV=3	Q2FJ93|EFG_STAA3	0.3	0.4	**0.35**
48	50S ribosomal protein L14 OS=Staphylococcus aureus (strain USA300) GN=rplN PE=3 SV=1	Q2FEP9|RL14_STAA3	0.4	0.4	**0.4**
55	UPF0457 protein SAUSA300_2132 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2132 PE=3 SV=1	Q2FEV9|Y2132_STAA3	0.4	0.4	**0.4**
31	30S ribosomal protein S5 OS=Staphylococcus aureus (strain USA300) GN=rpsE PE=3 SV=1	Q2FEQ6|RS5_STAA3	0.3	0.5	**0.4**
19	Transketolase OS=Staphylococcus aureus (strain USA300) GN=tkt PE=4 SV=1	Q2FH92|Q2FH92_STAA3	0.4	0.5	**0.45**
53	Alkyl hydroperoxide reductase, subunit F OS=Staphylococcus aureus (strain USA300) GN=ahpF PE=3 SV=1	Q2FJN5|Q2FJN5_STAA3	0.4	0.6	**0.5**
21	50S ribosomal protein L1 OS=Staphylococcus aureus (strain USA300) GN=rplA PE=3 SV=1	Q2FJA2|RL1_STAA3	0.5	0.6	**0.55**
57	50S ribosomal protein L13 OS=Staphylococcus aureus (strain USA300) GN=rplM PE=3 SV=1	Q2FES1|RL13_STAA3	0.4	0.7	**0.55**
27	50S ribosomal protein L3 OS=Staphylococcus aureus (strain USA300) GN=rplC PE=3 SV=1	Q2FEN9|RL3_STAA3	0.5	0.7	**0.6**
1	Elongation factor Tu OS=Staphylococcus aureus (strain USA300) GN=tuf PE=3 SV=1	Q2FJ92|EFTU_STAA3	0.6	0.7	**0.65**
15	Cell division protein ftsZ OS=Staphylococcus aureus (strain USA300) GN=ftsZ PE=3 SV=1	Q2FHQ1|Q2FHQ1_STAA3	0.6	0.7	**0.65**
17	Serine hydroxymethyltransferase OS=Staphylococcus aureus (strain USA300) GN=glyA PE=3 SV=1	Q2FF15|GLYA_STAA3	0.6	0.7	**0.65**
35	D-lactate dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=ddh PE=3 SV=1	Q2FDY1|Q2FDY1_STAA3	0.6	0.9	**0.75**

49	ATP synthase subunit alpha OS=Staphylococcus aureus (strain USA300) GN=atpA PE=3 SV=1	Q2FF22|ATPA_STAA3	0.7	1	**0.85**
10	Chaperone protein dnaK OS=Staphylococcus aureus (strain USA300) GN=dnaK PE=2 SV=1	Q2FGE3|DNAK_STAA3	1	1.1	**1.05**
29	30S ribosomal protein S2 OS=Staphylococcus aureus (strain USA300) GN=rpsB PE=3 SV=1	Q2FHI2|RS2_STAA3	1	1.1	**1.05**
61	Probable transglycosylase isaA OS=Staphylococcus aureus (strain USA300) GN=isaA PE=3 SV=1	Q2FDT8|ISAA_STAA3	1.2	1.7	**1.45**
41	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2473 PE=4 SV=1	Q2FDX1|Q2FDX1_STAA3	2.2	2.8	**2.5**
44	50S ribosomal protein L6 OS=Staphylococcus aureus (strain USA300) GN=rplF PE=3 SV=1	Q2FEQ4|RL6_STAA3	No Values	No Values	
45	Glucosamine--fructose-6-phosphate aminotransferase (Isomerizing) OS=Staphylococcus aureus (strain USA300) GN=glmS PE=3 SV=1	Q2FEX8|Q2FEX8_STAA3	No Values	No Values	
59	Transcription termination factor NusA OS=Staphylococcus aureus (strain USA300) GN=nusA PE=4 SV=1	Q2FHH2|Q2FHH2_STAA3	No Values	No Values	
58	Glyceraldehyde-3-phosphate dehydrogenase, type I OS=Staphylococcus aureus (strain USA300) GN=gap PE=3 SV=1	Q2FG50|Q2FG50_STAA3	Value Missing	Value Missing	

Table A11. Complete list of intracellular proteins identified from the USA 300 adaptive mutant at 8 hours.

#	Identified Proteins (796)	Accession Number	Fold Change from WT
213	Probable molybdate-binding protein OS=Staphylococcus aureus (strain N315) GN=modA PE=4 SV=1	Q99RZ3|Q99RZ3_STAAN	-4.4
30	Lipase 2 (lip2)	Q7A7P2|LIP2_STAAN	-3.7
161	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Staphylococcus aureus (strain N315) GN=purC PE=1 SV=1	P99064|PUR7_STAAN	-3.5
290	ATP synthase subunit delta OS=Staphylococcus aureus (strain N315) GN=atpH PE=1 SV=1	P99109|ATPD_STAAN	-3.5
251	Seryl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=serS PE=1 SV=1	P99178|SYS_STAAN	-3.3
318	SA0916 protein OS=Staphylococcus aureus (strain N315) GN=SA0916 PE=1 SV=1	Q7A696|Q7A696_STAAN	-3.3
493	Carbamate kinase 1 OS=Staphylococcus aureus (strain N315) GN=arcC1 PE=1 SV=1	Q7A627|ARCC1_STAAN	-3.3
33	Immunoglobulin-binding protein (sbi)	Q99RL2|SBI_STAAN	-3.2
248	Bifunctional protein pyrR OS=Staphylococcus aureus (strain N315) GN=pyrR PE=1 SV=1	P65944|PYRR_STAAN	-3.2
577	PTS system glucoside-specific EIICBA component OS=Staphylococcus aureus (strain N315) GN=glcB PE=1 SV=1	Q7A3G4|PTU3C_STAAN	-3.2
103	Ferritin OS=Staphylococcus aureus (strain N315) GN=ftnA PE=1 SV=1	Q7A4R2|FTN_STAAN	-3.1
114	Phosphoribosylamine--glycine ligase OS=Staphylococcus aureus (strain N315) GN=purD PE=1 SV=1	P65896|PUR2_STAAN	-3.1
167	Deoxyribose-phosphate aldolase 2 OS=Staphylococcus aureus (strain N315) GN=deoC2 PE=1 SV=1	P99174|DEOC2_STAAN	-3.1

386	SA0537 protein OS=Staphylococcus aureus (strain N315) GN=SA0537 PE=1 SV=1	Q7A765|Q7A765_STAAN	-3.1
413	UvrABC system protein A OS=Staphylococcus aureus (strain N315) GN=uvrA PE=1 SV=1	P63383|UVRA_STAAN	-3.1
32	Phosphoribosylformylglycinamidine synthase 2 (purL)	P65901|PURL_STAAN	-3
49	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (pdhC)	P65636|ODP2_STAAN	-3
106	L-lactate dehydrogenase 1 OS=Staphylococcus aureus (strain N315) GN=ldhA PE=1 SV=1	P65256|LDH1_STAAN	-3
199	PTS system glucose-specific EIICBA component OS=Staphylococcus aureus (strain N315) GN=ptsG PE=1 SV=1	Q7A807|PTG3C_STAAN	-3
282	SA0243 protein OS=Staphylococcus aureus (strain N315) GN=SA0243 PE=4 SV=1	Q7A7V2|Q7A7V2_STAAN	-3
320	Putative uncharacterized protein SA2101 OS=Staphylococcus aureus (strain N315) GN=SA2101 PE=4 SV=1	Q7A414|Q7A414_STAAN	-3
457	Uncharacterized lipoprotein SA2158 OS=Staphylococcus aureus (strain N315) GN=SA2158 PE=1 SV=1	Q7A3W5|Y2158_STAAN	-3
84	Bifunctional purine biosynthesis protein purH (purH)	P67544|PUR9_STAAN	-2.9
100	Ornithine aminotransferase 2 OS=Staphylococcus aureus (strain N315) GN=rocD2 PE=1 SV=1	P60298|OAT2_STAAN	-2.9
120	Pyrimidine-nucleoside phosphorylase OS=Staphylococcus aureus (strain N315) GN=pdp PE=1 SV=2	Q7A4D0|PDP_STAAN	-2.9
198	Phosphoribosylaminoimidazole carboxylase ATPase subunit OS=Staphylococcus aureus (strain N315) GN=purK PE=1 SV=1	Q7A695|PURK_STAAN	-2.9
264	Probable malate:quinone oxidoreductase 1 OS=Staphylococcus aureus (strain N315) GN=mqo1 PE=1 SV=1	P65422|MQO1_STAAN	-2.9
266	Glutamate-1-semialdehyde 2,1-aminomutase 1 OS=Staphylococcus aureus (strain N315) GN=hemL1 PE=1 SV=1	P99096|GSA1_STAAN	-2.9
324	SA0248 protein OS=Staphylococcus aureus (strain N315) GN=SA0248 PE=4 SV=1	Q7A7U7|Q7A7U7_STAAN	-2.9
419	Tyrosyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=tyrS PE=1 SV=1	Q7A537|SYY_STAAN	-2.9
9	Probable malate:quinone oxidoreductase 2 (mqo2)	P99115|MQO2_STAAN	-2.8
16	Dihydrolipoyl dehydrogenase (pdhD)	P99084|DLDH_STAAN	-2.8
34	SA0587 protein (SA0587)	Q7A719|Q7A719_STAAN	-2.8
73	Immunodominant staphylococcal antigen B (isaB)	Q7A377|ISAB_STAAN	-2.8
127	Ribose-phosphate pyrophosphokinase OS=Staphylococcus aureus (strain N315) GN=prs PE=1 SV=1	P65237|KPRS_STAAN	-2.8
221	ATP synthase subunit b OS=Staphylococcus aureus (strain N315) GN=atpF PE=1 SV=1	Q7A4E7|ATPF_STAAN	-2.8
253	ATP synthase gamma chain OS=Staphylococcus aureus (strain N315) GN=atpG PE=1 SV=1	Q7A4E8|ATPG_STAAN	-2.8
274	SA2302 protein OS=Staphylococcus aureus (strain N315) GN=SA2302 PE=4 SV=1	Q7A3I7|Q7A3I7_STAAN	-2.8
286	50S ribosomal protein L20 OS=Staphylococcus aureus (strain N315) GN=rplT PE=1 SV=1	P66108|RL20_STAAN	-2.8
480	Argininosuccinate synthase OS=Staphylococcus aureus (strain N315) GN=argG PE=3 SV=1	P63645|ASSY_STAAN	-2.8
35	50S ribosomal protein L5 (rplE)	Q7A465|RL5_STAAN	-2.7
56	SA0295 protein (SA0295)	Q7A7Q2|Q7A7Q2_STAAN	-2.7
145	L-lactate dehydrogenase 2 OS=Staphylococcus aureus (strain N315) GN=ldhB PE=1	P99119|LDH2_ST	-2.7

	SV=1	AAN	
307	Putative uncharacterized protein SA0618 OS=Staphylococcus aureus (strain N315) GN=SA0618 PE=4 SV=1	Q7A6Z0|Q7A6Z0_STAAN	-2.7
326	Putative uncharacterized protein SAS081 OS=Staphylococcus aureus (strain N315) GN=SA2054.1 PE=4 SV=1	Q7A450|Q7A450_STAAN	-2.7
387	DNA topoisomerase 4 subunit A OS=Staphylococcus aureus (strain N315) GN=parC PE=1 SV=1	Q93KF4|PARC_STAAN	-2.7
394	Putative uncharacterized protein SA2171 OS=Staphylococcus aureus (strain N315) GN=SA2171 PE=4 SV=1	Q7A3V3|Q7A3V3_STAAN	-2.7
406	D-alanine--poly(phosphoribitol) ligase subunit 2 OS=Staphylococcus aureus (strain N315) GN=dltC PE=3 SV=1	P0A019|DLTC_STAAN	-2.7
462	Ornithine carbamoyltransferase, catabolic OS=Staphylococcus aureus (strain N315) GN=arcB PE=1 SV=1	P65602|OTCC_STAAN	-2.7
570	Putative uncharacterized protein SA1649 OS=Staphylococcus aureus (strain N315) GN=SA1649 PE=4 SV=1	Q7A4W5|Q7A4W5_STAAN	-2.7
632	Branched-chain alpha-keto acid dehydrogenase E1 OS=Staphylococcus aureus (strain N315) GN=bfmBAA PE=4 SV=1	Q7A5F7|Q7A5F7_STAAN	-2.7
38	Carbamoyl-phosphate synthase large chain (carB)	P63740|CARB_STAAN	-2.6
71	NADH dehydrogenase-like protein SA0802 (SA0802)	Q7A6J4|Y802_STAAN	-2.6
146	50S ribosomal protein L14 OS=Staphylococcus aureus (strain N315) GN=rplN PE=1 SV=1	Q7A463|RL14_STAAN	-2.6
162	SA1224 protein OS=Staphylococcus aureus (strain N315) GN=SA1224 PE=4 SV=1	Q7A5Q0|Q7A5Q0_STAAN	-2.6
183	GTPase obg OS=Staphylococcus aureus (strain N315) GN=obg PE=1 SV=1	Q7A584|OBG_STAAN	-2.6
197	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Staphylococcus aureus (strain N315) GN=gpmI PE=1 SV=1	P64270|GPMI_STAAN	-2.6
334	SA0589 protein OS=Staphylococcus aureus (strain N315) GN=SA0589 PE=4 SV=1	Q7A717|Q7A717_STAAN	-2.6
347	Glycerol kinase OS=Staphylococcus aureus (strain N315) GN=glpK PE=1 SV=1	P99113|GLPK_STAAN	-2.6
441	SA1606 protein OS=Staphylococcus aureus (strain N315) GN=SA1606 PE=1 SV=1	Q7A4Z8|Q7A4Z8_STAAN	-2.6
455	Phosphoribosylformylglycinamidine synthase 1 OS=Staphylococcus aureus (strain N315) GN=purQ PE=1 SV=1	P99166|PURQ_STAAN	-2.6
612	Putative uncharacterized protein SA0637 OS=Staphylococcus aureus (strain N315) GN=SA0637 PE=4 SV=1	Q7A6X4|Q7A6X4_STAAN	-2.6
729	SA0682 protein OS=Staphylococcus aureus (strain N315) GN=SA0682 PE=3 SV=1	Q7A6T5|Q7A6T5_STAAN	-2.6
44	D-lactate dehydrogenase (ldhD)	P99116|LDHD_STAAN	-2.5
94	Asparaginyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=asnS PE=1 SV=1	P67572|SYN_STAAN	-2.5
279	GTP-binding protein engA OS=Staphylococcus aureus (strain N315) GN=engA PE=1 SV=1	P64060|ENGA_STAAN	-2.5
364	SA1989 protein OS=Staphylococcus aureus (strain N315) GN=SA1989 PE=1 SV=1	Q7A492|Q7A492_STAAN	-2.5
415	SA1749 protein OS=Staphylococcus aureus (strain N315) GN=SA1749 PE=4 SV=1	Q7A4N0|Q7A4N0_STAAN	-2.5
469	Kanamycin nucleotidyltransferase OS=Staphylococcus aureus (strain N315) GN=aadD PE=4 SV=1	Q7A8D0|Q7A8D0_STAAN	-2.5
477	Protein-export membrane protein SecDF OS=Staphylococcus aureus (strain N315) GN=secF PE=4 SV=1	Q7A586|Q7A586_STAAN	-2.5
617	UPF0297 protein SA1445 OS=Staphylococcus aureus (strain N315) GN=SA1445 PE=1 SV=1	P60359|Y1445_STAAN	-2.5
667	Putative uncharacterized protein SA0814 OS=Staphylococcus aureus (strain N315) GN=SA0814 PE=4 SV=1	Q7A6I2|Q7A6I2_STAAN	-2.5

6	Formate acetyltransferase (pflB)	Q7A7X6|PFLB_STAAN	-2.4
53	Protein translocase subunit secA 1 (secA1)	Q7A6R5|SECA1_STAAN	-2.4
54	ATP synthase subunit alpha (atpA)	P99111|ATPA_STAAN	-2.4
66	Probable quinol oxidase subunit 2 (qoxA)	Q7A698|QOX2_STAAN	-2.4
116	50S ribosomal protein L19 OS=Staphylococcus aureus (strain N315) GN=rplS PE=1 SV=1	P66083|RL19_STAAN	-2.4
139	Phosphate acetyltransferase OS=Staphylococcus aureus (strain N315) GN=pta PE=1 SV=1	P99092|PTA_STAAN	-2.4
340	Putative uncharacterized protein SA0933 OS=Staphylococcus aureus (strain N315) GN=SA0933 PE=4 SV=1	Q7A687|Q7A687_STAAN	-2.4
356	GTP pyrophosphokinase OS=Staphylococcus aureus (strain N315) GN=relA PE=1 SV=2	Q99TL8|RELA_STAAN	-2.4
450	Virulence factor esxA OS=Staphylococcus aureus (strain N315) GN=esxA PE=1 SV=1	ESXA_STAAN (+1)	-2.4
573	Molybdopterin synthase sulfur carrier subunit OS=Staphylococcus aureus (strain N315) GN=moaD PE=1 SV=1	Q7A441|MOAD_STAAN	-2.4
631	SA2201 protein OS=Staphylococcus aureus (strain N315) GN=SA2201 PE=3 SV=1	Q7A3S5|Q7A3S5_STAAN	-2.4
82	Fructose-bisphosphate aldolase (fba)	P99075|ALF2_STAAN	-2.3
83	PBP2 (pbp2)	Q7A5K8|Q7A5K8_STAAN	-2.3
96	50S ribosomal protein L13 OS=Staphylococcus aureus (strain N315) GN=rplM PE=1 SV=1	Q7A473|RL13_STAAN	-2.3
137	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase OS=Staphylococcus aureus (strain N315) GN=gpmA PE=1 SV=1	P99153|GPMA_STAAN	-2.3
140	Probable catabolite control protein A OS=Staphylococcus aureus (strain N315) GN=ccpA PE=1 SV=1	P99175|CCPA_STAAN	-2.3
142	N-acetylmuramoyl-L-alanine amidase sle1 OS=Staphylococcus aureus (strain N315) GN=sle1 PE=1 SV=1	Q7A7E0|SLE1_STAAN	-2.3
220	Acetoin(diacetyl) reductase OS=Staphylococcus aureus (strain N315) GN=butA PE=1 SV=1	P99120|BUTA_STAAN	-2.3
223	Ffh protein OS=Staphylococcus aureus (strain N315) GN=ffh PE=4 SV=1	Q7A5Z0|Q7A5Z0_STAAN	-2.3
332	DNA polymerase I OS=Staphylococcus aureus (strain N315) GN=polA PE=3 SV=1	Q7A565|Q7A565_STAAN	-2.3
363	DegV domain-containing protein SA1258 OS=Staphylococcus aureus (strain N315) GN=SA1258 PE=1 SV=1	P67371|Y1258_STAAN	-2.3
384	Putative uncharacterized protein SA1933 OS=Staphylococcus aureus (strain N315) GN=SA1933 PE=4 SV=1	Q7A4D3|Q7A4D3_STAAN	-2.3
393	Carbamoyl-phosphate synthase small chain OS=Staphylococcus aureus (strain N315) GN=carA PE=1 SV=1	P99147|CARA_STAAN	-2.3
420	50S ribosomal protein L24 OS=Staphylococcus aureus (strain N315) GN=rplX PE=1 SV=1	P60735|RL24_STAAN	-2.3
491	Amidophosphoribosyltransferase OS=Staphylococcus aureus (strain N315) GN=purF PE=1 SV=1	P99164|PUR1_STAAN	-2.3
506	Glycerol-3-phosphate dehydrogenase [NAD(P)+] OS=Staphylococcus aureus (strain N315) GN=gpsA PE=1 SV=1	P64191|GPDA_STAAN	-2.3
621	Putative uncharacterized protein SA1168 OS=Staphylococcus aureus (strain N315) GN=SA1168 PE=4 SV=1	Q7A5T3|Q7A5T3_STAAN	-2.3
785	Ribonuclease 3 OS=Staphylococcus aureus (strain N315) GN=rnc PE=1 SV=1	P66668|RNC_STAAN	-2.3
18	ATP synthase subunit beta (atpD)	P99112|ATPB_STAAN	-2.2
40	Aconitate hydratase (acnA)	P99148|ACON_ST	-2.2

		AAN	
51	50S ribosomal protein L1 (rplA)	Q99W68|RL1_STAAN	-2.2
69	50S ribosomal protein L6 (rplF)	Q7A466|RL6_STAAN	-2.2
77	Glucose-6-phosphate isomerase (pgi)	P99078|G6PI_STAAN	-2.2
92	Succinate dehydrogenase flavoprotein subunit OS=Staphylococcus aureus (strain N315) GN=sdhA PE=4 SV=1	Q7A642|Q7A642_STAAN	-2.2
104	Formate--tetrahydrofolate ligase OS=Staphylococcus aureus (strain N315) GN=fhs PE=1 SV=1	Q7A535|FTHS_STAAN	-2.2
105	Aerobic glycerol-3-phosphate dehydrogenase OS=Staphylococcus aureus (strain N315) GN=glpD PE=1 SV=2	Q7A5V7|GLPD_STAAN	-2.2
115	Threonyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=thrS PE=1 SV=1	P67585|SYT_STAAN	-2.2
130	50S ribosomal protein L22 OS=Staphylococcus aureus (strain N315) GN=rplV PE=1 SV=1	Q7A460|RL22_STAAN	-2.2
141	NAD-specific glutamate dehydrogenase OS=Staphylococcus aureus (strain N315) GN=gluD PE=1 SV=1	Q7A6H8|DHE2_STAAN	-2.2
156	Transcription termination-antitermination factor OS=Staphylococcus aureus (strain N315) GN=nusA PE=4 SV=1	Q7A5Y2|Q7A5Y2_STAAN	-2.2
157	50S ribosomal protein L4 OS=Staphylococcus aureus (strain N315) GN=rplD PE=1 SV=1	P61059|RL4_STAAN	-2.2
180	Adenylosuccinate lyase OS=Staphylococcus aureus (strain N315) GN=purB PE=1 SV=1	Q7A4Q3|PUR8_STAAN	-2.2
196	SA1599 protein OS=Staphylococcus aureus (strain N315) GN=SA1599 PE=4 SV=1	Q7A501|Q7A501_STAAN	-2.2
205	HTH-type transcriptional regulator mgrA OS=Staphylococcus aureus (strain N315) GN=mgrA PE=1 SV=3	Q7A6X2|MGRA_STAAN	-2.2
230	UPF0355 protein SA0372 OS=Staphylococcus aureus (strain N315) GN=SA0372 PE=1 SV=1	Q7A7I6|UP355_STAAN	-2.2
247	ATP-dependent Clp protease ATP-binding subunit clpX OS=Staphylococcus aureus (strain N315) GN=clpX PE=1 SV=1	P63790|CLPX_STAAN	-2.2
268	Putative uncharacterized protein SA0633 OS=Staphylococcus aureus (strain N315) GN=SA0633 PE=4 SV=1	Q7A6X7|Q7A6X7_STAAN	-2.2
283	Putative uncharacterized protein SA0919 OS=Staphylococcus aureus (strain N315) GN=SA0919 PE=4 SV=1	Q7A694|Q7A694_STAAN	-2.2
305	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Staphylococcus aureus (strain N315) GN=accA PE=1 SV=1	Q7A558|ACCA_STAAN	-2.2
333	Putative uncharacterized protein SA1331 OS=Staphylococcus aureus (strain N315) GN=SA1331 PE=1 SV=1	Q7A5H1|Q7A5H1_STAAN	-2.2
362	Serine-protein kinase rsbW OS=Staphylococcus aureus (strain N315) GN=rsbW PE=1 SV=1	P0A0H7|RSBW_STAAN	-2.2
411	SA1585 protein OS=Staphylococcus aureus (strain N315) GN=SA1585 PE=4 SV=1	Q7A512|Q7A512_STAAN	-2.2
454	Cytidylate kinase OS=Staphylococcus aureus (strain N315) GN=cmk PE=3 SV=1	P63806|KCY_STAAN	-2.2
481	Uncharacterized peptidase SA1530 OS=Staphylococcus aureus (strain N315) GN=SA1530 PE=1 SV=2	Q7A552|Y1530_STAAN	-2.2
519	UPF0173 metal-dependent hydrolase SA1529 OS=Staphylococcus aureus (strain N315) GN=SA1529 PE=1 SV=1	P99149|Y1529_STAAN	-2.2
536	SA0658 protein OS=Staphylococcus aureus (strain N315) GN=SA0658 PE=4 SV=1	Q7A6V6|Q7A6V6_STAAN	-2.2
598	SA1450 protein OS=Staphylococcus aureus (strain N315) GN=SA1450 PE=4 SV=1	Q7A595|Q7A595_STAAN	-2.2
691	UvrABC system protein B OS=Staphylococcus aureus (strain N315) GN=uvrB PE=1 SV=1	P67425|UVRB_STAAN	-2.2
718	(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase OS=Staphylococcus aureus (strain N315) GN=fabZ PE=3 SV=1	P64108|FABZ_STAAN	-2.2

7	Penicillin binding protein 2 prime (mecA)	Q7A8C6|Q7A8C6_STAAN	-2.1
39	1-pyrroline-5-carboxylate dehydrogenase (rocA)	P99076|ROCA_STAAN	-2.1
50	30S ribosomal protein S5 (rpsE)	P66579|RS5_STAAN	-2.1
65	Transketolase (tkt)	P99161|TKT_STAAN	-2.1
68	30S ribosomal protein S11 (rpsK)	P66357|RS11_STAAN	-2.1
86	Cell division protein (ftsA)	P63765|FTSA_STAAN	-2.1
88	Translation initiation factor IF-2 (infB)	P65134|IF2_STAAN	-2.1
147	Naphthoate synthase OS=Staphylococcus aureus (strain N315) GN=menB PE=1 SV=1	Q7A6A9|MENB_STAAN	-2.1
159	Uncharacterized protein SA1069 OS=Staphylococcus aureus (strain N315) GN=SA1069 PE=1 SV=1	Q7A5Z4|Y1069_STAAN	-2.1
160	Copper chaperone copZ OS=Staphylococcus aureus (strain N315) GN=copZ PE=1 SV=1	Q7A3E5|COPZ_STAAN	-2.1
172	SA0859 protein OS=Staphylococcus aureus (strain N315) GN=SA0859 PE=1 SV=1	Q7A6E5|Q7A6E5_STAAN	-2.1
176	6-phosphofructokinase OS=Staphylococcus aureus (strain N315) GN=pfkA PE=1 SV=1	P99165|K6PF_STAAN	-2.1
217	50S ribosomal protein L21 OS=Staphylococcus aureus (strain N315) GN=rplU PE=1 SV=1	Q7A583|RL21_STAAN	-2.1
225	Xanthine phosphoribosyltransferase OS=Staphylococcus aureus (strain N315) GN=xpt PE=1 SV=1	Q7A7I5|XPT_STAAN	-2.1
276	Trans-2-enoyl-ACP reductase OS=Staphylococcus aureus (strain N315) GN=fabI PE=4 SV=1	Q7A6D8|Q7A6D8_STAAN	-2.1
299	30S ribosomal protein S18 OS=Staphylococcus aureus (strain N315) GN=rpsR PE=1 SV=1	P66468|RS18_STAAN	-2.1
304	Urocanate hydratase OS=Staphylococcus aureus (strain N315) GN=hutU PE=1 SV=1	P67417|HUTU_STAAN	-2.1
350	SA1969 protein OS=Staphylococcus aureus (strain N315) GN=SA1969 PE=4 SV=1	Q7A4A8|Q7A4A8_STAAN	-2.1
369	30S ribosomal protein S17 OS=Staphylococcus aureus (strain N315) GN=rpsQ PE=1 SV=1	Q7A462|RS17_STAAN	-2.1
379	Putative uncharacterized protein SA2309 OS=Staphylococcus aureus (strain N315) GN=SA2309 PE=4 SV=1	Q7A3I0|Q7A3I0_STAAN	-2.1
381	Aminoacyltransferase femB OS=Staphylococcus aureus (strain N315) GN=femB PE=1 SV=1	P0A0A7|FEMB_STAAN	-2.1
400	SA0884 protein OS=Staphylococcus aureus (strain N315) GN=SA0884 PE=4 SV=1	Q7A6C5|Q7A6C5_STAAN	-2.1
404	Anti-sigma-B factor antagonist OS=Staphylococcus aureus (strain N315) GN=rsbV PE=1 SV=1	P66838|RSBV_STAAN	-2.1
432	SA1054 protein OS=Staphylococcus aureus (strain N315) GN=SA1054 PE=4 SV=1	Q7A605|Q7A605_STAAN	-2.1
436	Putative uncharacterized protein SAS053 OS=Staphylococcus aureus (strain N315) GN=SA1670.1 PE=4 SV=1	Q7A4U6|Q7A4U6_STAAN	-2.1
488	ATP-dependent DNA helicase pcrA OS=Staphylococcus aureus (strain N315) GN=pcrA PE=1 SV=1	P64319|PCRA_STAAN	-2.1
496	Putative uncharacterized protein SA1534 OS=Staphylococcus aureus (strain N315) GN=SA1534 PE=4 SV=1	Q7A550|Q7A550_STAAN	-2.1
503	Putative uncharacterized protein SA2247 OS=Staphylococcus aureus (strain N315) GN=SA2247 PE=4 SV=1	Q7A3N9|Q7A3N9_STAAN	-2.1
563	Probable ribokinase OS=Staphylococcus aureus (strain N315) GN=rbsK PE=3 SV=1	Q7A7T7|Q7A7T7_STAAN	-2.1
640	Putative uncharacterized protein SA1455 OS=Staphylococcus aureus (strain N315)	Q7A590|Q7A590_	-2.1

	GN=SA1455 PE=4 SV=1	STAAN	
663	Uridine kinase OS=Staphylococcus aureus (strain N315) GN=udk PE=1 SV=1	P67411|URK_STAAN	-2.1
698	P0A0I2|SECE_STAAN	P0A0I2|SECE_STAAN	-2.1
26	DNA-directed RNA polymerase subunit beta' (rpoC)	P60285|RPOC_STAAN	-2
45	Putative universal stress protein SA1532 (SA1532)	Q7A551|Y1532_STAAN	-2
62	ATP-dependent Clp protease ATP-binding subunit (clpL)	Q7A3F4|CLPL_STAAN	-2
64	Catalase (katA)	Q7A5T2|CATA_STAAN	-2
107	UPF0342 protein SA1663 OS=Staphylococcus aureus (strain N315) GN=SA1663 PE=1 SV=1	Q7A4V3|Y1663_STAAN	-2
164	SA0351 protein OS=Staphylococcus aureus (strain N315) GN=SA0351 PE=4 SV=1	Q7A7K4|Q7A7K4_STAAN	-2
170	Putative uncharacterized protein SA1607 OS=Staphylococcus aureus (strain N315) GN=SA1607 PE=4 SV=1	Q7A4Z7|Q7A4Z7_STAAN	-2
178	UPF0356 protein SA0941 OS=Staphylococcus aureus (strain N315) GN=SA0941 PE=3 SV=2	Q99V08|Y941_STAAN	-2
208	SA2119 protein OS=Staphylococcus aureus (strain N315) GN=SA2119 PE=1 SV=1	Q7A3Z5_STAAN	-2
210	Citrate synthase II OS=Staphylococcus aureus (strain N315) GN=citZ PE=1 SV=1	Q7A561|Q7A561_STAAN	-2
249	30S ribosomal protein S10 OS=Staphylococcus aureus (strain N315) GN=rpsJ PE=1 SV=1	P66334|RS10_STAAN	-2
252	Putative 2-hydroxyacid dehydrogenase SA2098 OS=Staphylococcus aureus (strain N315) GN=SA2098 PE=1 SV=1	Q7A417|Y2098_STAAN	-2
261	Extracellular matrix protein-binding protein emp OS=Staphylococcus aureus (strain N315) GN=emp PE=1 SV=1	Q7A6P4|EMP_STAAN	-2
267	SA1524 protein OS=Staphylococcus aureus (strain N315) GN=SA1524 PE=3 SV=1	Q7A556|Q7A556_STAAN	-2
308	Uncharacterized oxidoreductase SA2266 OS=Staphylococcus aureus (strain N315) GN=SA2266 PE=1 SV=1	Q7A3L9|Y2266_STAAN	-2
309	ATP-dependent protease ATPase subunit HslU OS=Staphylococcus aureus (strain N315) GN=hslU PE=1 SV=1	P63797|HSLU_STAAN	-2
313	Putative phosphotransferase SA1392 OS=Staphylococcus aureus (strain N315) GN=SA1392 PE=3 SV=1	P67200|Y1392_STAAN	-2
316	Uncharacterized epimerase/dehydratase SA0511 OS=Staphylococcus aureus (strain N315) GN=SA0511 PE=1 SV=1	Q7A788|Y511_STAAN	-2
342	Uncharacterized N-acetyltransferase SA1019 OS=Staphylococcus aureus (strain N315) GN=SA1019 PE=1 SV=1	Q99UT4|Y1019_STAAN	-2
408	Lipoyl synthase OS=Staphylococcus aureus (strain N315) GN=lipA PE=1 SV=1	P65286|LIPA_STAAN	-2
486	Putative uncharacterized protein SA0319 OS=Staphylococcus aureus (strain N315) GN=SA0319 PE=4 SV=1	Q7A7N3|Q7A7N3_STAAN	-2
495	Glutathione peroxidase homolog BsaA OS=Staphylococcus aureus (strain N315) GN=bsaA PE=1 SV=1	P99097|BSAA_STAAN	-2
509	Putative uncharacterized protein SA2143 OS=Staphylococcus aureus (strain N315) GN=SA2143 PE=4 SV=1	Q7A3X9|Q7A3X9_STAAN	-2
560	Pyrimidine nucleoside transport protein OS=Staphylococcus aureus (strain N315) GN=nupC PE=4 SV=1	Q7A7A0|Q7A7A0_STAAN	-2
594	30S ribosomal protein S14 type Z OS=Staphylococcus aureus (strain N315) GN=rpsZ PE=3 SV=1	P66412|RS14Z_STAAN	-2
603	SA1155 protein OS=Staphylococcus aureus (strain N315) GN=SA1155 PE=4 SV=1	Q7A5U5|Q7A5U5_STAAN	-2
645	UPF0039 protein SA0906 OS=Staphylococcus aureus (strain N315) GN=SA0906 PE=3 SV=1	P0A0M7|Y906_STAAN	-2

671	SA2166 protein OS=Staphylococcus aureus (strain N315) GN=SA2166 PE=4 SV=1	Q7A3V7|Q7A3V7_STAAN	-2
673	SA0572 protein OS=Staphylococcus aureus (strain N315) GN=SA0572 PE=4 SV=1	Q7A733|Q7A733_STAAN	-2
730	Putative uncharacterized protein SA0626 OS=Staphylococcus aureus (strain N315) GN=SA0626 PE=4 SV=1	Q7A6Y4|Q7A6Y4_STAAN	-2
12	Pyruvate kinase (pyk)	Q7A559|KPYK_STAAN	-1.9
23	Cysteine synthase (cysK)	P63871|CYSK_STAAN	-1.9
36	Phosphoglycerate kinase (pgk)	P99135|PGK_STAAN	-1.9
47	Pyruvate dehydrogenase E1 component subunit alpha (pdhA)	Q820A6|ODPA_STAAN	-1.9
59	50S ribosomal protein L2 (rplB)	P60432|RL2_STAAN	-1.9
60	Acetate kinase (ackA)	Q99TF2|ACKA_STAAN	-1.9
67	UPF0478 protein SA1560 (SA1560)	Q7A531|Y1560_STAAN	-1.9
78	Isocitrate dehydrogenase [NADP] (icd)	P99167|IDH_STAAN	-1.9
80	DNA polymerase III subunit beta (dnaN)	P99103|DPO3B_STAAN	-1.9
85	Putative aldehyde dehydrogenase SA1924 (SA1924)	Q7A4D8|ALD1_STAAN	-1.9
93	30S ribosomal protein S7 OS=Staphylococcus aureus (strain N315) GN=rpsG PE=1 SV=1	P66616|RS7_STAAN	-1.9
126	6-phosphogluconate dehydrogenase, decarboxylating OS=Staphylococcus aureus (strain N315) GN=gnd PE=1 SV=1	P63334|6PGD_STAAN	-1.9
128	30S ribosomal protein S13 OS=Staphylococcus aureus (strain N315) GN=rpsM PE=1 SV=1	P66388|RS13_STAAN	-1.9
134	Prolyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=proS PE=1 SV=1	Q7A5Y3|SYP_STAAN	-1.9
138	30S ribosomal protein S12 OS=Staphylococcus aureus (strain N315) GN=rpsL PE=1 SV=1	P0A0G8|RS12_STAAN	-1.9
144	30S ribosomal protein S8 OS=Staphylococcus aureus (strain N315) GN=rpsH PE=1 SV=1	P66630|RS8_STAAN	-1.9
151	Phosphoglucosamine mutase OS=Staphylococcus aureus (strain N315) GN=glmM PE=1 SV=1	P99087|GLMM_STAAN	-1.9
171	Putative dipeptidase SA1572 OS=Staphylococcus aureus (strain N315) GN=SA1572 PE=1 SV=1	Q7A522|PEPVL_STAAN	-1.9
174	Putative aldehyde dehydrogenase AldA OS=Staphylococcus aureus (strain N315) GN=aldA PE=1 SV=1	Q7A825|ALDA_STAAN	-1.9
188	SA0959 protein OS=Staphylococcus aureus (strain N315) GN=SA0959 PE=4 SV=1	Q7A671|Q7A671_STAAN	-1.9
204	UPF0477 protein SA0873 OS=Staphylococcus aureus (strain N315) GN=SA0873 PE=1 SV=1	Q7A6D4|Y873_STAAN	-1.9
209	50S ribosomal protein L23 OS=Staphylococcus aureus (strain N315) GN=rplW PE=1 SV=1	Q7A459|RL23_STAAN	-1.9
214	Succinate dehydrogenase iron-sulfur protein subunit OS=Staphylococcus aureus (strain N315) GN=sdhB PE=4 SV=1	Q99UV7|Q99UV7_STAAN	-1.9
228	Probable thiol peroxidase OS=Staphylococcus aureus (strain N315) GN=tpx PE=1 SV=1	P99146|TPX_STAAN	-1.9
291	SA1387 protein OS=Staphylococcus aureus (strain N315) GN=SA1387 PE=4 SV=1	Q7A5D2|Q7A5D2_STAAN	-1.9
294	Glucokinase OS=Staphylococcus aureus (strain N315) GN=glcK PE=4 SV=1	Q7A5D8|Q7A5D8_STAAN	-1.9
306	UPF0051 protein SA0778 OS=Staphylococcus aureus (strain N315) GN=SA0778 PE=1	Q7A6L4|Y778_ST	-1.9

	SV=1	AAN	
322	Transcriptional regulatory protein srrA OS=Staphylococcus aureus (strain N315) GN=srrA PE=1 SV=1	Q7A5H6|SRRA_STAAN	-1.9
345	GTP-binding protein era homolog OS=Staphylococcus aureus (strain N315) GN=era PE=1 SV=1	P64085|ERA_STAAN	-1.9
360	SA1548 protein OS=Staphylococcus aureus (strain N315) GN=SA1548 PE=4 SV=1	Q7A539|Q7A539_STAAN	-1.9
377	SA0317 protein OS=Staphylococcus aureus (strain N315) GN=SA0317 PE=4 SV=1	Q7A7N5|Q7A7N5_STAAN	-1.9
378	SA2202 protein OS=Staphylococcus aureus (strain N315) GN=SA2202 PE=4 SV=1	Q99RL6|Q99RL6_STAAN	-1.9
391	Methionyl-tRNA formyltransferase OS=Staphylococcus aureus (strain N315) GN=fmt PE=1 SV=1	P99127|FMT_STAAN	-1.9
392	Mannitol-1-phosphate 5-dehydrogenase OS=Staphylococcus aureus (strain N315) GN=mtlD PE=1 SV=1	P99140|MTLD_STAAN	-1.9
399	PhoH protein OS=Staphylococcus aureus (strain N315) GN=phoH PE=4 SV=1	Q7A5C7|Q7A5C7_STAAN	-1.9
412	Acetyl-CoA synthetase OS=Staphylococcus aureus (strain N315) GN=acsA PE=4 SV=1	Q99TD1|Q99TD1_STAAN	-1.9
466	Fructose specific permease OS=Staphylococcus aureus (strain N315) GN=fruA PE=4 SV=1	Q7A6V9|Q7A6V9_STAAN	-1.9
475	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2 OS=Staphylococcus aureus (strain N315) GN=murA2 PE=1 SV=1	P65457|MURA2_STAAN	-1.9
485	Putative uncharacterized protein SA1242 OS=Staphylococcus aureus (strain N315) GN=SA1242 PE=4 SV=1	Q7A5N6|Q7A5N6_STAAN	-1.9
568	Probable DNA-directed RNA polymerase subunit delta OS=Staphylococcus aureus (strain N315) GN=rpoE PE=1 SV=1	P66715|RPOE_STAAN	-1.9
627	50S ribosomal protein L32 OS=Staphylococcus aureus (strain N315) GN=rpmF PE=1 SV=1	P66210|RL32_STAAN	-1.9
629	Dihydrofolate reductase OS=Staphylococcus aureus (strain N315) GN=folA PE=1 SV=2	P99079|DYR_STAAN	-1.9
647	50S ribosomal protein L9 OS=Staphylococcus aureus (strain N315) GN=rplI PE=1 SV=1	P66318|RL9_STAAN	-1.9
660	Membrane-associated protein tcaA OS=Staphylococcus aureus (strain N315) GN=tcaA PE=2 SV=1	Q7A3X6|TCAA_STAAN	-1.9
672	Putative uncharacterized protein SA1068 OS=Staphylococcus aureus (strain N315) GN=SA1068 PE=4 SV=1	Q7A5Z5|Q7A5Z5_STAAN	-1.9
687	Putative uncharacterized protein SA1086 OS=Staphylococcus aureus (strain N315) GN=SA1086 PE=4 SV=1	Q7A5Y9|Q7A5Y9_STAAN	-1.9
767	Putative uncharacterized protein SA1062 OS=Staphylococcus aureus (strain N315) GN=SA1062 PE=4 SV=1	Q7A5Z9|Q7A5Z9_STAAN	-1.9
1	Elongation factor Tu (tuf)	P99152|EFTU_STAAN	-1.8
2	Bifunctional autolysin (atl)	Q99V41|ATL_STAAN	-1.8
29	Pyruvate dehydrogenase E1 component subunit beta (pdhB)	P99063|ODPB_STAAN	-1.8
48	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (gatB)	P99169|GATB_STAAN	-1.8
58	Glutamyl-tRNA(Gln) amidotransferase subunit A (gatA)	P63489|GATA_STAAN	-1.8
75	Ribonucleoside-diphosphate reductase (nrdE)	Q7A6T2|Q7A6T2_STAAN	-1.8
122	SA1745 protein OS=Staphylococcus aureus (strain N315) GN=SA1745 PE=4 SV=1	Q7A4N5|Q7A4N5_STAAN	-1.8
129	DNA-directed RNA polymerase subunit alpha OS=Staphylococcus aureus (strain N315) GN=rpoA PE=1 SV=1	P66706|RPOA_STAAN	-1.8
148	Pyridoxal biosynthesis lyase pdxS OS=Staphylococcus aureus (strain N315) GN=pdxS PE=1 SV=1	P60798|PDXS_STAAN	-1.8

166	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Staphylococcus aureus (strain N315) GN=sucD PE=1 SV=1	P99070|SUCD_STAAN	-1.8
179	Glycine cleavage system H protein OS=Staphylococcus aureus (strain N315) GN=gcvH PE=1 SV=1	P64214|GCSH_STAAN	-1.8
219	D-alanine aminotransferase OS=Staphylococcus aureus (strain N315) GN=dat PE=1 SV=1	P99090|DAAA_STAAN	-1.8
229	3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Staphylococcus aureus (strain N315) GN=fabF PE=1 SV=1	Q7A6F8|FABF_STAAN	-1.8
233	Putative 8-amino-7-oxononanoate synthase/2-amino-3-ketobutyrate coenzyme A ligase OS=Staphylococcus aureus (strain N315) GN=SA0508 PE=1 SV=1	P60120|BIKB_STAAN	-1.8
235	D-alanine--poly(phosphoribitol) ligase subunit 1 OS=Staphylococcus aureus (strain N315) GN=dltA PE=1 SV=1	P99107|DLTA_STAAN	-1.8
241	30S ribosomal protein S6 OS=Staphylococcus aureus (strain N315) GN=rpsF PE=1 SV=1	P99142|RS6_STAAN	-1.8
245	Uridylate kinase OS=Staphylococcus aureus (strain N315) GN=pyrH PE=1 SV=1	P65936|PYRH_STAAN	-1.8
257	Chaperone protein hchA OS=Staphylococcus aureus (strain N315) GN=hchA PE=1 SV=1	P64313|HCHA_STAAN	-1.8
280	CTP synthase OS=Staphylococcus aureus (strain N315) GN=pyrG PE=1 SV=1	P99072|PYRG_STAAN	-1.8
285	D-alanine--D-alanine ligase OS=Staphylococcus aureus (strain N315) GN=ddl PE=1 SV=1	P63892|DDL_STAAN	-1.8
293	Putative NAD(P)H nitroreductase SA2311 OS=Staphylococcus aureus (strain N315) GN=SA2311 PE=1 SV=1	Q7A3H8|Y2311_STAAN	-1.8
300	30S ribosomal protein S9 OS=Staphylococcus aureus (strain N315) GN=rpsI PE=1 SV=1	P66646|RS9_STAAN	-1.8
302	50S ribosomal protein L31 type B OS=Staphylococcus aureus (strain N315) GN=rpmE2 PE=1 SV=1	P66196|RL31B_STAAN	-1.8
311	Imidazolonepropionase OS=Staphylococcus aureus (strain N315) GN=hutI PE=1 SV=1	P64418|HUTI_STAAN	-1.8
329	50S ribosomal protein L29 OS=Staphylococcus aureus (strain N315) GN=rpmC PE=1 SV=1	P66173|RL29_STAAN	-1.8
358	Putative uncharacterized protein SA1657 OS=Staphylococcus aureus (strain N315) GN=SA1657 PE=4 SV=1	Q7A4V9|Q7A4V9_STAAN	-1.8
361	PTS system EIIBC component SA0186 OS=Staphylococcus aureus (strain N315) GN=SA0186 PE=1 SV=1	Q7A804|PTXBC_STAAN	-1.8
366	Ribonuclease J 2 OS=Staphylococcus aureus (strain N315) GN=SA1118 PE=1 SV=1	Q7A5X6|RNJ2_STAAN	-1.8
383	Hypoxanthine-guanine phosphoribosyltransferase OS=Staphylococcus aureus (strain N315) GN=hpt PE=1 SV=1	P99085|HPRT_STAAN	-1.8
398	30S ribosomal protein S16 OS=Staphylococcus aureus (strain N315) GN=rpsP PE=1 SV=1	P66440|RS16_STAAN	-1.8
459	Glutamate-1-semialdehyde 2,1-aminomutase 2 OS=Staphylococcus aureus (strain N315) GN=hemL2 PE=1 SV=1	Q7A4T5|GSA2_STAAN	-1.8
473	Leucyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=leuS PE=1 SV=1	P67513|SYL_STAAN	-1.8
499	30S ribosomal protein S20 OS=Staphylococcus aureus (strain N315) GN=rpsT PE=1 SV=1	Q7A5C0|RS20_STAAN	-1.8
624	Response regulator protein vraR OS=Staphylococcus aureus (strain N315) GN=vraR PE=1 SV=1	Q7A4R9|VRAR_STAAN	-1.8
652	Protein nagD homolog OS=Staphylococcus aureus (strain N315) GN=nagD PE=3 SV=1	Q7A6K4|NAGD_STAAN	-1.8
701	Putative uncharacterized protein SA1453 OS=Staphylococcus aureus (strain N315) GN=SA1453 PE=4 SV=1	Q7A592|Q7A592_STAAN	-1.8
17	Protein map (map)	P69775|MAP1_STAAN	-1.7
24	Fructose-bisphosphate aldolase class 1 (fda)	P99117|ALF1_STAAN	-1.7
42	UPF0365 protein SA1402 (SA1402)	Q7A5C5|Y1402_S	-1.7

		TAAN	
57	Uncharacterized protein SA0829 (SA0829)	Q7A6H3|Y829_STAAN	-1.7
79	Glutamine synthetase (glnA)	P99095|GLNA_STAAN	-1.7
98	60 kDa chaperonin OS=Staphylococcus aureus (strain N315) GN=groL PE=1 SV=1	P99083|CH60_STAAN	-1.7
99	Triosephosphate isomerase OS=Staphylococcus aureus (strain N315) GN=tpiA PE=1 SV=1	P99133|TPIS_STAAN	-1.7
101	50S ribosomal protein L10 OS=Staphylococcus aureus (strain N315) GN=rplJ PE=1 SV=1	P99155|RL10_STAAN	-1.7
113	Septation ring formation regulator ezrA OS=Staphylococcus aureus (strain N315) GN=ezrA PE=1 SV=1	P64003|EZRA_STAAN	-1.7
119	GTP-sensing transcriptional pleiotropic repressor codY OS=Staphylococcus aureus (strain N315) GN=codY PE=1 SV=1	P63844|CODY_STAAN	-1.7
143	Protein recA OS=Staphylococcus aureus (strain N315) GN=recA PE=1 SV=1	P68844|RECA_STAAN	-1.7
149	50S ribosomal protein L7/L12 OS=Staphylococcus aureus (strain N315) GN=rplL PE=1 SV=1	P99154|RL7_STAAN	-1.7
152	Putative uncharacterized protein SA1986 OS=Staphylococcus aureus (strain N315) GN=SA1986 PE=4 SV=1	Q7A493|Q7A493_STAAN	-1.7
193	Putative uncharacterized protein SA0359 OS=Staphylococcus aureus (strain N315) GN=SA0359 PE=4 SV=1	Q7A7J8|Q7A7J8_STAAN	-1.7
200	Putative uncharacterized protein SA1528 OS=Staphylococcus aureus (strain N315) GN=SA1528 PE=4 SV=1	Q7A553|Q7A553_STAAN	-1.7
232	Transcription antitermination protein nusG OS=Staphylococcus aureus (strain N315) GN=nusG PE=1 SV=1	P0A096|NUSG_STAAN	-1.7
236	Glycerol phosphate lipoteichoic acid synthase OS=Staphylococcus aureus (strain N315) GN=ltaS PE=1 SV=1	Q7A6U1|LTAS_STAAN	-1.7
254	Elastin-binding protein ebpS OS=Staphylococcus aureus (strain N315) GN=ebpS PE=1 SV=3	Q7A5I6|EBPS_STAAN	-1.7
263	UDP-N-acetylmuramoylalanine--D-glutamate ligase OS=Staphylococcus aureus (strain N315) GN=murD PE=1 SV=1	P0A090|MURD_STAAN	-1.7
270	Arginyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=argS PE=1 SV=1	Q99W05|SYR_STAAN	-1.7
272	Orotidine 5'-phosphate decarboxylase OS=Staphylococcus aureus (strain N315) GN=pyrF PE=1 SV=1	P99145|PYRF_STAAN	-1.7
277	Alcohol-acetaldehyde dehydrogenase OS=Staphylococcus aureus (strain N315) GN=adhE PE=4 SV=1	Q7A843|Q7A843_STAAN	-1.7
317	50S ribosomal protein L17 OS=Staphylococcus aureus (strain N315) GN=rplQ PE=1 SV=1	Q7A469|RL17_STAAN	-1.7
390	Translation initiation factor IF-3 OS=Staphylococcus aureus (strain N315) GN=infC PE=1 SV=1	P65140|IF3_STAAN	-1.7
395	Putative uncharacterized protein SA1946 OS=Staphylococcus aureus (strain N315) GN=SA1946 PE=1 SV=1	Q7A4C4|Q7A4C4_STAAN	-1.7
421	SA1565 protein OS=Staphylococcus aureus (strain N315) GN=SA1565 PE=4 SV=1	Q7A527|Q7A527_STAAN	-1.7
433	Cystathionine gamma-synthase OS=Staphylococcus aureus (strain N315) GN=metB PE=3 SV=1	Q99WE2|Q99WE2_STAAN	-1.7
437	Phosphate acyltransferase OS=Staphylococcus aureus (strain N315) GN=plsX PE=1 SV=1	P65739|PLSX_STAAN	-1.7
446	Putative uncharacterized protein SA1840 OS=Staphylococcus aureus (strain N315) GN=SA1840 PE=1 SV=1	Q7A4J0|Q7A4J0_STAAN	-1.7
500	Ribosomal RNA small subunit methyltransferase H OS=Staphylococcus aureus (strain N315) GN=rsmH PE=1 SV=1	P60392|RSMH_STAAN	-1.7
514	Putative uncharacterized protein SA0635 OS=Staphylococcus aureus (strain N315) GN=SA0635 PE=4 SV=1	Q7A6X5|Q7A6X5_STAAN	-1.7
555	Putative uncharacterized protein SA1464 OS=Staphylococcus aureus (strain N315) GN=SA1464 PE=4 SV=1	Q7A585|Q7A585_STAAN	-1.7

579	SA0675 protein OS=Staphylococcus aureus (strain N315) GN=SA0675 PE=4 SV=1	Q7A6U0|Q7A6U0_STAAN	-1.7
628	tRNA modification GTPase mnmE OS=Staphylococcus aureus (strain N315) GN=mnmE PE=3 SV=1	P66972|MNME_STAAN	-1.7
669	Chaperone protein dnaJ OS=Staphylococcus aureus (strain N315) GN=dnaJ PE=1 SV=1	P63971|DNAJ_STAAN	-1.7
11	Cell division protein ftsZ (ftsZ)	P99108|FTSZ_STAAN	-1.6
27	Staphylococcal secretory antigen (ssaA2)	Q7A423|SSAA2_STAAN	-1.6
72	DNA-directed RNA polymerase subunit beta (rpoB)	P60278|RPOB_STAAN	-1.6
90	Trigger factor OS=Staphylococcus aureus (strain N315) GN=tig PE=1 SV=1	P99080|TIG_STAAN	-1.6
121	Putative formate dehydrogenase SA2102 OS=Staphylococcus aureus (strain N315) GN=SA2102 PE=1 SV=1	Q99RW4|FDHL_STAAN	-1.6
175	Adenylosuccinate synthetase OS=Staphylococcus aureus (strain N315) GN=purA PE=1 SV=1	P99099|PURA_STAAN	-1.6
181	Putative uncharacterized protein SA1263 OS=Staphylococcus aureus (strain N315) GN=SA1263 PE=4 SV=1	Q7A5M5|Q7A5M5_STAAN	-1.6
182	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 OS=Staphylococcus aureus (strain N315) GN=murA1 PE=1 SV=1	P84058|MURA1_STAAN	-1.6
239	Putative uncharacterized protein SA1743 OS=Staphylococcus aureus (strain N315) GN=SA1743 PE=1 SV=1	Q7A4N7|Q7A4N7_STAAN	-1.6
242	Chaperone protein clpB OS=Staphylococcus aureus (strain N315) GN=clpB PE=1 SV=1	Q7A6G6|CLPB_STAAN	-1.6
281	Thioredoxin reductase OS=Staphylococcus aureus (strain N315) GN=trxB PE=1 SV=1	P99101|TRXB_STAAN	-1.6
298	DNA gyrase subunit A OS=Staphylococcus aureus (strain N315) GN=gyrA PE=1 SV=1	Q99XG5|GYRA_STAAN	-1.6
314	Ribosome-recycling factor OS=Staphylococcus aureus (strain N315) GN=frr PE=1 SV=1	P99130|RRF_STAAN	-1.6
328	Putative septation protein spoVG OS=Staphylococcus aureus (strain N315) GN=spoVG PE=1 SV=2	Q7A7B5|SP5G_STAAN	-1.6
365	Aspartate semialdehyde dehydrogenase OS=Staphylococcus aureus (strain N315) GN=asd PE=3 SV=1	Q7A5P8|Q7A5P8_STAAN	-1.6
397	Branched-chain alpha-keto acid dehydrogenase E2 OS=Staphylococcus aureus (strain N315) GN=bmfBB PE=3 SV=1	Q7A5F9|Q7A5F9_STAAN	-1.6
414	10 kDa chaperonin OS=Staphylococcus aureus (strain N315) GN=groS PE=1 SV=1	P99104|CH10_STAAN	-1.6
470	Putative uncharacterized protein SAS056 OS=Staphylococcus aureus (strain N315) GN=SA1738.1 PE=4 SV=1	Q7A4P2|Q7A4P2_STAAN	-1.6
483	Pyrroline-5-carboxylate reductase OS=Staphylococcus aureus (strain N315) GN=proC PE=1 SV=1	Q7A5G8|P5CR_STAAN	-1.6
511	Arginase OS=Staphylococcus aureus (strain N315) GN=arg PE=1 SV=1	P60088|ARGI_STAAN	-1.6
539	SA2056 protein OS=Staphylococcus aureus (strain N315) GN=SA2056 PE=4 SV=1	Q7A448|Q7A448_STAAN	-1.6
540	Menaquinone biosynthesis methyltransferase ubiE OS=Staphylococcus aureus (strain N315) GN=ubiE PE=1 SV=1	P67062|UBIE_STAAN	-1.6
554	50S ribosomal protein L28 OS=Staphylococcus aureus (strain N315) GN=rpmB PE=3 SV=1	P66153|RL28_STAAN	-1.6
585	Uncharacterized protein SA1737 OS=Staphylococcus aureus (strain N315) GN=SA1737 PE=1 SV=1	Q7A4P4|Y1737_STAAN	-1.6
593	Single-stranded DNA-binding protein OS=Staphylococcus aureus (strain N315) GN=ssb PE=4 SV=1	Q7A7K2_STAAN (+1)	-1.6
680	Ribosome-binding factor A OS=Staphylococcus aureus (strain N315) GN=rbfA PE=1 SV=1	P65967|RBFA_STAAN	-1.6
3	Elongation factor G (fusA)	P68789|EFG_STA	-1.5

		AN	
10	Inosine-5'-monophosphate dehydrogenase (guaB)	P99106|IMDH_STAAN	-1.5
19	Enolase (eno)	P99088|ENO_STAAN	-1.5
25	30S ribosomal protein S2 (rpsB)	P66544|RS2_STAAN	-1.5
28	30S ribosomal protein S3 (rpsC)	P66553|RS3_STAAN	-1.5
55	Alkyl hydroperoxide reductase subunit C (ahpC)	P99074|AHPC_STAAN	-1.5
74	Phosphocarrier protein HPr (ptsH)	P99143|PTHP_STAAN	-1.5
76	GMP synthase [glutamine-hydrolyzing] (guaA)	P99105|GUAA_STAAN	-1.5
91	Lysyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=lysS PE=1 SV=1	P67610|SYK_STAAN	-1.5
102	Probable branched-chain-amino-acid aminotransferase OS=Staphylococcus aureus (strain N315) GN=ilvE PE=1 SV=1	P99138|ILVE_STAAN	-1.5
108	50S ribosomal protein L3 OS=Staphylococcus aureus (strain N315) GN=rplC PE=1 SV=1	P60449|RL3_STAAN	-1.5
125	Bifunctional protein folD OS=Staphylococcus aureus (strain N315) GN=folD PE=1 SV=1	Q7A697|FOLD_STAAN	-1.5
133	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Staphylococcus aureus (strain N315) GN=sucC PE=1 SV=1	P99071|SUCC_STAAN	-1.5
165	UPF0133 protein SA0437 OS=Staphylococcus aureus (strain N315) GN=SA0437 PE=1 SV=1	P99126|Y437_STAAN	-1.5
186	S-adenosylmethionine synthase OS=Staphylococcus aureus (strain N315) GN=metK PE=1 SV=1	P66767|METK_STAAN	-1.5
195	50S ribosomal protein L18 OS=Staphylococcus aureus (strain N315) GN=rplR PE=1 SV=1	Q7A467|RL18_STAAN	-1.5
202	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Staphylococcus aureus (strain N315) GN=gapA2 PE=1 SV=1	P99067|G3P2_STAAN	-1.5
215	Glutamyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=gltX PE=1 SV=1	P99170|SYE_STAAN	-1.5
222	Putative uncharacterized protein SA1661 OS=Staphylococcus aureus (strain N315) GN=SA1661 PE=4 SV=1	Q7A4V5|Q7A4V5_STAAN	-1.5
224	Putative peptidyl-prolyl cis-trans isomerase OS=Staphylococcus aureus (strain N315) GN=SA0815 PE=1 SV=1	Q7A6I1|PPI1_STAAN	-1.5
238	Aspartyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=aspS PE=1 SV=1	P67015|SYD_STAAN	-1.5
250	Uracil phosphoribosyltransferase OS=Staphylococcus aureus (strain N315) GN=upp PE=1 SV=1	P67396|UPP_STAAN	-1.5
258	DNA gyrase subunit B OS=Staphylococcus aureus (strain N315) GN=gyrB PE=1 SV=2	P66937|GYRB_STAAN	-1.5
287	30S ribosomal protein S4 OS=Staphylococcus aureus (strain N315) GN=rpsD PE=1 SV=1	P66563|RS4_STAAN	-1.5
327	Putative uncharacterized protein SA1668 OS=Staphylococcus aureus (strain N315) GN=SA1668 PE=4 SV=1	Q7A4U8|Q7A4U8_STAAN	-1.5
335	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--L-lysine ligase OS=Staphylococcus aureus (strain N315) GN=murE PE=1 SV=1	P65480|MURE_STAAN	-1.5
346	Peptide methionine sulfoxide reductase msrA 2 OS=Staphylococcus aureus (strain N315) GN=msrA2 PE=1 SV=1	P65446|MSRA2_STAAN	-1.5
352	SA1243 protein OS=Staphylococcus aureus (strain N315) GN=SA1243 PE=4 SV=1	Q7A5N5|Q7A5N5_STAAN	-1.5
374	SA0758 protein OS=Staphylococcus aureus (strain N315) GN=SA0758 PE=4 SV=1	Q7A6M7|Q7A6M7_STAAN	-1.5
401	Mannitol-specific phosphotransferase enzyme IIA component OS=Staphylococcus aureus (strain N315) GN=mtlF PE=3 SV=2	P0A0D8|PTMA_STAAN	-1.5

403	Dephospho-CoA kinase OS=Staphylococcus aureus (strain N315) GN=coaE PE=1 SV=1	P63831|COAE_STAAN	-1.5
428	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase OS=Staphylococcus aureus (strain N315) GN=murF PE=3 SV=1	Q7A4F9|Q7A4F9_STAAN	-1.5
449	(Dimethylallyl)adenosine tRNA methylthiotransferase miaB OS=Staphylococcus aureus (strain N315) GN=miaB PE=1 SV=1	Q7A5W3|MIAB_STAAN	-1.5
508	RNA polymerase sigma factor rpoD OS=Staphylococcus aureus (strain N315) GN=rpoD PE=1 SV=1	Q99TT5|RPOD_STAAN	-1.5
517	Conserved virulence factor B OS=Staphylococcus aureus (strain N315) GN=cvfB PE=1 SV=1	Q7A5Q1|CVFB_STAAN	-1.5
557	UPF0312 protein SA2479 OS=Staphylococcus aureus (strain N315) GN=SA2479 PE=1 SV=1	Q7A339|Y2479_STAAN	-1.5
699	GMP reductase OS=Staphylococcus aureus (strain N315) GN=guaC PE=1 SV=1	P60563|GUAC_STAAN	-1.5
761	Methicillin resistance mecR1 protein OS=Staphylococcus aureus (strain N315) GN=mecR1 PE=1 SV=1	P0A0B0|MECR_STAAN	-1.5
769	SA0777 protein OS=Staphylococcus aureus (strain N315) GN=SA0777 PE=4 SV=1	Q7A6L5|Q7A6L5_STAAN	-1.5
21	Glyceraldehyde-3-phosphate dehydrogenase 1 (gapA1)	P99136|G3P1_STAAN	-1.4
109	Phosphoenolpyruvate-protein phosphotransferase OS=Staphylococcus aureus (strain N315) GN=ptsI PE=1 SV=1	Q99V14|PT1_STAAN	-1.4
110	Putative uncharacterized protein SA1698 OS=Staphylococcus aureus (strain N315) GN=SA1698 PE=4 SV=1	Q7A4S0|Q7A4S0_STAAN	-1.4
118	Putative uncharacterized protein SA0775 OS=Staphylococcus aureus (strain N315) GN=SA0775 PE=4 SV=1	Q7A6L6|Q7A6L6_STAAN	-1.4
154	Serine hydroxymethyltransferase OS=Staphylococcus aureus (strain N315) GN=glyA PE=1 SV=1	P99091|GLYA_STAAN	-1.4
191	SA1549 protein OS=Staphylococcus aureus (strain N315) GN=SA1549 PE=4 SV=1	Q7A538|Q7A538_STAAN	-1.4
237	50S ribosomal protein L30 OS=Staphylococcus aureus (strain N315) GN=rpmD PE=1 SV=1	RL30_STAAN (+1)	-1.4
262	50S ribosomal protein L16 OS=Staphylococcus aureus (strain N315) GN=rplP PE=1 SV=1	Q7A461|RL16_STAAN	-1.4
265	Alanyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=alaS PE=1 SV=1	P67011|SYA_STAAN	-1.4
292	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C OS=Staphylococcus aureus (strain N315) GN=gatC PE=1 SV=1	P68808|GATC_STAAN	-1.4
315	Signal transduction protein TRAP OS=Staphylococcus aureus (strain N315) GN=traP PE=1 SV=1	Q7A4W3|TRAP_STAAN	-1.4
319	Acetate-CoA ligase OS=Staphylococcus aureus (strain N315) GN=SA2402 PE=4 SV=1	Q7A3A2|Q7A3A2_STAAN	-1.4
343	DNA-directed RNA polymerase subunit omega OS=Staphylococcus aureus (strain N315) GN=rpoZ PE=1 SV=1	P66726|RPOZ_STAAN	-1.4
388	Putative uncharacterized protein SAS040 OS=Staphylococcus aureus (strain N315) GN=SA1154.1 PE=4 SV=1	Q7A5U6|Q7A5U6_STAAN	-1.4
418	UPF0637 protein SA0957 OS=Staphylococcus aureus (strain N315) GN=SA0957 PE=1 SV=1	Q99UZ6|Y957_STAAN	-1.4
447	Branched-chain alpha-keto acid dehydrogenase E1 OS=Staphylococcus aureus (strain N315) GN=bfmBAB PE=4 SV=1	Q7A5F8|Q7A5F8_STAAN	-1.4
489	Lipase 1 OS=Staphylococcus aureus (strain N315) GN=lip1 PE=3 SV=2	P65289|LIP1_STAAN	-1.4
492	Organic hydroperoxide resistance protein-like OS=Staphylococcus aureus (strain N315) GN=SA0755 PE=1 SV=1	Q7A6M9|OHRL_STAAN	-1.4
501	Methionine aminopeptidase OS=Staphylococcus aureus (strain N315) GN=map PE=1 SV=1	P99121|AMPM_STAAN	-1.4
43	Glycyl-tRNA synthetase (glyQS)	P99129|SYG_STAAN	-1.3
87	UPF0457 protein SA1975.1 (SA1975.1)	Q99S93|Y197A_ST	-1.3

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95	Cell-division protein OS=Staphylococcus aureus (strain N315) GN=ftsH PE=4 SV=1	Q7A7A5|Q7A7A5_STAAN	-1.3
117	Putative uncharacterized protein SAS030 OS=Staphylococcus aureus (strain N315) GN=SA0930.1 PE=4 SV=1	Q7A690|Q7A690_STAAN	-1.3
123	Putative uncharacterized protein SA1671 OS=Staphylococcus aureus (strain N315) GN=SA1671 PE=1 SV=1	Q7A4U5|Q7A4U5_STAAN	-1.3
132	Foldase protein prsA OS=Staphylococcus aureus (strain N315) GN=prsA PE=1 SV=1	P60748|PRSA_STAAN	-1.3
155	Alkyl hydroperoxide reductase subunit F OS=Staphylococcus aureus (strain N315) GN=ahpF PE=1 SV=1	P99118|AHPF_STAAN	-1.3
168	Uncharacterized hydrolase SA2367 OS=Staphylococcus aureus (strain N315) GN=SA2367 PE=1 SV=1	Q7A3C4|Y2367_STAAN	-1.3
190	Translation initiation factor IF-1 OS=Staphylococcus aureus (strain N315) GN=infA PE=1 SV=1	P65119|IF1_STAAN	-1.3
194	SA2095 protein OS=Staphylococcus aureus (strain N315) GN=SA2095 PE=4 SV=1	Q7A420|Q7A420_STAAN	-1.3
203	3-oxoacyl-[acyl-carrier-protein] reductase OS=Staphylococcus aureus (strain N315) GN=fabG PE=1 SV=1	P99093|FABG_STAAN	-1.3
227	Adenylate kinase OS=Staphylococcus aureus (strain N315) GN=adk PE=1 SV=1	P99062|KAD_STAAN	-1.3
255	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Staphylococcus aureus (strain N315) GN=odhB PE=1 SV=1	Q7A5N4|ODO2_STAAN	-1.3
338	Probable uridylyltransferase SA1974 OS=Staphylococcus aureus (strain N315) GN=SA1974 PE=1 SV=1	Q7A4A4|URTF_STAAN	-1.3
373	Elongation factor P OS=Staphylococcus aureus (strain N315) GN=efp PE=1 SV=1	P99066|EFP_STAAN	-1.3
382	Staphopain A OS=Staphylococcus aureus (strain N315) GN=sspP PE=3 SV=1	P65826|SSPP_STAAN	-1.3
402	HTH-type transcriptional regulator sarR OS=Staphylococcus aureus (strain N315) GN=sarR PE=1 SV=3	Q7A425|SARR_STAAN	-1.3
435	50S ribosomal protein L33 1 OS=Staphylococcus aureus (strain N315) GN=rpmG1 PE=3 SV=1	P66228|RL331_STAAN	-1.3
440	Hit-like protein involved in cell-cycle regulation OS=Staphylococcus aureus (strain N315) GN=hit PE=4 SV=1	Q7A4W0|Q7A4W0_STAAN	-1.3
505	Putative uncharacterized protein SAS027 OS=Staphylococcus aureus (strain N315) GN=SA0884.1 PE=4 SV=1	Q7A6C4|Q7A6C4_STAAN	-1.3
556	Cold shock protein cspB OS=Staphylococcus aureus (strain N315) GN=cspB PE=3 SV=1	Q7A326|Q7A326_STAAN	-1.3
633	Uncharacterized protein SA1186 OS=Staphylococcus aureus (strain N315) GN=SA1186 PE=1 SV=1	Q7A5S4|Y1186_STAAN	-1.3
5	DNA-binding protein HU (hup)	Q7A5J1|DBH_STAAN	-1.2
14	30S ribosomal protein S1 (rpsA)	Q7A5J0|RS1_STAAN	-1.2
37	Thioredoxin (trxA)	P99122|THIO_STAAN	-1.2
81	SA0774 protein (SA0774)	Q7A6L7|Q7A6L7_STAAN	-1.2
124	Polyribonucleotide nucleotidyltransferase OS=Staphylococcus aureus (strain N315) GN=pnp PE=1 SV=1	Q7A5X7|PNP_STAAN	-1.2
177	2-oxoglutarate dehydrogenase E1 component OS=Staphylococcus aureus (strain N315) GN=odhA PE=1 SV=1	Q99U74|ODO1_STAAN	-1.2
207	Methionyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=metG PE=1 SV=1	P67579|SYM_STAAN	-1.2
297	Regulatory protein msrR OS=Staphylococcus aureus (strain N315) GN=msrR PE=1 SV=1	Q99Q02|MSRR_STAAN	-1.2

351	Glucose-6-phosphate 1-dehydrogenase OS=Staphylococcus aureus (strain N315) GN=SA1336 PE=3 SV=1	Q7A5G7|Q7A5G7_STAAN	-1.2
375	NH(3)-dependent NAD(+) synthetase OS=Staphylococcus aureus (strain N315) GN=nadE PE=1 SV=1	P99150|NADE_STAAN	-1.2
430	Peptide methionine sulfoxide reductase msrB OS=Staphylococcus aureus (strain N315) GN=msrB PE=1 SV=1	P99065|MSRB_STAAN	-1.2
443	Redox-sensing transcriptional repressor rex OS=Staphylococcus aureus (strain N315) GN=rex PE=3 SV=1	P60386|REX_STAAN	-1.2
543	Chromosome segregation SMC protein OS=Staphylococcus aureus (strain N315) GN=smc PE=4 SV=1	Q7A5Z2|Q7A5Z2_STAAN	-1.2
136	Putative uncharacterized protein SA0570 OS=Staphylococcus aureus (strain N315) GN=SA0570 PE=4 SV=1	Q7A735|Q7A735_STAAN	-1.1
295	Malonyl CoA-acyl carrier protein transacylase OS=Staphylococcus aureus (strain N315) GN=fabD PE=1 SV=1	Q7A5Z3|FABD_STAAN	-1.1
301	Transcription elongation factor greA OS=Staphylococcus aureus (strain N315) GN=greA PE=1 SV=1	P99156|GREA_STAAN	-1.1
344	30S ribosomal protein S19 OS=Staphylococcus aureus (strain N315) GN=rpsS PE=1 SV=1	P66494|RS19_STAAN	-1.1
348	Probable cysteine desulfurase OS=Staphylococcus aureus (strain N315) GN=csd PE=1 SV=1	P99177|CSD_STAAN	-1.1
359	S-ribosylhomocysteine lyase OS=Staphylococcus aureus (strain N315) GN=luxS PE=1 SV=1	P65330|LUXS_STAAN	-1.1
368	Probable glycine dehydrogenase [decarboxylating] subunit 2 OS=Staphylococcus aureus (strain N315) GN=gcvPB PE=1 SV=1	P99168|GCSPB_STAAN	-1.1
464	SA1035 protein OS=Staphylococcus aureus (strain N315) GN=SA1035 PE=1 SV=1	Q7A612|Q7A612_STAAN	-1.1
465	Putative uncharacterized protein SA2262 OS=Staphylococcus aureus (strain N315) GN=SA2262 PE=4 SV=1	Q7A3M3|Q7A3M3_STAAN	-1.1
526	Low molecular weight protein-tyrosine-phosphatase ptpA OS=Staphylococcus aureus (strain N315) GN=ptpA PE=1 SV=1	Q7A4S1|PTPA_STAAN	-1.1
550	Probable transglycosylase sceD OS=Staphylococcus aureus (strain N315) GN=sceD PE=2 SV=1	Q7A4F2|SCED_STAAN	-1.1
578	OppF protein OS=Staphylococcus aureus (strain N315) GN=oppF PE=4 SV=1	Q7A6F3|Q7A6F3_STAAN	-1.1
618	3-phosphoshikimate 1-carboxyvinyltransferase OS=Staphylococcus aureus (strain N315) GN=aroA PE=1 SV=1	P63585|AROA_STAAN	-1.1
620	SA1475 protein OS=Staphylococcus aureus (strain N315) GN=SA1475 PE=4 SV=1	Q7A581|Q7A581_STAAN	-1.1
646	Aminomethyltransferase OS=Staphylococcus aureus (strain N315) GN=gcvT PE=1 SV=1	P64225|GCST_STAAN	-1.1
4	UPF0337 protein SA0772 (SA0772)	Q7A6L9|Y772_STAAN	-1
41	Acyl carrier protein (acpP)	P0A002|ACP_STAAN	-1
46	Uncharacterized leukocidin-like protein 2 (SA1813)	Q99SN7|LUKL2_STAAN	-1
89	Probable manganese-dependent inorganic pyrophosphatase (ppaC)	P65753|PPAC_STAAN	-1
185	50S ribosomal protein L11 OS=Staphylococcus aureus (strain N315) GN=rplK PE=1 SV=2	P0A0F2|RL11_STAAN	-1
442	Homoserine dehydrogenase OS=Staphylococcus aureus (strain N315) GN=dhoM PE=3 SV=1	Q7A5T6|Q7A5T6_STAAN	-1
467	Cysteinyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=cysS PE=1 SV=1	Q99W73|SYC_STAAN	-1
504	Bla regulator protein blaR1 OS=Staphylococcus aureus (strain N315) GN=blaR1 PE=4 SV=1	Q9AC79|Q9AC79_STAAN	-1
523	FMN-dependent NADPH-azoreductase OS=Staphylococcus aureus (strain N315) GN=azo1 PE=1 SV=1	Q7A782|AZO1_STAAN	-1
548	tRNA uridine 5-carboxymethylaminomethyl modification enzyme mnmG	P64230|MNMG_S	-1

	OS=Staphylococcus aureus (strain N315) GN=mnmG PE=1 SV=1	TAAN	
613	UPF0447 protein SA0544 OS=Staphylococcus aureus (strain N315) GN=SA0544 PE=1 SV=1	Q7A759|Y544_STAAN	-1
716	Putative trmH family tRNA/rRNA methyltransferase OS=Staphylococcus aureus (strain N315) GN=SA0490 PE=1 SV=1	Q7A794|TRMHL_STAAN	-1
746	UPF0154 protein SA1178 OS=Staphylococcus aureus (strain N315) GN=SA1178 PE=1 SV=1	P67291|Y1178_STAAN	-1
750	SA0605 protein OS=Staphylococcus aureus (strain N315) GN=SA0605 PE=4 SV=1	Q7A701|Q7A701_STAAN	-1
8	Alkaline shock protein 23 (asp23)	P99157|ASP23_STAAN	-0.9
111	50S ribosomal protein L27 OS=Staphylococcus aureus (strain N315) GN=rpmA PE=1 SV=1	P66133|RL27_STAAN	-0.9
112	SA2327 protein OS=Staphylococcus aureus (strain N315) GN=SA2327 PE=4 SV=1	Q7A3G3|Q7A3G3_STAAN	-0.9
163	ATP-dependent Clp protease ATP-binding subunit clpC OS=Staphylococcus aureus (strain N315) GN=clpC PE=1 SV=1	Q7A797|CLPC_STAAN	-0.9
192	3-hexulose-6-phosphate synthase OS=Staphylococcus aureus (strain N315) GN=SA0528 PE=1 SV=1	Q7A774|HPS_STAAN	-0.9
246	Valyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=valS PE=1 SV=1	Q99TJ8|SYV_STAAN	-0.9
310	Probable glycine dehydrogenase [decarboxylating] subunit 1 OS=Staphylococcus aureus (strain N315) GN=gcvPA PE=1 SV=1	P64218|GCSPA_STAAN	-0.9
380	Ribonucleoside-diphosphate reductase minor subunit OS=Staphylococcus aureus (strain N315) GN=nrdF PE=4 SV=1	Q7A6T1|Q7A6T1_STAAN	-0.9
490	SA1558 protein OS=Staphylococcus aureus (strain N315) GN=SA1558 PE=4 SV=1	Q7A533|Q7A533_STAAN	-0.9
522	Probable ctpA-like serine protease OS=Staphylococcus aureus (strain N315) GN=SA1253 PE=1 SV=1	Q7A5M9|CTPAL_STAAN	-0.9
527	Putative uncharacterized protein SA0936 OS=Staphylococcus aureus (strain N315) GN=SA0936 PE=4 SV=1	Q7A686|Q7A686_STAAN	-0.9
600	Putative uncharacterized protein SA1293 OS=Staphylococcus aureus (strain N315) GN=SA1293 PE=4 SV=1	Q7A5J9|Q7A5J9_STAAN	-0.9
766	Threonine synthase OS=Staphylococcus aureus (strain N315) GN=thrC PE=4 SV=1	Q7A5T5|Q7A5T5_STAAN	-0.9
97	Phosphoenolpyruvate carboxykinase [ATP] OS=Staphylococcus aureus (strain N315) GN=pckA PE=1 SV=1	P99128|PCKA_STAAN	-0.8
189	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase 2 OS=Staphylococcus aureus (strain N315) GN=ispD2 PE=1 SV=1	Q7A7V0|ISPD2_STAAN	-0.8
405	Cold-shock protein C OS=Staphylococcus aureus (strain N315) GN=cspC PE=3 SV=1	Q7A6P1|Q7A6P1_STAAN	-0.8
422	Glucose-specific phosphotransferase enzyme IIA component OS=Staphylococcus aureus (strain N315) GN=crr PE=1 SV=1	P60857|PTGA_STAAN	-0.8
478	ATP-binding cassette transporter A OS=Staphylococcus aureus (strain N315) GN=SA0599 PE=4 SV=1	Q7A708|Q7A708_STAAN	-0.8
623	Iron-regulated ABC transporter siderophore-binding protein SirA OS=Staphylococcus aureus (strain N315) GN=sirA PE=4 SV=1	Q7A869|Q7A869_STAAN	-0.8
135	Transcriptional regulator sarA OS=Staphylococcus aureus (strain N315) GN=sarA PE=1 SV=3	Q7A732|SARA_STAAN	-0.7
206	General stress protein 20U OS=Staphylococcus aureus (strain N315) GN=dps PE=3 SV=1	Q7A4C8|Q7A4C8_STAAN	-0.7
212	Uncharacterized protein SA0707 OS=Staphylococcus aureus (strain N315) GN=SA0707 PE=1 SV=1	Q7A6R6|Y707_STAAN	-0.7
303	UPF0082 protein SA0624 OS=Staphylococcus aureus (strain N315) GN=SA0624 PE=1 SV=1	P67182|Y624_STAAN	-0.7
532	Penicillin-binding protein 1 OS=Staphylococcus aureus (strain N315) GN=pbpA PE=4 SV=1	Q7A619|Q7A619_STAAN	-0.7
602	Putative uncharacterized protein SA1593 OS=Staphylococcus aureus (strain N315) GN=SA1593 PE=4 SV=1	Q99T94|Q99T94_STAAN	-0.7

711	Putative uncharacterized protein SA2221 OS=Staphylococcus aureus (strain N315) GN=SA2221 PE=4 SV=1	Q7A3R1|Q7A3R1_STAAN	-0.7
712	Aminopeptidase ampS OS=Staphylococcus aureus (strain N315) GN=ampS PE=4 SV=1	Q7A4S3|Q7A4S3_STAAN	-0.7
717	Na(+)/H(+) antiporter subunit E1 OS=Staphylococcus aureus (strain N315) GN=mnhE1 PE=1 SV=1	P60689|MNHE1_STAAN	-0.7
153	Isoleucyl-tRNA synthetase OS=Staphylococcus aureus (strain N315) GN=ileS PE=1 SV=1	P67509|SYI_STAAN	-0.6
158	Putative uncharacterized protein SA1573 OS=Staphylococcus aureus (strain N315) GN=SA1573 PE=4 SV=1	Q7A521|Q7A521_STAAN	-0.6
169	Probable DEAD-box ATP-dependent RNA helicase SA1885 OS=Staphylococcus aureus (strain N315) GN=SA1885 PE=1 SV=1	Q7A4G0|Y1885_STAAN	-0.6
289	Superoxide dismutase [Mn/Fe] 1 OS=Staphylococcus aureus (strain N315) GN=sodA PE=1 SV=1	P99098|SODM1_STAAN	-0.6
367	SA0691 protein OS=Staphylococcus aureus (strain N315) GN=SA0691 PE=4 SV=1	Q7A6S7|Q7A6S7_STAAN	-0.6
448	Epimerase family protein SA0724 OS=Staphylococcus aureus (strain N315) GN=SA0724 PE=1 SV=1	Q7A6Q5|Y724_STAAN	-0.6
476	SA1563 protein OS=Staphylococcus aureus (strain N315) GN=SA1563 PE=1 SV=1	Q7A529|Q7A529_STAAN	-0.6
705	Putative uncharacterized protein SA0711 OS=Staphylococcus aureus (strain N315) GN=SA0711 PE=4 SV=1	Q7A6R2|Q7A6R2_STAAN	-0.6
187	Cell cycle protein gpsB OS=Staphylococcus aureus (strain N315) GN=gpsB PE=1 SV=1	Q7A5L1|GPSB_STAAN	-0.5
284	Superoxide dismutase [Mn/Fe] 2 OS=Staphylococcus aureus (strain N315) GN=sodM PE=1 SV=1	P66831|SODM2_STAAN	-0.5
479	Aminoacyltransferase femA OS=Staphylococcus aureus (strain N315) GN=femA PE=1 SV=1	Q7A5R3|FEMA_STAAN	-0.5
482	HTH-type transcriptional regulator sarS OS=Staphylococcus aureus (strain N315) GN=sarS PE=1 SV=1	Q7A872|SARS_STAAN	-0.5
582	Putative uncharacterized protein SA0695 OS=Staphylococcus aureus (strain N315) GN=SA0695 PE=4 SV=1	Q7A6S4|Q7A6S4_STAAN	-0.5
625	SA0422 protein OS=Staphylococcus aureus (strain N315) GN=SA0422 PE=4 SV=1	Q7A7E1|Q7A7E1_STAAN	-0.5
715	Peptide deformylase OS=Staphylococcus aureus (strain N315) GN=def PE=1 SV=1	P99077|DEF_STAAN	-0.5
271	FMN-dependent NADH-azoreductase OS=Staphylococcus aureus (strain N315) GN=azoR PE=1 SV=1	Q99X11|AZOR_STAAN	-0.4
552	Lytic regulatory protein truncated with Tn554 OS=Staphylococcus aureus (strain N315) GN=truncated-SA PE=4 SV=1	Q99SB2|Q99SB2_STAAN	-0.4
553	Clumping factor A OS=Staphylococcus aureus (strain N315) GN=clfA PE=1 SV=1	Q99VJ4|CLFA_STAAN	-0.4
20	Chaperone protein dnaK (dnaK)	P99110|DNAK_STAAN	-0.3
321	Hydroxamate siderophore binding lipoprotein OS=Staphylococcus aureus (strain N315) GN=fhuD2 PE=4 SV=1	Q7A433|Q7A433_STAAN	-0.3
664	Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase trmFO OS=Staphylococcus aureus (strain N315) GN=trmFO PE=1 SV=1	P64235|TRMFO_STAAN	-0.3
752	Putative uncharacterized protein SA2267 OS=Staphylococcus aureus (strain N315) GN=SA2267 PE=4 SV=1	Q99RF4|Q99RF4_STAAN	-0.3
765	Putative uncharacterized protein SA1957 OS=Staphylococcus aureus (strain N315) GN=SA1957 PE=4 SV=1	Q7A4B6|Q7A4B6_STAAN	-0.2
31	SA2437 protein (SA2437)	Q7A371|Q7A371_STAAN	-0.1
216	SA1979 protein OS=Staphylococcus aureus (strain N315) GN=SA1979 PE=1 SV=1	Q7A499|Q7A499_STAAN	-0.1
288	2',3'-cyclic-nucleotide 2'-phosphodiesterase OS=Staphylococcus aureus (strain N315) GN=cvfA PE=1 SV=1	P67278|CNPD_STAAN	-0.1
444	Anti repressor OS=Staphylococcus aureus (strain N315) GN=SA1801 PE=4 SV=1	Q99SP8|Q99SP8_S	-0.1

		TAAN	
545	Putative uncharacterized protein SA1274 OS=Staphylococcus aureus (strain N315) GN=SA1274 PE=4 SV=1	Q7A5L6|Q7A5L6_STAAN	-0.1
22	Probable transglycosylase isaA (isaA)	P99160|ISAA_STAAN	0
735	Heme-degrading monooxygenase isdI OS=Staphylococcus aureus (strain N315) GN=isdI PE=1 SV=1	Q7A827|ISDI_STAAN	0
275	UPF0435 protein SA1696 OS=Staphylococcus aureus (strain N315) GN=SA1696 PE=1 SV=1	Q7A4S2|Y1696_STAAN	0.1
575	Putative uncharacterized protein SA0943 OS=Staphylococcus aureus (strain N315) GN=SA0943 PE=4 SV=1	Q7A681|Q7A681_STAAN	0.1
708	SA1343 protein OS=Staphylococcus aureus (strain N315) GN=SA1343 PE=4 SV=1	Q7A5G2|Q7A5G2_STAAN	0.1
325	6,7-dimethyl-8-ribityllumazine synthase OS=Staphylococcus aureus (strain N315) GN=ribH PE=1 SV=1	P99141|RISB_STAAN	0.2
15	Elongation factor Ts (tsf)	P99171|EFTS_STAAN	0.4
218	50S ribosomal protein L25 OS=Staphylococcus aureus (strain N315) GN=rplY PE=1 SV=1	Q7A7B3|RL25_STAAN	0.4
52	Putative uncharacterized protein SAS049 (SA1451.1)	Q7A594|Q7A594_STAAN	0.5
63	Putative uncharacterized protein SA2323 (SA2323)	Q7A3G7|Q7A3G7_STAAN	0.5
259	UPF0337 protein SA1452 OS=Staphylococcus aureus (strain N315) GN=SA1452 PE=1 SV=1	Q7A593|Y1452_STAAN	0.7
355	GTP cyclohydrolase folE2 OS=Staphylococcus aureus (strain N315) GN=folE2 PE=1 SV=1	Q7A777|GCH4_STAAN	0.8
547	Delta-hemolysin OS=Staphylococcus aureus (strain N315) GN=hld PE=1 SV=2	P0A0M2|HLD_STAAN	0.8
240	SA0246 protein OS=Staphylococcus aureus (strain N315) GN=SA0246 PE=4 SV=1	Q7A7U9|Q7A7U9_STAAN	No Values
312	UDP-N-acetylmuramate--L-alanine ligase OS=Staphylococcus aureus (strain N315) GN=murC PE=1 SV=1	P65475|MURC_STAAN	No Values
353	Pseudouridine synthase OS=Staphylococcus aureus (strain N315) GN=SA1040 PE=3 SV=1	Q7A610|Q7A610_STAAN	No Values
385	Probable cytosol aminopeptidase OS=Staphylococcus aureus (strain N315) GN=ampA PE=4 SV=1	Q7A6J3|Q7A6J3_STAAN	No Values
396	Aldehyde dehydrogenase OS=Staphylococcus aureus (strain N315) GN=aldH PE=4 SV=1	Q7A4P5|Q7A4P5_STAAN	No Values
407	Fumarate hydratase class II OS=Staphylococcus aureus (strain N315) GN=fumC PE=1 SV=1	P64173|FUMC_STAAN	No Values
416	Putative uncharacterized protein SA0908 OS=Staphylococcus aureus (strain N315) GN=SA0908 PE=4 SV=1	Q7A6A3|Q7A6A3_STAAN	No Values
424	Bleomycin resistance protein OS=Staphylococcus aureus (strain N315) GN=ble PE=1 SV=2	Q7A8D1|BLE_STAAN	No Values
425	Protein grpE OS=Staphylococcus aureus (strain N315) GN=grpE PE=1 SV=1	P99086|GRPE_STAAN	No Values
434	Putative uncharacterized protein SAS010 OS=Staphylococcus aureus (strain N315) GN=SA0359.1 PE=4 SV=1	Q7A7J7|Q7A7J7_STAAN	No Values
453	Exodeoxyribonuclease 7 small subunit OS=Staphylococcus aureus (strain N315) GN=xseB PE=3 SV=1	P67461|EX7S_STAAN	No Values
456	Serine-aspartate repeat-containing protein D OS=Staphylococcus aureus (strain N315) GN=sdrD PE=1 SV=1	Q7A780|SDRD_STAAN	No Values
460	Putative uncharacterized protein SA1277 OS=Staphylococcus aureus (strain N315) GN=SA1277 PE=4 SV=1	Q7A5L3|Q7A5L3_STAAN	No Values
468	50S ribosomal protein L15 OS=Staphylococcus aureus (strain N315) GN=rplO PE=1 SV=1	P0A0F6|RL15_STAAN	No Values
471	30S ribosomal protein S15 OS=Staphylococcus aureus (strain N315) GN=rpsO PE=1 SV=1	Q7A5X8|RS15_STAAN	No Values

497	Methionine import ATP-binding protein MetN 2 OS=Staphylococcus aureus (strain N315) GN=metN2 PE=1 SV=1	Q7A6M2|METN2_STAAN	No Values
498	Putative uncharacterized protein SA1363 OS=Staphylococcus aureus (strain N315) GN=SA1363 PE=4 SV=1	Q7A5E8|Q7A5E8_STAAN	No Values
502	SA0182 protein OS=Staphylococcus aureus (strain N315) GN=SA0182 PE=1 SV=1	Q7A808|Q7A808_STAAN	No Values
510	SA1559 protein OS=Staphylococcus aureus (strain N315) GN=SA1559 PE=4 SV=1	Q7A532|Q7A532_STAAN	No Values
513	Protein kinase OS=Staphylococcus aureus (strain N315) GN=SA1063 PE=4 SV=1	Q7A5Z8|Q7A5Z8_STAAN	No Values
516	SA2140 protein OS=Staphylococcus aureus (strain N315) GN=SA2140 PE=4 SV=1	Q7A3Y2|Q7A3Y2_STAAN	No Values
518	3-methyl-2-oxobutanoate hydroxymethyltransferase OS=Staphylococcus aureus (strain N315) GN=panB PE=1 SV=1	P65656|PANB_STAAN	No Values
525	ATP synthase epsilon chain OS=Staphylococcus aureus (strain N315) GN=atpC PE=1 SV=1	P63665|ATPE_STAAN	No Values
528	SA2346 protein OS=Staphylococcus aureus (strain N315) GN=SA2346 PE=4 SV=1	Q7A3E4|Q7A3E4_STAAN	No Values
529	Uncharacterized protein SA0370 OS=Staphylococcus aureus (strain N315) GN=SA0370 PE=1 SV=1	P60855|Y370_STAAN	No Values
531	Coenzyme A disulfide reductase OS=Staphylococcus aureus (strain N315) GN=cdr PE=1 SV=3	Q7A6H1|CDR_STAAN	No Values
533	Molybdopterin molybdenumtransferase OS=Staphylococcus aureus (strain N315) GN=moeA PE=1 SV=1	P99139|MOEA_STAAN	No Values
535	Putative uncharacterized protein SA1031 OS=Staphylococcus aureus (strain N315) GN=SA1031 PE=3 SV=1	Q7A616|Q7A616_STAAN	No Values
537	SA1121 protein OS=Staphylococcus aureus (strain N315) GN=SA1121 PE=3 SV=1	Q7A5X4|Q7A5X4_STAAN	No Values
538	Putative uncharacterized protein SA2160 OS=Staphylococcus aureus (strain N315) GN=SA2160 PE=4 SV=1	Q7A3W3|Q7A3W3_STAAN	No Values
541	Adenine phosphoribosyltransferase OS=Staphylococcus aureus (strain N315) GN=apt PE=1 SV=1	P68779|APT_STAAN	No Values
542	SA1311 protein OS=Staphylococcus aureus (strain N315) GN=SA1311 PE=4 SV=1	Q7A5I7|Q7A5I7_STAAN	No Values
546	SA2434 protein OS=Staphylococcus aureus (strain N315) GN=SA2434 PE=4 SV=1	Q7A374|Q7A374_STAAN	No Values
558	SA2332 protein OS=Staphylococcus aureus (strain N315) GN=SA2332 PE=4 SV=1	Q7A3F8|Q7A3F8_STAAN	No Values
561	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase OS=Staphylococcus aureus (strain N315) GN=dapH PE=3 SV=1	Q7A5P7|DAPH_STAAN	No Values
566	TelA-like protein SA1238 OS=Staphylococcus aureus (strain N315) GN=SA1238 PE=1 SV=1	P60108|TELL_STAAN	No Values
567	Putative uncharacterized protein SA2374 OS=Staphylococcus aureus (strain N315) GN=SA2374 PE=4 SV=1	Q7A3B7|Q7A3B7_STAAN	No Values
571	Putative uncharacterized protein SA0721 OS=Staphylococcus aureus (strain N315) GN=SA0721 PE=4 SV=1	Q7A6Q7|Q7A6Q7_STAAN	No Values
576	Chorismate synthase OS=Staphylococcus aureus (strain N315) GN=aroC PE=3 SV=1	P63614|AROC_STAAN	No Values
580	PurR protein OS=Staphylococcus aureus (strain N315) GN=purR PE=4 SV=1	Q7A7B7|Q7A7B7_STAAN	No Values
583	DNA topoisomerase 1 OS=Staphylococcus aureus (strain N315) GN=topA PE=1 SV=1	Q7A5Y5|TOP1_STAAN	No Values
584	SA2200 protein OS=Staphylococcus aureus (strain N315) GN=SA2200 PE=4 SV=1	Q7A3S6|Q7A3S6_STAAN	No Values
590	SA2490 protein OS=Staphylococcus aureus (strain N315) GN=SA2490 PE=1 SV=1	Q7A331|Q7A331_STAAN	No Values
591	Putative uncharacterized protein SA1454 OS=Staphylococcus aureus (strain N315) GN=SA1454 PE=4 SV=1	Q7A591|Q7A591_STAAN	No Values
596	Nucleoside-triphosphatase OS=Staphylococcus aureus (strain N315) GN=SA0998 PE=1	P99094|NTPA_ST	No Values

	SV=1	AAN	
597	Purine nucleoside phosphorylase OS=Staphylococcus aureus (strain N315) GN=deoD PE=1 SV=1	Q7A4C9|Q7A4C9_STAAN	No Values
599	UPF0473 protein SA1443 OS=Staphylococcus aureus (strain N315) GN=SA1443 PE=1 SV=1	Q7A598|Y1443_STAAN	No Values
601	Glycolytic operon regulator OS=Staphylococcus aureus (strain N315) GN=gapR PE=4 SV=1	Q7A6Q3|Q7A6Q3_STAAN	No Values
608	Putative uncharacterized protein SA1405 OS=Staphylococcus aureus (strain N315) GN=SA1405 PE=4 SV=1	Q7A5C4|Q7A5C4_STAAN	No Values
609	Putative uncharacterized protein SA1451 OS=Staphylococcus aureus (strain N315) GN=SA1451 PE=4 SV=1	Q99TM6|Q99TM6_STAAN	No Values
610	Sensor protein srrB OS=Staphylococcus aureus (strain N315) GN=srrB PE=1 SV=2	Q7A5H7|SRRB_STAAN	No Values
611	Phosphoglucomutase OS=Staphylococcus aureus (strain N315) GN=pgcA PE=1 SV=2	PGCA_STAAN	No Values
619	Putative uncharacterized protein SAS054 OS=Staphylococcus aureus (strain N315) GN=SA1692.1 PE=4 SV=1	Q7A4S5|Q7A4S5_STAAN	No Values
626	SA0247 protein OS=Staphylococcus aureus (strain N315) GN=SA0247 PE=4 SV=1	Q7A7U8|Q7A7U8_STAAN	No Values
630	SA2244 protein OS=Staphylococcus aureus (strain N315) GN=SA2244 PE=4 SV=1	Q7A3P2|Q7A3P2_STAAN	No Values
636	UPF0349 protein SA0800 OS=Staphylococcus aureus (strain N315) GN=SA0800 PE=3 SV=1	Q7A6J6|Y800_STAAN	No Values
638	Glycine betaine transporter OS=Staphylococcus aureus (strain N315) GN=opuD PE=4 SV=1	Q99UC9|Q99UC9_STAAN	No Values
639	Glutamate racemase OS=Staphylococcus aureus (strain N315) GN=murI PE=1 SV=1	P63638|MURI_STAAN	No Values
641	Putative uncharacterized protein SA1795 OS=Staphylococcus aureus (strain N315) GN=SA1795 PE=4 SV=1	Q99SQ6|Q99SQ6_STAAN	No Values
642	DNA ligase OS=Staphylococcus aureus (strain N315) GN=ligA PE=3 SV=1	Q7A4Q5|DNLJ_STAAN	No Values
643	SA2498 protein OS=Staphylococcus aureus (strain N315) GN=SA2498 PE=4 SV=1	Q7A321|Q7A321_STAAN	No Values
644	SA0817 protein OS=Staphylococcus aureus (strain N315) GN=SA0817 PE=1 SV=1	Q7A6H9|Q7A6H9_STAAN	No Values
650	SA1566 protein OS=Staphylococcus aureus (strain N315) GN=SA1566 PE=4 SV=1	Q7A526|Q7A526_STAAN	No Values
651	Alpha-D-1,4-glucosidase OS=Staphylococcus aureus (strain N315) GN=malA PE=1 SV=1	Q7A5G5|Q7A5G5_STAAN	No Values
653	Putative uncharacterized protein SA0696 OS=Staphylococcus aureus (strain N315) GN=SA0696 PE=1 SV=1	Q7A6S3|Q7A6S3_STAAN	No Values
654	Putative uncharacterized protein SA0529 OS=Staphylococcus aureus (strain N315) GN=SA0529 PE=4 SV=1	Q7A773|Q7A773_STAAN	No Values
655	SA0165 protein OS=Staphylococcus aureus (strain N315) GN=SA0165 PE=4 SV=1	Q7A821|Q7A821_STAAN	No Values
657	Alanine dehydrogenase 2 OS=Staphylococcus aureus (strain N315) GN=ald2 PE=1 SV=1	Q99TF4|DHA2_STAAN	No Values
658	SA1216 protein OS=Staphylococcus aureus (strain N315) GN=SA1216 PE=4 SV=1	Q7A5Q5|Q7A5Q5_STAAN	No Values
659	UTP--glucose-1-phosphate uridylyltransferase OS=Staphylococcus aureus (strain N315) GN=gtaB PE=1 SV=1	Q7A3J9|GTAB_STAAN	No Values
668	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Staphylococcus aureus (strain N315) GN=glmS PE=1 SV=2	GLMS_STAAN	No Values
676	Bifunctional protein glmU OS=Staphylococcus aureus (strain N315) GN=glmU PE=1 SV=1	Q7A7B4|GLMU_STAAN	No Values
677	SA0229 protein OS=Staphylococcus aureus (strain N315) GN=SA0229 PE=4 SV=1	Q7A7W6|Q7A7W6_STAAN	No Values
678	PTS enzyme II, phosphoenolpyruvate-dependent, trehalose-specific OS=Staphylococcus aureus (strain N315) GN=treP PE=4 SV=1	Q7A7D1|Q7A7D1_STAAN	No Values

681	SA0557 protein OS=Staphylococcus aureus (strain N315) GN=SA0557 PE=4 SV=1	Q7A747|Q7A747_STAAN	No Values
683	SA2170 protein OS=Staphylococcus aureus (strain N315) GN=SA2170 PE=4 SV=1	Q7A3V4|Q7A3V4_STAAN	No Values
684	Transcription-repair-coupling factor OS=Staphylococcus aureus (strain N315) GN=mfd PE=1 SV=1	Q7A7B2|MFD_STAAN	No Values
688	SA0677 protein OS=Staphylococcus aureus (strain N315) GN=SA0677 PE=4 SV=1	Q7A6T8|Q7A6T8_STAAN	No Values
689	SA2248 protein OS=Staphylococcus aureus (strain N315) GN=SA2248 PE=4 SV=1	Q7A3N8|Q7A3N8_STAAN	No Values
690	UDP-N-acetylglucosamine 2-epimerase OS=Staphylococcus aureus (strain N315) GN=mnaA PE=3 SV=1	Q7A4E3|Q7A4E3_STAAN	No Values
692	SA2240 protein OS=Staphylococcus aureus (strain N315) GN=SA2240 PE=3 SV=1	Q7A3P6|Q7A3P6_STAAN	No Values
693	Putative uncharacterized protein SA1966 OS=Staphylococcus aureus (strain N315) GN=SA1966 PE=4 SV=1	Q7A4B0|Q7A4B0_STAAN	No Values
694	Transcriptional repressor nrdR OS=Staphylococcus aureus (strain N315) GN=nrdR PE=3 SV=1	P67316|NRDR_STAAN	No Values
695	Uroporphyrinogen decarboxylase OS=Staphylococcus aureus (strain N315) GN=hemE PE=1 SV=1	P67420|DCUP_STAAN	No Values
696	SA0902 protein OS=Staphylococcus aureus (strain N315) GN=SA0902 PE=3 SV=1	Q7A6A5|Q7A6A5_STAAN	No Values
697	SA2099 protein OS=Staphylococcus aureus (strain N315) GN=SA2099 PE=4 SV=1	Q7A416|Q7A416_STAAN	No Values
702	Pseudouridine synthase OS=Staphylococcus aureus (strain N315) GN=rluB PE=3 SV=1	Q7A5H5|Q7A5H5_STAAN	No Values
707	Putative uncharacterized protein SA0013 OS=Staphylococcus aureus (strain N315) GN=SA0013 PE=4 SV=1	Q7A8E3|Q7A8E3_STAAN	No Values
709	Putative uncharacterized protein SAS032 OS=Staphylococcus aureus (strain N315) GN=SA0959.1 PE=4 SV=1	Q7A670|Q7A670_STAAN	No Values
710	Formimidoylglutamase OS=Staphylococcus aureus (strain N315) GN=hutG PE=1 SV=1	P99158|HUTG_STAAN	No Values
713	Probable GTP-binding protein engB OS=Staphylococcus aureus (strain N315) GN=engB PE=1 SV=1	P64071|ENGB_STAAN	No Values
714	Putative uncharacterized protein SA2298 OS=Staphylococcus aureus (strain N315) GN=SA2298 PE=4 SV=1	Q7A3J0|Q7A3J0_STAAN	No Values
719	Delta-aminolevulinic acid dehydratase OS=Staphylococcus aureus (strain N315) GN=hemB PE=1 SV=1	P64334|HEM2_STAAN	No Values
721	Serine acetyltransferase OS=Staphylococcus aureus (strain N315) GN=cysE PE=1 SV=1	P67765|CYSE_STAAN	No Values
723	SA2436 protein OS=Staphylococcus aureus (strain N315) GN=SA2436 PE=4 SV=1	Q7A372|Q7A372_STAAN	No Values
724	Diacylglycerol kinase OS=Staphylococcus aureus (strain N315) GN=dagK PE=3 SV=1	Q7A4Q8|DAGK_STAAN	No Values
725	Putative uncharacterized protein SA1546 OS=Staphylococcus aureus (strain N315) GN=SA1546 PE=4 SV=1	Q7A541|Q7A541_STAAN	No Values
726	SA1291 protein OS=Staphylococcus aureus (strain N315) GN=SA1291 PE=4 SV=1	Q7A5K1|Q7A5K1_STAAN	No Values
727	Putative uncharacterized protein SA1017 OS=Staphylococcus aureus (strain N315) GN=SA1017 PE=4 SV=1	Q7A623|Q7A623_STAAN	No Values
731	SA0590 protein OS=Staphylococcus aureus (strain N315) GN=SA0590 PE=4 SV=1	Q7A716|Q7A716_STAAN	No Values
732	Protein esaA OS=Staphylococcus aureus (strain N315) GN=esaA PE=3 SV=1	Q7A7S3|ESAA_STAAN	No Values
733	SA0270 protein OS=Staphylococcus aureus (strain N315) GN=SA0270 PE=4 SV=1	Q7A7S5_STAAN (+1)	No Values
734	Ribonuclease R OS=Staphylococcus aureus (strain N315) GN=rnr PE=4 SV=1	Q99VK1|Q99VK1_STAAN	No Values
736	Putative uncharacterized protein SA0447 OS=Staphylococcus aureus (strain N315)	Q7A7C1|Q7A7C1_	No Values

	GN=SA0447 PE=4 SV=1	STAAN	
737	UPF0403 protein SA1261 OS=Staphylococcus aureus (strain N315) GN=SA1261 PE=1 SV=1	Q7A5M6|Y1261_STAAN	No Values
738	Uncharacterized lipoprotein SA2273 OS=Staphylococcus aureus (strain N315) GN=SA2273 PE=1 SV=1	Q7A3L3|Y2273_STAAN	No Values
739	DNA polymerase III polC-type OS=Staphylococcus aureus (strain N315) GN=polC PE=1 SV=1	P63982|DPO3_STAAN	No Values
741	HmrA protein OS=Staphylococcus aureus (strain N315) GN=hmrA PE=4 SV=1	Q99Q45|Q99Q45_STAAN	No Values
742	Putative uncharacterized protein SA2238 OS=Staphylococcus aureus (strain N315) GN=SA2238 PE=4 SV=1	Q99RI2|Q99RI2_STAAN	No Values
743	Queuine tRNA-ribosyltransferase OS=Staphylococcus aureus (strain N315) GN=tgt PE=1 SV=1	P66905|TGT_STAAN	No Values
744	Streptomycin 3"-adenylyltransferase OS=Staphylococcus aureus (strain N315) GN=ant1 PE=1 SV=1	P0A0D1|S3AD_STAAN	No Values
745	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Staphylococcus aureus (strain N315) GN=metE PE=3 SV=1	P65343|METE_STAAN	No Values
748	Glycine betaine/carnitine/choline ABC transporter opuCC OS=Staphylococcus aureus (strain N315) GN=opuCC PE=4 SV=1	Q7A3Q0|Q7A3Q0_STAAN	No Values
749	Putative uncharacterized protein SA2224 OS=Staphylococcus aureus (strain N315) GN=SA2224 PE=4 SV=1	Q7A3Q8|Q7A3Q8_STAAN	No Values
751	SA0530 protein OS=Staphylococcus aureus (strain N315) GN=SA0530 PE=4 SV=1	Q7A772|Q7A772_STAAN	No Values
753	Putative uncharacterized protein SA1403 OS=Staphylococcus aureus (strain N315) GN=SA1403 PE=4 SV=1	Q99TS2|Q99TS2_STAAN	No Values
756	Ribosomal RNA small subunit methyltransferase G OS=Staphylococcus aureus (strain N315) GN=rsmG PE=3 SV=1	P64240|RSMG_STAAN	No Values
757	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta OS=Staphylococcus aureus (strain N315) GN=accD PE=1 SV=1	Q7A557|ACCD_STAAN	No Values
758	Porphobilinogen deaminase OS=Staphylococcus aureus (strain N315) GN=hemC PE=1 SV=1	P64341|HEM3_STAAN	No Values
760	Peptide methionine sulfoxide reductase msrA 1 OS=Staphylococcus aureus (strain N315) GN=msrA1 PE=1 SV=1	P0A082|MSRA1_STAAN	No Values
762	Glycine betaine aldehyde dehydrogenase gbsA OS=Staphylococcus aureus (strain N315) GN=gbsA PE=4 SV=1	Q7A399|Q7A399_STAAN	No Values
763	Preprotein translocase subunit secY OS=Staphylococcus aureus (strain N315) GN=secY PE=1 SV=1	Q7A468|SECY_STAAN	No Values
764	Putative uncharacterized protein SA1985 OS=Staphylococcus aureus (strain N315) GN=SA1985 PE=4 SV=1	Q7A494|Q7A494_STAAN	No Values
768	Putative uncharacterized protein SA1018 OS=Staphylococcus aureus (strain N315) GN=SA1018 PE=4 SV=1	Q7A622|Q7A622_STAAN	No Values
772	Serine-aspartate repeat-containing protein E OS=Staphylococcus aureus (strain N315) GN=sdrE PE=1 SV=1	Q99W46|SDRE_STAAN	No Values
773	Peptidase T OS=Staphylococcus aureus (strain N315) GN=pepT PE=3 SV=1	P65806|PEPT_STAAN	No Values
775	DNA topoisomerase 3 OS=Staphylococcus aureus (strain N315) GN=topB PE=3 SV=1	Q7A455|TOP3_STAAN	No Values
776	Ferredoxin--NADP reductase OS=Staphylococcus aureus (strain N315) GN=SA2162 PE=1 SV=2	Q7A3W1|FENR_STAAN	No Values
777	SA0849 protein OS=Staphylococcus aureus (strain N315) GN=SA0849 PE=4 SV=1	Q7A6F2|Q7A6F2_STAAN	No Values
779	SA2194 protein OS=Staphylococcus aureus (strain N315) GN=SA2194 PE=3 SV=1	Q7A3T2|RANDOM_Q7A3T2_STAAN-R	No Values
780	Putative uncharacterized protein SA0673 OS=Staphylococcus aureus (strain N315) GN=SA0673 PE=4 SV=1	Q7A6U2|Q7A6U2_STAAN	No Values
781	Guanylate kinase OS=Staphylococcus aureus (strain N315) GN=gmk PE=1 SV=1	P99176|KGUA_STAAN	No Values

782	Glycerol uptake facilitator OS=Staphylococcus aureus (strain N315) GN=glpF PE=3 SV=1	Q7A5V8|Q7A5V8_STAAN	No Values
783	Putative uncharacterized protein SA0960 OS=Staphylococcus aureus (strain N315) GN=SA0960 PE=4 SV=1	Q7A669|Q7A669_STAAN	No Values
784	Putative uncharacterized protein SA1742 OS=Staphylococcus aureus (strain N315) GN=SA1742 PE=4 SV=1	Q7A4N8|Q7A4N8_STAAN	No Values
786	MutS2 protein OS=Staphylococcus aureus (strain N315) GN=mutS2 PE=1 SV=1	P65496|MUTS2_STAAN	No Values
787	SA2324 protein OS=Staphylococcus aureus (strain N315) GN=SA2324 PE=4 SV=1	Q7A3G6|Q7A3G6_STAAN	No Values
788	SA1562 protein OS=Staphylococcus aureus (strain N315) GN=SA1562 PE=4 SV=1	Q7A530|Q7A530_STAAN	No Values
789	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase OS=Staphylococcus aureus (strain N315) GN=menD PE=3 SV=1	Q7A6B1|MEND_STAAN	No Values
790	Sensor protein kinase walK OS=Staphylococcus aureus (strain N315) GN=walK PE=1 SV=1	Q7A8E0|WALK_STAAN	No Values
792	Thymidylate synthase OS=Staphylococcus aureus (strain N315) GN=thyA PE=3 SV=1	P67047|TYSY_STAAN	No Values
793	UPF0124 protein SA1030 OS=Staphylococcus aureus (strain N315) GN=SA1030 PE=3 SV=1	Q7A617|Y1030_STAAN	No Values
794	DNA polymerase III gamma and tau subunits OS=Staphylococcus aureus (strain N315) GN=dnaX PE=4 SV=1	Q7A7C7|Q7A7C7_STAAN	No Values
795	Dehydrosqualene desaturase OS=Staphylococcus aureus (strain N315) GN=crtN PE=1 SV=1	Q7A3E2|CRTN_STAAN	No Values
796	Pantothenate synthetase OS=Staphylococcus aureus (strain N315) GN=panC PE=1 SV=1	P65659|PANC_STAAN	No Values
354	Putative uncharacterized protein SA0771 OS=Staphylococcus aureus (strain N315) GN=SA0771 PE=4 SV=1	Q7A6M0|Q7A6M0_STAAN	Reference Missing
569	SA2422 protein OS=Staphylococcus aureus (strain N315) GN=SA2422 PE=4 SV=1	Q7A383|Q7A383_STAAN	Reference Missing
662	Primosomal protein OS=Staphylococcus aureus (strain N315) GN=dnaI PE=4 SV=1	Q7A568|Q7A568_STAAN	Reference Missing
13	Cold shock protein (cspA)	Q7A5P3|CSPA_STAAN	Value Missing
61	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (glmS)	P64228|GLMS_STAAN	Value Missing
70	Uncharacterized leukocidin-like protein 1 (SA1812)	Q7A4L0|LUKL1_STAAN	Value Missing
131	Immunoglobulin G-binding protein A OS=Staphylococcus aureus (strain N315) GN=spa PE=1 SV=1	SPA_STAAN	Value Missing
150	Phosphoribosylformylglycinamidine cyclo-ligase OS=Staphylococcus aureus (strain N315) GN=purM PE=1 SV=1	P99163|PUR5_STAAN	Value Missing
173	Alcohol dehydrogenase OS=Staphylococcus aureus (strain N315) GN=adh PE=1 SV=1	Q7A742|ADH_STAAN	Value Missing
184	Pyruvate carboxylase OS=Staphylococcus aureus (strain N315) GN=pycA PE=4 SV=1	Q7A666|Q7A666_STAAN	Value Missing
201	Threonine dehydratase catabolic OS=Staphylococcus aureus (strain N315) GN=tdcB PE=1 SV=1	Q7A5L8|THD2_STAAN	Value Missing
211	Alpha-Hemolysin OS=Staphylococcus aureus (strain N315) GN=SA1007 PE=4 SV=1	Q7A632|Q7A632_STAAN	Value Missing
226	SA0231 protein OS=Staphylococcus aureus (strain N315) GN=SA0231 PE=1 SV=1	Q7A7W3|Q7A7W3_STAAN	Value Missing
231	Probable quinol oxidase subunit 1 OS=Staphylococcus aureus (strain N315) GN=qoxB PE=1 SV=1	Q7A699|QOX1_STAAN	Value Missing
234	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase OS=Staphylococcus aureus (strain N315) GN=murG PE=1 SV=1	P65482|MURG_STAAN	Value Missing
243	Poly D-alanine transfer protein OS=Staphylococcus aureus (strain N315) GN=dltD PE=4 SV=1	Q7A6K0|Q7A6K0_STAAN	Value Missing

244	Transcriptional regulatory protein walR OS=Staphylococcus aureus (strain N315) GN=walR PE=1 SV=2	Q7A8E1|WALR_STAAN	Value Missing
256	SA0759 protein OS=Staphylococcus aureus (strain N315) GN=SA0759 PE=4 SV=1	Q7A6M6|Q7A6M6_STAAN	Value Missing
260	SA1000 protein OS=Staphylococcus aureus (strain N315) GN=SA1000 PE=4 SV=1	Q7A639|Q7A639_STAAN	Value Missing
269	Transcription termination factor Rho OS=Staphylococcus aureus (strain N315) GN=rho PE=4 SV=1	Q99SD7|Q99SD7_STAAN	Value Missing
273	3-hydroxy-3-methylglutaryl CoA synthase OS=Staphylococcus aureus (strain N315) GN=mvaS PE=1 SV=1	Q7A3F6|Q7A3F6_STAAN	Value Missing
278	Accessory gene regulator protein A OS=Staphylococcus aureus (strain N315) GN=agrA PE=1 SV=1	P0A0I5|AGRA_STAAN	Value Missing
296	Putative uncharacterized protein SA0663 OS=Staphylococcus aureus (strain N315) GN=SA0663 PE=4 SV=1	Q7A6V1|Q7A6V1_STAAN	Value Missing
323	SA0969 protein OS=Staphylococcus aureus (strain N315) GN=SA0969 PE=4 SV=1	Q7A661|Q7A661_STAAN	Value Missing
330	UDP-N-acetylenolpyruvoylglucosamine reductase OS=Staphylococcus aureus (strain N315) GN=murB PE=1 SV=1	P65463|MURB_STAAN	Value Missing
331	Aminoacyltransferase femX OS=Staphylococcus aureus (strain N315) GN=femX PE=1 SV=1	Q7A447|FEMX_STAAN	Value Missing
336	Dihydroorotase OS=Staphylococcus aureus (strain N315) GN=pyrC PE=1 SV=1	P65906|PYRC_STAAN	Value Missing
337	Chromosomal replication initiator protein dnaA OS=Staphylococcus aureus (strain N315) GN=dnaA PE=1 SV=1	P68866|DNAA_STAAN	Value Missing
339	Putative uncharacterized protein SA1868 OS=Staphylococcus aureus (strain N315) GN=SA1868 PE=4 SV=1	Q7A4H1|Q7A4H1_STAAN	Value Missing
341	Putative uncharacterized protein SA0606 OS=Staphylococcus aureus (strain N315) GN=SA0606 PE=1 SV=1	Q7A700|Q7A700_STAAN	Value Missing
349	SA2375 protein OS=Staphylococcus aureus (strain N315) GN=SA2375 PE=3 SV=1	Q7A3B6|Q7A3B6_STAAN	Value Missing
357	Nucleoside diphosphate kinase OS=Staphylococcus aureus (strain N315) GN=ndk PE=1 SV=1	NDK_STAAN	Value Missing
370	Putative uncharacterized protein SA0517 OS=Staphylococcus aureus (strain N315) GN=SA0517 PE=1 SV=1	Q7A783|Q7A783_STAAN	Value Missing
371	Probable acetyl-CoA acyltransferase OS=Staphylococcus aureus (strain N315) GN=SA0342 PE=1 SV=1	Q7A7L2|THLA_STAAN	Value Missing
372	Ferrochelatase OS=Staphylococcus aureus (strain N315) GN=hemH PE=1 SV=1	P64125|HEMH_STAAN	Value Missing
376	Alpha-acetolactate synthase OS=Staphylococcus aureus (strain N315) GN=alsS PE=4 SV=1	Q7A481|Q7A481_STAAN	Value Missing
389	Protein fmtA OS=Staphylococcus aureus (strain N315) GN=fmtA PE=1 SV=1	Q7A6A2|FMTA_STAAN	Value Missing
409	Phosphopentomutase OS=Staphylococcus aureus (strain N315) GN=deoB PE=1 SV=1	P99100|DEOB_STAAN	Value Missing
410	SigmaB regulation protein RsbU OS=Staphylococcus aureus (strain N315) GN=rsbU PE=4 SV=1	Q7A4H0|Q7A4H0_STAAN	Value Missing
417	Xaa-Pro dipeptidase OS=Staphylococcus aureus (strain N315) GN=SA1360 PE=3 SV=1	Q99TW4|Q99TW4_STAAN	Value Missing
423	ATP-dependent Clp protease proteolytic subunit OS=Staphylococcus aureus (strain N315) GN=clpP PE=1 SV=1	P99089|CLPP_STAAN	Value Missing
426	SA1626 protein OS=Staphylococcus aureus (strain N315) GN=SA1626 PE=4 SV=1	Q7A4Y5|Q7A4Y5_STAAN (+1)	Value Missing
427	Ribonuclease J 1 OS=Staphylococcus aureus (strain N315) GN=SA0940 PE=1 SV=1	Q7A682|RNJ1_STAAN	Value Missing
429	D-3-phosphoglycerate dehydrogenase OS=Staphylococcus aureus (strain N315) GN=serA PE=4 SV=1	Q7A542|Q7A542_STAAN	Value Missing
431	Phosphoribosylglycinamide formyltransferase OS=Staphylococcus aureus (strain N315) GN=purN PE=1 SV=1	P99162|PUR3_STAAN	Value Missing
438	Ornithine carbamoyltransferase OS=Staphylococcus aureus (strain N315) GN=argF	P99073|OTC_STA	Value

	PE=1 SV=1	AN	Missing
439	Alanine dehydrogenase 1 OS=Staphylococcus aureus (strain N315) GN=ald1 PE=1 SV=1	P99151|DHA1_STAAN	Value Missing
445	Peptide chain release factor 3 OS=Staphylococcus aureus (strain N315) GN=prfC PE=1 SV=1	Q99V72|RF3_STAAN	Value Missing
451	DNA repair protein OS=Staphylococcus aureus (strain N315) GN=recN PE=4 SV=1	Q7A5F5|Q7A5F5_STAAN	Value Missing
452	HTH-type transcriptional regulator rot OS=Staphylococcus aureus (strain N315) GN=rot PE=1 SV=2	Q7A514|ROT_STAAN	Value Missing
458	Glycine betaine/carnitine/choline ABC transporter opuCA OS=Staphylococcus aureus (strain N315) GN=opuCA PE=4 SV=1	Q7A3P8|Q7A3P8_STAAN	Value Missing
461	Putative uncharacterized protein SA1161 OS=Staphylococcus aureus (strain N315) GN=SA1161 PE=4 SV=1	Q7A5T9|Q7A5T9_STAAN	Value Missing
463	SA2297 protein OS=Staphylococcus aureus (strain N315) GN=SA2297 PE=4 SV=1	Q7A3J1_STAAN (+1)	Value Missing
472	tRNA pseudouridine synthase B OS=Staphylococcus aureus (strain N315) GN=truB PE=1 SV=1	P65855|TRUB_STAAN	Value Missing
474	Alkaline phosphatase synthesis transcriptional regulatory protein OS=Staphylococcus aureus (strain N315) GN=phoP PE=4 SV=1	Q7A562|Q7A562_STAAN	Value Missing
484	Putative uncharacterized protein SA1364 OS=Staphylococcus aureus (strain N315) GN=SA1364 PE=4 SV=1	Q7A5E7|Q7A5E7_STAAN	Value Missing
487	SA2156 protein OS=Staphylococcus aureus (strain N315) GN=SA2156 PE=4 SV=1	Q7A3W7|Q7A3W7_STAAN	Value Missing
494	HPr kinase/phosphorylase OS=Staphylococcus aureus (strain N315) GN=hprK PE=1 SV=1	P60701|HPRK_STAAN	Value Missing
507	DNA topoisomerase 4 subunit B OS=Staphylococcus aureus (strain N315) GN=parE PE=1 SV=1	P66939|PARE_STAAN	Value Missing
512	Arginine deiminase OS=Staphylococcus aureus (strain N315) GN=arcA PE=1 SV=1	P63554|ARCA_STAAN	Value Missing
515	Histidine protein kinase saeS OS=Staphylococcus aureus (strain N315) GN=saeS PE=1 SV=1	Q7A6V4|SAES_STAAN	Value Missing
520	Accessory gene regulator C OS=Staphylococcus aureus (strain N315) GN=agrC PE=4 SV=1	Q7A4I6|Q7A4I6_STAAN	Value Missing
521	Putative uncharacterized protein SA1423 OS=Staphylococcus aureus (strain N315) GN=SA1423 PE=4 SV=1	Q7A5B3|Q7A5B3_STAAN	Value Missing
524	Glutamine amidotransferase subunit pdxT OS=Staphylococcus aureus (strain N315) GN=pdxT PE=1 SV=1	Q7A7A1|PDXT_STAAN	Value Missing
530	SA1708 protein OS=Staphylococcus aureus (strain N315) GN=SA1708 PE=4 SV=1	Q7A4R3|Q7A4R3_STAAN	Value Missing
534	Protoporphyrinogen oxidase OS=Staphylococcus aureus (strain N315) GN=hemY PE=4 SV=1	Q7A4W4|Q7A4W4_STAAN	Value Missing
544	Putative uncharacterized protein SA1662 OS=Staphylococcus aureus (strain N315) GN=SA1662 PE=4 SV=1	Q7A4V4_STAAN	Value Missing
549	Phenylalanyl-tRNA synthetase beta chain OS=Staphylococcus aureus (strain N315) GN=pheT PE=1 SV=1	P67041|SYFB_STAAN	Value Missing
551	SA0791 protein OS=Staphylococcus aureus (strain N315) GN=SA0791 PE=4 SV=1	Q7A6K3|Q7A6K3_STAAN	Value Missing
559	SA2278 protein OS=Staphylococcus aureus (strain N315) GN=SA2278 PE=4 SV=1	Q7A3K8|Q7A3K8_STAAN	Value Missing
562	Cmp-binding-factor 1 OS=Staphylococcus aureus (strain N315) GN=cbf1 PE=4 SV=1	Q7A4V6|Q7A4V6_STAAN	Value Missing
564	UPF0316 protein SA1727 OS=Staphylococcus aureus (strain N315) GN=SA1727 PE=1 SV=1	P61544|Y1727_STAAN	Value Missing
565	Putative uncharacterized protein SA1426 OS=Staphylococcus aureus (strain N315) GN=SA1426 PE=4 SV=1	Q7A5B1|Q7A5B1_STAAN	Value Missing
572	Penicillin binding protein 4 OS=Staphylococcus aureus (strain N315) GN=pbp4 PE=3 SV=1	Q7A709|Q7A709_STAAN	Value Missing
574	Putative uncharacterized protein SA0513 OS=Staphylococcus aureus (strain N315) GN=SA0513 PE=4 SV=1	Q7A787|Q7A787_STAAN	Value Missing

581	tRNA-specific 2-thiouridylase mnmA OS=Staphylococcus aureus (strain N315) GN=mnmA PE=1 SV=1	Q99TM8|MNMA_STAAN	Value Missing
586	Thymidylate kinase OS=Staphylococcus aureus (strain N315) GN=tmk PE=3 SV=1	P65249|KTHY_STAAN	Value Missing
587	GTP-binding protein lepA OS=Staphylococcus aureus (strain N315) GN=lepA PE=1 SV=1	P65272|LEPA_STAAN	Value Missing
588	DNA mismatch repair protein mutL OS=Staphylococcus aureus (strain N315) GN=mutL PE=1 SV=1	P65492|MUTL_STAAN	Value Missing
589	Aspartate carbamoyltransferase OS=Staphylococcus aureus (strain N315) GN=pyrB PE=1 SV=1	P65618|PYRB_STAAN	Value Missing
592	Penicillin-binding protein 3 OS=Staphylococcus aureus (strain N315) GN=pbp3 PE=4 SV=1	Q7A5D5|Q7A5D5_STAAN	Value Missing
595	SA0357 protein OS=Staphylococcus aureus (strain N315) GN=SA0357 PE=4 SV=1	Q7A7K0|Q7A7K0_STAAN	Value Missing
604	Fibrinogen-binding protein OS=Staphylococcus aureus (strain N315) GN=fib PE=1 SV=1	P68800|FIB_STAAN	Value Missing
605	4,4'-diaponeurosporene oxidase OS=Staphylococcus aureus (strain N315) GN=crtP PE=1 SV=1	Q7A3D9|CRTP_STAAN	Value Missing
606	SA2243 protein OS=Staphylococcus aureus (strain N315) GN=SA2243 PE=4 SV=1	Q7A3P3_STAAN (+1)	Value Missing
607	SA2103 protein OS=Staphylococcus aureus (strain N315) GN=SA2103 PE=4 SV=1	Q7A413|Q7A413_STAAN	Value Missing
614	Membrane protein oxaA OS=Staphylococcus aureus (strain N315) GN=oxaA PE=1 SV=1	P65629|OXAA_STAAN	Value Missing
615	SA1329 protein OS=Staphylococcus aureus (strain N315) GN=SA1329 PE=4 SV=1	Q7A5H3|Q7A5H3_STAAN	Value Missing
616	Competence-damage inducible protein cinA OS=Staphylococcus aureus (strain N315) GN=cinA PE=4 SV=1	Q7A5W9|Q7A5W9_STAAN	Value Missing
622	Putative uncharacterized protein SA0449 OS=Staphylococcus aureus (strain N315) GN=SA0449 PE=4 SV=1	Q7A7C0|Q7A7C0_STAAN	Value Missing
634	OppD protein OS=Staphylococcus aureus (strain N315) GN=oppD PE=4 SV=1	Q7A6F4|Q7A6F4_STAAN	Value Missing
635	Putative uncharacterized protein SA0832 OS=Staphylococcus aureus (strain N315) GN=SA0832 PE=4 SV=1	Q7A6H0|Q7A6H0_STAAN	Value Missing
637	Transcriptional regulator ctsR OS=Staphylococcus aureus (strain N315) GN=ctsR PE=1 SV=1	Q7A799|CTSR_STAAN	Value Missing
648	Ribose-5-phosphate isomerase A OS=Staphylococcus aureus (strain N315) GN=rpiA PE=3 SV=1	P66695|RPIA_STAAN	Value Missing
649	Putative uncharacterized protein SA2090 OS=Staphylococcus aureus (strain N315) GN=SA2090 PE=4 SV=1	Q7A424|Q7A424_STAAN	Value Missing
656	SA2132 protein OS=Staphylococcus aureus (strain N315) GN=SA2132 PE=4 SV=1	Q99RT2|Q99RT2_STAAN	Value Missing
661	2-dehydropantoate 2-reductase OS=Staphylococcus aureus (strain N315) GN=SA2232 PE=3 SV=1	Q7A3Q3|Q7A3Q3_STAAN	Value Missing
665	Putative uncharacterized protein SA0184 OS=Staphylococcus aureus (strain N315) GN=SA0184 PE=4 SV=1	Q7A806|Q7A806_STAAN	Value Missing
666	Gamma-hemolysin component B OS=Staphylococcus aureus (strain N315) GN=hlgB PE=1 SV=1	P0A075|HLGB_STAAN	Value Missing
670	Mannose-6-phosphate isomerase OS=Staphylococcus aureus (strain N315) GN=pmi PE=3 SV=1	Q7A373|Q7A373_STAAN	Value Missing
674	SA0566 protein OS=Staphylococcus aureus (strain N315) GN=SA0566 PE=4 SV=1	Q7A739|Q7A739_STAAN	Value Missing
675	Putative uncharacterized protein SA0561 OS=Staphylococcus aureus (strain N315) GN=SA0561 PE=4 SV=1	Q7A743|Q7A743_STAAN	Value Missing
679	Putative uncharacterized protein SA0954 OS=Staphylococcus aureus (strain N315) GN=SA0954 PE=4 SV=1	Q7A675|Q7A675_STAAN	Value Missing
682	Peptide chain release factor 1 OS=Staphylococcus aureus (strain N315) GN=prfA PE=3 SV=1	P66019|RF1_STAAN	Value Missing
685	Putative uncharacterized protein SA0739 OS=Staphylococcus aureus (strain N315)	Q7A6P8|Q7A6P8_	Value

	GN=SA0739 PE=4 SV=1	STAAN	Missing
686	Putative zinc metalloprotease SA1105 OS=Staphylococcus aureus (strain N315) GN=SA1105 PE=1 SV=1	P63333|Y1105_STAAN	Value Missing
700	Putative uncharacterized protein SA1942 OS=Staphylococcus aureus (strain N315) GN=SA1942 PE=4 SV=1	Q7A4C7|Q7A4C7_STAAN	Value Missing
703	SA0958 protein OS=Staphylococcus aureus (strain N315) GN=SA0958 PE=4 SV=1	Q7A673|Q7A673_STAAN	Value Missing
704	SA0734 protein OS=Staphylococcus aureus (strain N315) GN=SA0734 PE=4 SV=1	Q7A6Q0|Q7A6Q0_STAAN	Value Missing
706	Putative uncharacterized protein SA0296 OS=Staphylococcus aureus (strain N315) GN=SA0296 PE=4 SV=1	Q7A7Q1|Q7A7Q1_STAAN	Value Missing
720	Undecaprenyl-diphosphatase OS=Staphylococcus aureus (strain N315) GN=uppP PE=3 SV=1	P67391|UPPP_STAAN	Value Missing
722	Carbamate kinase 2 OS=Staphylococcus aureus (strain N315) GN=arcC2 PE=1 SV=1	P99069|ARCC2_STAAN	Value Missing
728	SA0895 protein OS=Staphylococcus aureus (strain N315) GN=SA0895 PE=4 SV=1	Q7A6B2|Q7A6B2_STAAN	Value Missing
740	Urease accessory protein ureG OS=Staphylococcus aureus (strain N315) GN=ureG PE=1 SV=1	Q7A427|UREG_STAAN	Value Missing
747	Orotate phosphoribosyltransferase OS=Staphylococcus aureus (strain N315) GN=pyrE PE=1 SV=1	PYRE_STAAN (+1)	Value Missing
754	Sulfite reductase flavoprotein OS=Staphylococcus aureus (strain N315) GN=SA2413 PE=3 SV=1	Q7A392|Q7A392_STAAN	Value Missing
755	SA1699 protein OS=Staphylococcus aureus (strain N315) GN=SA1699 PE=4 SV=1	Q99SZ8|Q99SZ8_STAAN	Value Missing
759	Putative uncharacterized protein SA1672 OS=Staphylococcus aureus (strain N315) GN=SA1672 PE=4 SV=1	Q7A4U4|Q7A4U4_STAAN	Value Missing
770	Putative uncharacterized protein SA0601 OS=Staphylococcus aureus (strain N315) GN=SA0601 PE=3 SV=1	Q7A705|Q7A705_STAAN	Value Missing
771	NADPH-dependent oxidoreductase OS=Staphylococcus aureus (strain N315) GN=nfrA PE=3 SV=1	Q7A7J0|NFRA_STAAN	Value Missing
774	Putative uncharacterized protein SA1526 OS=Staphylococcus aureus (strain N315) GN=SA1526 PE=4 SV=1	Q7A555|Q7A555_STAAN	Value Missing
778	30S ribosomal protein S5 OS=Staphylococcus aureus (strain N315) GN=rpsE PE=1 SV=1	RS5_STAAN	Value Missing
791	Dihydrolipoyl dehydrogenase OS=Staphylococcus aureus (strain N315) GN=SA1349 PE=3 SV=1	Q7A5F6|Q7A5F6_STAAN	Value Missing

Table A12. Complete list of intracellular proteins identified from the USA 100 adaptive mutant at 15 hours.

#	Identified Proteins (791)	Accession Number	Fold Change from WT
47	Uncharacterized leukocidin-like protein 2 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1975 PE=3 SV=1	Q2FFA2|LUKL2_STAA3	-4.4
67	Uncharacterized leukocidin-like protein 1 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1974 PE=3 SV=1	Q2FFA3|LUKL1_STAA3	-4.4
429	Glycosyl transferase, group 1 family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0939 PE=4 SV=1	Q2FI41|Q2FI41_STAA3	-4.4
428	Proline dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=putA PE=4 SV=1	Q2FFX4|Q2FFX4_STAA3	-4.3
671	Hydrolase, alpha/beta hydrolase fold family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0604 PE=4 SV=1	Q2FJ21|Q2FJ21_STAA3	-4.1

338	Dihydroxyacetone kinase, DhaL subunit OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0637 PE=4 SV=1	Q2FIY8|Q2FIY8_STAA3	-4
521	Accessory gene regulator protein C OS=Staphylococcus aureus (strain USA300) GN=agrC PE=4 SV=1	Q2FF86|Q2FF86_STAA3	-3.8
205	PTS system glucose-specific EIICBA component OS=Staphylococcus aureus (strain USA300) GN=ptsG PE=3 SV=1	Q2FK73|PTG3C_STAA3	-3.6
436	Alanine dehydrogenase 1 OS=Staphylococcus aureus (strain USA300) GN=ald1 PE=3 SV=1	Q2FH00|DHA1_STAA3	-3.6
552	UPF0316 protein SAUSA300_1892 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1892 PE=3 SV=1	Q2FFI4|Y1892_STAA3	-3.6
587	Putative staphylococcal enterotoxin OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0370 PE=4 SV=1	Q2FJP4|Q2FJP4_STAA3	-3.5
31	Phosphoribosylformylglycinamidine synthase 2 OS=Staphylococcus aureus (strain USA300) GN=purL PE=3 SV=1	Q2FI09|PURL_STAA3	-3.4
244	Uracil phosphoribosyltransferase OS=Staphylococcus aureus (strain USA300) GN=upp PE=3 SV=1	Q2FF16|UPP_STAA3	-3.4
579	GTP-binding protein lepA OS=Staphylococcus aureus (strain USA300) GN=lepA PE=3 SV=1	Q2FGD9|LEPA_STAA3	-3.4
269	Hydroxymethylglutaryl-CoA synthase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2484 PE=4 SV=1	Q2FDW0|Q2FDW0_STAA3	-3.3
392	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2328 PE=4 SV=1	Q2FEB5|Q2FEB5_STAA3	-3.3
453	Glutamate-1-semialdehyde 2,1-aminomutase 2 OS=Staphylococcus aureus (strain USA300) GN=hemL2 PE=3 SV=1	Q2FFN1|GSA2_STAA3	-3.3
8	Formate acetyltransferase OS=Staphylococcus aureus (strain USA300) GN=pflB PE=3 SV=1	Q2FK44|PFLB_STAA3	-3.2
65	Probable quinol oxidase subunit 2 OS=Staphylococcus aureus (strain USA300) GN=qoxA PE=3 SV=1	Q2FI17|QOX2_STAA3	-3.2
305	ATP-dependent hsl protease ATP-binding subunit hslU OS=Staphylococcus aureus (strain USA300) GN=hslU PE=3 SV=1	Q2FHI4|HSLU_STAA3	-3.2
319	Accessory gene regulator protein A OS=Staphylococcus aureus (strain USA300) GN=agrA PE=4 SV=1	Q2FF85|Q2FF85_STAA3	-3.2
534	AcrB/AcrD/AcrF family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2213 PE=4 SV=1	Q2FEN0|Q2FEN0_STAA3	-3.2
662	Uridine kinase OS=Staphylococcus aureus (strain USA300) GN=udk PE=3 SV=1	Q2FGB5|URK_STAA3	-3.2
146	Phosphoribosylformylglycinamidine cyclo-ligase OS=Staphylococcus aureus (strain USA300) GN=purM PE=3 SV=1	Q2FI07|PUR5_STAA3	-3.1
278	Putative teichoic acid biosynthesis protein B OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0247 PE=4 SV=1	Q2FK17|Q2FK17_STAA3	-3.1
297	Putative lipoprotein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0693 PE=4 SV=1	Q2FIT2|Q2FIT2_STAA3	-3.1

327	Aminoacyltransferase femX OS=Staphylococcus aureus (strain USA300) GN=femX PE=3 SV=1	Q2FEM9|FEMX_STAA3	-3.1
339	Chromosomal replication initiator protein dnaA OS=Staphylococcus aureus (strain USA300) GN=dnaA PE=3 SV=1	Q2FKQ5|DNAA_STAA3	-3.1
361	Hydrolase, haloacid dehalogenase-like family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0544 PE=4 SV=1	Q2FJ81|Q2FJ81_STAA3	-3.1
411	Lipoyl synthase OS=Staphylococcus aureus (strain USA300) GN=lipA PE=3 SV=1	Q2FIE9|LIPA_STAA3	-3.1
61	Glucosamine--fructose-6-phosphate aminotransferase (Isomerizing) OS=Staphylococcus aureus (strain USA300) GN=glmS PE=3 SV=1	Q2FEX8|Q2FEX8_STAA3	-3
171	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1729 PE=4 SV=1	Q2FFV7|Q2FFV7_STAA3	-3
116	Phosphoribosylamine--glycine ligase OS=Staphylococcus aureus (strain USA300) GN=purD PE=3 SV=1	Q2FI04|Q2FI04_STAA3	-2.9
148	Pyridoxal biosynthesis lyase pdxS OS=Staphylococcus aureus (strain USA300) GN=pdxS PE=3 SV=1	Q2FJC1|PDXS_STAA3	-2.9
200	Glyceraldehyde-3-phosphate dehydrogenase, type I OS=Staphylococcus aureus (strain USA300) GN=gap PE=3 SV=1	Q2FG50|Q2FG50_STAA3	-2.9
333	ABC transporter ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0620 PE=4 SV=1	Q2FJ05|Q2FJ05_STAA3	-2.9
442	DNA repair protein RecN OS=Staphylococcus aureus (strain USA300) GN=recN PE=4 SV=1	Q2FGL4|Q2FGL4_STAA3	-2.9
228	Probable quinol oxidase subunit 1 OS=Staphylococcus aureus (strain USA300) GN=qoxB PE=3 SV=1	Q2FI18|QOX1_STAA3	-2.8
270	Alcohol dehydrogenase, iron-containing OS=Staphylococcus aureus (strain USA300) GN=adhE PE=4 SV=1	Q2FKB2|Q2FKB2_STAA3	-2.8
452	Oxidoreductase, aldo/keto reductase family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0688 PE=4 SV=1	Q2FIT7|Q2FIT7_STAA3	-2.8
471	Protein-export membrane protein SecF OS=Staphylococcus aureus (strain USA300) GN=secF PE=4 SV=1	Q2FG90|Q2FG90_STAA3	-2.8
668	Chaperone protein dnaJ OS=Staphylococcus aureus (strain USA300) GN=dnaJ PE=3 SV=1	Q2FGE4|DNAJ_STAA3	-2.8
159	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Staphylococcus aureus (strain USA300) GN=purC PE=3 SV=1	Q2FI12|PUR7_STAA3	-2.7
271	ABC transporter, ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2453 PE=4 SV=1	Q2FDZ1|Q2FDZ1_STAA3	-2.7
357	Ribonuclease J 2 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1168 PE=3 SV=2	Q2FHG3|RNJ2_STAA3	-2.7
225	Acetoin(Diacetyl) reductase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0129 PE=3 SV=1	Q2FKD2|Q2FKD2_STAA3	-2.6
232	ATP synthase subunit delta OS=Staphylococcus aureus (strain USA300) GN=atpH PE=3 SV=1	Q2FF21|ATPD_STAA3	-2.6

276	UPF0637 protein SAUSA300_1006 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1006 PE=3 SV=1	Q2FHX4|Y1006_STAA3	-2.6
341	Dihydroorotate dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=pyrD PE=3 SV=1	Q2FDR8|Q2FDR8_STAA3	-2.6
359	Glycosyl transferase, group 2 family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0252 PE=4 SV=1	Q2FK12|Q2FK12_STAA3	-2.6
383	Staphopain A OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1890 PE=4 SV=1	Q2FFI6|Q2FFI6_STAA3	-2.6
404	HTH-type transcriptional regulator sarR OS=Staphylococcus aureus (strain USA300) GN=sarR PE=3 SV=3	Q2FEJ8|SARR_STAA3	-2.6
752	Dihydroxyacetone kinase, DhaK subunit OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0636 PE=4 SV=1	Q2FIY9|Q2FIY9_STAA3	-2.6
759	RNA methyltransferase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1805 PE=4 SV=1	Q2FFP0|Q2FFP0_STAA3	-2.6
788	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2378 PE=4 SV=1	Q2FE65|RANDOM_Q2FE65_STAA3-R	-2.6
15	Cold shock protein cspA OS=Staphylococcus aureus (strain USA300) GN=cspA PE=3 SV=1	Q2FH36|CSPA_STAA3	-2.5
35	50S ribosomal protein L5 OS=Staphylococcus aureus (strain USA300) GN=rplE PE=3 SV=1	Q2FEQ1|RL5_STAA3	-2.5
55	ATP synthase subunit alpha OS=Staphylococcus aureus (strain USA300) GN=atpA PE=3 SV=1	Q2FF22|ATPA_STAA3	-2.5
154	L-lactate dehydrogenase 2 OS=Staphylococcus aureus (strain USA300) GN=ldh2 PE=3 SV=1	Q2FDQ7|LDH2_STAA3	-2.5
235	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase OS=Staphylococcus aureus (strain USA300) GN=murG PE=3 SV=1	Q2FH20|MURG_STAA3	-2.5
330	Oxidoreductase, aldo/keto reductase family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1450 PE=4 SV=1	Q2FGN2|Q2FGN2_STAA3	-2.5
387	Phosphomethylpyrimidine kinase OS=Staphylococcus aureus (strain USA300) GN=thiD PE=4 SV=1	Q2FJ63|Q2FJ63_STAA3	-2.5
426	Amidophosphoribosyltransferase OS=Staphylococcus aureus (strain USA300) GN=purF PE=4 SV=1	Q2FI08|Q2FI08_STAA3	-2.5
450	Cytidylate kinase OS=Staphylococcus aureus (strain USA300) GN=cmk PE=4 SV=1	Q2FGW4|Q2FGW4_STAA3	-2.5
516	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0278 PE=4 SV=1	Q2FJY6|Q2FJY6_STAA3	-2.5
582	Aspartate carbamoyltransferase OS=Staphylococcus aureus (strain USA300) GN=pyrB PE=3 SV=1	Q2FHN8|PYRB_STAA3	-2.5
603	Membrane protein oxaA OS=Staphylococcus aureus (strain USA300) GN=oxaA PE=3 SV=1	Q2FF36|OXAA_STAA3	-2.5
32	ABC transporter, substrate-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0618 PE=3 SV=1	Q2FJ07|Q2FJ07_STAA3	-2.4

39	Carbamoyl-phosphate synthase large chain OS=Staphylococcus aureus (strain USA300) GN=carB PE=3 SV=1	Q2FHN5|CARB_STAA3	-2.4
196	Phosphoribosylaminoimidazole carboxylase, ATPase subunit OS=Staphylococcus aureus (strain USA300) GN=purK PE=4 SV=1	Q2FI13|Q2FI13_STAA3	-2.4
217	ATP synthase subunit b OS=Staphylococcus aureus (strain USA300) GN=atpF PE=3 SV=1	Q2FF20|ATPF_STAA3	-2.4
249	Bifunctional protein pyrR OS=Staphylococcus aureus (strain USA300) GN=pyrR PE=3 SV=1	Q2FHP0|PYRR_STAA3	-2.4
334	Dihydroorotase OS=Staphylococcus aureus (strain USA300) GN=pyrC PE=3 SV=1	Q2FHN7|Q2FHN7_STAA3	-2.4
440	Glycine betaine/carnitine/choline ABC transporter ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=opuCa PE=4 SV=1	Q2FE50|Q2FE50_STAA3	-2.4
486	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0331 PE=4 SV=1	Q2FJT3|Q2FJT3_STAA3	-2.4
496	Carbamate kinase 1 OS=Staphylococcus aureus (strain USA300) GN=arcC1 PE=3 SV=1	Q2FHR7|ARCC1_STAA3	-2.4
559	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1780 PE=4 SV=1	Q2FFR5|Q2FFR5_STAA3	-2.4
699	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1583 PE=4 SV=1	Q2FGA0|Q2FGA0_STAA3	-2.4
53	Protein translocase subunit secA 1 OS=Staphylococcus aureus (strain USA300) GN=secA1 PE=3 SV=1	Q2FIN8|SECA1_STAA3	-2.3
89	Bifunctional purine biosynthesis protein purH OS=Staphylococcus aureus (strain USA300) GN=purH PE=3 SV=1	Q2FI05|PUR9_STAA3	-2.3
138	Catabolite control protein A OS=Staphylococcus aureus (strain USA300) GN=ccpA PE=4 SV=1	Q2FG02|Q2FG02_STAA3	-2.3
188	Putative serine protease HtrA OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1674 PE=4 SV=1	Q2FG10|Q2FG10_STAA3	-2.3
354	Serine-protein kinase rsbW OS=Staphylococcus aureus (strain USA300) GN=rsbW PE=3 SV=1	Q2FF59|RSBW_STAA3	-2.3
399	Methionyl-tRNA formyltransferase OS=Staphylococcus aureus (strain USA300) GN=fmt PE=3 SV=1	Q2FHM2|FMT_STAA3	-2.3
696	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2093 PE=4 SV=1	Q2FEY9|Q2FEY9_STAA3	-2.3
71	Ribonucleoside-diphosphate reductase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0716 PE=3 SV=1	Q2FIQ9|Q2FIQ9_STAA3	-2.2
336	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0982 PE=4 SV=1	Q2FHZ8|Q2FHZ8_STAA3	-2.2
390	Fmt protein OS=Staphylococcus aureus (strain USA300) GN=fmt PE=4 SV=1	Q2FI21|Q2FI21_STAA3	-2.2
523	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1554 PE=4 SV=1	Q2FGC9|Q2FGC9_STAA3	-2.2

548	Pyrimidine nucleoside transport protein OS=Staphylococcus aureus (strain USA300) GN=nupC PE=4 SV=1	Q2FJB9|Q2FJB9_STAA3	-2.2
557	ABC transporter, permease protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2358 PE=3 SV=1	Q2FE85|Q2FE85_STAA3	-2.2
621	tRNA modification GTPase mnmE OS=Staphylococcus aureus (strain USA300) GN=mnmE PE=3 SV=1	Q2FDE8|MNME_STAA3	-2.2
737	Heme-degrading monooxygenase isdI OS=Staphylococcus aureus (strain USA300) GN=isdI PE=3 SV=1	Q2FK96|ISDI_STAA3	-2.2
9	Penicillin-binding protein 2' OS=Staphylococcus aureus (strain USA300) GN=mecA PE=4 SV=1	Q2FKM6|Q2FKM6_STAA3	-2.1
19	ATP synthase subunit beta OS=Staphylococcus aureus (strain USA300) GN=atpD PE=3 SV=1	Q2FF24|ATPB_STAA3	-2.1
29	30S ribosomal protein S3 OS=Staphylococcus aureus (strain USA300) GN=rpsC PE=3 SV=1	Q2FEP5|RS3_STAA3	-2.1
136	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase OS=Staphylococcus aureus (strain USA300) GN=gpmA PE=3 SV=1	Q2FE81|GPMA_STAA3	-2.1
160	Alcohol dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=adh PE=3 SV=1	Q2FJ31|ADH_STAA3	-2.1
223	Xanthine phosphoribosyltransferase OS=Staphylococcus aureus (strain USA300) GN=xpt PE=3 SV=1	Q2FJM8|XPT_STAA3	-2.1
230	Putative pyridoxal phosphate-dependent acyltransferase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0535 PE=3 SV=1	Q2FJ90|Q2FJ90_STAA3	-2.1
251	Putative arsenate reductase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0790 PE=4 SV=1	Q2FII8|Q2FII8_STAA3	-2.1
282	50S ribosomal protein L20 OS=Staphylococcus aureus (strain USA300) GN=rplT PE=3 SV=1	Q2FG58|RL20_STAA3	-2.1
315	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2212 PE=4 SV=1	Q2FEN1|Q2FEN1_STAA3	-2.1
371	ATP-binding protein, Mrp/Nbp35 family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2125 PE=4 SV=1	Q2FEW6|Q2FEW6_STAA3	-2.1
403	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1223 PE=4 SV=1	Q2FHA8|Q2FHA8_STAA3	-2.1
412	Phosphopentomutase OS=Staphylococcus aureus (strain USA300) GN=deoB PE=3 SV=1	Q2FKC0|DEOB_STAA3	-2.1
504	Putative lipoprotein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2403 PE=4 SV=1	Q2FE40|Q2FE40_STAA3	-2.1
506	3-phosphoshikimate 1-carboxyvinyltransferase OS=Staphylococcus aureus (strain USA300) GN=aroA PE=3 SV=1	Q2FGX6|AROA_STAA3	-2.1
508	Glycerol-3-phosphate dehydrogenase [NAD(P)+] OS=Staphylococcus aureus (strain USA300) GN=gpsA PE=3 SV=1	Q2FGW8|GPDA_STAA3	-2.1
729	Amino acid/peptide transporter (Peptide:H+ symporter) OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0712 PE=3 SV=1	Q2FIR3|Q2FIR3_STAA3	-2.1

11	Malate:quinone-oxidoreductase OS=Staphylococcus aureus (strain USA300) GN=mqo PE=3 SV=1	Q2FDQ3|Q2FDQ3_STAA3	-2
42	UPF0365 protein SAUSA300_1533 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1533 PE=3 SV=1	Q2FGF0|Y1533_STAA3	-2
46	Putative universal stress protein SAUSA300_1656 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1656 PE=3 SV=1	Q2FG28|Y1656_STAA3	-2
48	50S ribosomal protein L1 OS=Staphylococcus aureus (strain USA300) GN=rplA PE=3 SV=1	Q2FJA2|RL1_STAA3	-2
68	UPF0478 protein SAUSA300_1685 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1685 PE=3 SV=1	Q2FFZ9|Y1685_STAA3	-2
73	NADH dehydrogenase-like protein SAUSA300_0844 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0844 PE=3 SV=1	Q2FID4|Y844_STAA3	-2
179	GTPase obg OS=Staphylococcus aureus (strain USA300) GN=obg PE=3 SV=1	Q2FG83|OBG_STAA3	-2
209	Succinate dehydrogenase, iron-sulfur protein OS=Staphylococcus aureus (strain USA300) GN=sdhB PE=4 SV=1	Q2FHT2|Q2FHT2_STAA3	-2
262	Transcription termination factor Rho OS=Staphylococcus aureus (strain USA300) GN=rho PE=4 SV=1	Q2FF07|Q2FF07_STAA3	-2
285	Elastin-binding protein ebpS OS=Staphylococcus aureus (strain USA300) GN=ebpS PE=3 SV=3	Q2FGW1|EBPS_STAA3	-2
301	Trans-2-enoyl-ACP reductase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0912 PE=4 SV=1	Q2FI66|Q2FI66_STAA3	-2
316	Putative AMP-binding enzyme OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2542 PE=4 SV=1	Q2FDQ2|Q2FDQ2_STAA3	-2
317	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2257 PE=4 SV=1	Q2FEI6|Q2FEI6_STAA3	-2
344	Glucose-6-phosphate 1-dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=zwf PE=3 SV=1	Q2FGM8|Q2FGM8_STAA3	-2
437	Ornithine carbamoyltransferase OS=Staphylococcus aureus (strain USA300) GN=argF PE=3 SV=1	Q2FHR8|Q2FHR8_STAA3	-2
485	Hydrolase, MutT/nudix family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2432 PE=4 SV=1	Q2FE12|Q2FE12_STAA3	-2
490	ATP-dependent DNA helicase, PcrA OS=Staphylococcus aureus (strain USA300) GN=pcrA PE=4 SV=1	Q2FFJ0|Q2FFJ0_STAA3	-2
491	Mur ligase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1873 PE=4 SV=1	Q2FFK3|Q2FFK3_STAA3	-2
517	Histidine protein kinase saeS OS=Staphylococcus aureus (strain USA300) GN=saeS PE=3 SV=1	Q2FIT5|SAES_STAA3	-2
641	Putative lipoprotein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0769 PE=4 SV=1	Q2FIK9|Q2FIK9_STAA3	-2
670	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1118 PE=4 SV=1	Q2FHL3|Q2FHL3_STAA3	-2

750	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1240 PE=4 SV=1	Q2FH91|Q2FH91_STAA3	-2
37	Triacylglycerol lipase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0320 PE=4 SV=1	Q2FJU4|Q2FJU4_STAA3	-1.9
78	Isocitrate dehydrogenase [NADP] OS=Staphylococcus aureus (strain USA300) GN=icd PE=3 SV=1	Q2FG43|Q2FG43_STAA3	-1.9
91	Translation initiation factor IF-2 OS=Staphylococcus aureus (strain USA300) GN=infB PE=3 SV=1	Q2FHG9|IF2_STAA3	-1.9
94	Asparaginyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=asnS PE=3 SV=1	Q2FGY6|SYN_STAA3	-1.9
103	Formate--tetrahydrofolate ligase OS=Staphylococcus aureus (strain USA300) GN=fhs PE=3 SV=1	Q2FG06|FTHS_STAA3	-1.9
109	50S ribosomal protein L3 OS=Staphylococcus aureus (strain USA300) GN=rplC PE=3 SV=1	Q2FEN9|RL3_STAA3	-1.9
130	Ribose-phosphate pyrophosphokinase OS=Staphylococcus aureus (strain USA300) GN=prs PE=3 SV=1	Q2FJE1|Q2FJE1_STAA3	-1.9
155	50S ribosomal protein L4 OS=Staphylococcus aureus (strain USA300) GN=rplD PE=3 SV=1	Q2FEP0|RL4_STAA3	-1.9
156	Uncharacterized protein SAUSA300_1119 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1119 PE=4 SV=1	Q2FHL2|Y1119_STAA3	-1.9
210	UPF0477 protein SAUSA300_0916 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0916 PE=3 SV=1	Q2FI62|Y916_STAA3	-1.9
264	Glutamate-1-semialdehyde 2,1-aminomutase 1 OS=Staphylococcus aureus (strain USA300) GN=hemL1 PE=3 SV=1	Q2FG69|GSA1_STAA3	-1.9
273	ATP synthase gamma chain OS=Staphylococcus aureus (strain USA300) GN=atpG PE=3 SV=1	Q2FF23|Q2FF23_STAA3	-1.9
300	Threonine dehydratase catabolic OS=Staphylococcus aureus (strain USA300) GN=tdcB PE=3 SV=1	Q2FH01|THD2_STAA3	-1.9
311	Putative phosphotransferase SAUSA300_1523 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1523 PE=3 SV=1	Q2FGG0|Y1523_STAA3	-1.9
355	DegV family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1318 PE=4 SV=1	Q2FH13|Q2FH13_STAA3	-1.9
388	Hypoxanthine phosphoribosyltransferase OS=Staphylococcus aureus (strain USA300) GN=hpt PE=4 SV=1	Q2FJD1|Q2FJD1_STAA3	-1.9
497	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1658 PE=4 SV=1	Q2FG26|Q2FG26_STAA3	-1.9
551	Ribokinase OS=Staphylococcus aureus (strain USA300) GN=rbsK PE=3 SV=1	Q2FK02|Q2FK02_STAA3	-1.9
567	tRNA-specific 2-thiouridylase mnmA OS=Staphylococcus aureus (strain USA300) GN=mnmA PE=3 SV=2	Q2FGA5|MNMA_STAA3	-1.9
666	Mannose-6-phosphate isomerase, class I OS=Staphylococcus aureus (strain USA300) GN=manA PE=3 SV=1	Q2FDL7|Q2FDL7_STAA3	-1.9

697	Delta-hemolysin OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1988 PE=4 SV=1	Q2FF89|Q2FF89_STAA3	-1.9
751	Orotate phosphoribosyltransferase OS=Staphylococcus aureus (strain USA300) GN=pyrE PE=3 SV=1	Q2FHN3|Q2FHN3_STAA3	-1.9
70	30S ribosomal protein S11 OS=Staphylococcus aureus (strain USA300) GN=rpsK PE=3 SV=1	Q2FER4|RS11_STAA3	-1.8
81	DNA polymerase III, beta subunit OS=Staphylococcus aureus (strain USA300) GN=dnaN PE=3 SV=1	Q2FKQ4|Q2FKQ4_STAA3	-1.8
92	Succinate dehydrogenase, flavoprotein subunit OS=Staphylococcus aureus (strain USA300) GN=sdhA PE=4 SV=1	Q2FHT3|Q2FHT3_STAA3	-1.8
125	50S ribosomal protein L19 OS=Staphylococcus aureus (strain USA300) GN=rplS PE=3 SV=1	Q2FHJ7|RL19_STAA3	-1.8
167	ABC transporter, ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1285 PE=4 SV=1	Q2FH46|Q2FH46_STAA3	-1.8
204	Transcriptional regulator, MarR family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0672 PE=4 SV=1	Q2FIV3|Q2FIV3_STAA3	-1.8
216	Oxidoreductase, short chain dehydrogenase/reductase family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2275 PE=4 SV=1	Q2FEG8|Q2FEG8_STAA3	-1.8
220	Signal recognition particle protein OS=Staphylococcus aureus (strain USA300) GN=ffh PE=4 SV=1	Q2FHK1|Q2FHK1_STAA3	-1.8
237	D-alanine-activating enzyme/D-alanine-D-alanyl, dltD protein OS=Staphylococcus aureus (strain USA300) GN=dltD PE=4 SV=1	Q2FIE0|Q2FIE0_STAA3	-1.8
247	Extracellular matrix protein-binding protein emp OS=Staphylococcus aureus (strain USA300) GN=emp PE=3 SV=1	Q2FIK4|EMP_STAA3	-1.8
292	Putative NADP-dependent malic enzyme OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1648 PE=3 SV=1	Q2FG36|Q2FG36_STAA3	-1.8
294	GTP-binding protein engA OS=Staphylococcus aureus (strain USA300) GN=engA PE=3 SV=1	Q2FGW7|ENGA_STAA3	-1.8
304	Urocanate hydratase OS=Staphylococcus aureus (strain USA300) GN=hutU PE=4 SV=1	Q2FEG5|Q2FEG5_STAA3	-1.8
306	UPF0051 protein SAUSA300_0822 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0822 PE=3 SV=1	Q2FIF6|Y822_STAA3	-1.8
340	DNA-directed RNA polymerase subunit omega OS=Staphylococcus aureus (strain USA300) GN=rpoZ PE=3 SV=1	Q2FHM8|RPOZ_STAA3	-1.8
367	Putative thioredoxin OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0789 PE=4 SV=1	Q2FII9|Q2FII9_STAA3	-1.8
568	Oligopeptide ABC transporter, ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=oppF PE=4 SV=1	Q2FI88|Q2FI88_STAA3	-1.8
585	Single-stranded DNA-binding protein OS=Staphylococcus aureus (strain USA300) GN=ssb PE=4 SV=1	Q2FJP7|Q2FJP7_STAA3	-1.8
586	30S ribosomal protein S14 type Z OS=Staphylococcus aureus (strain USA300) GN=rpsZ PE=3 SV=2	Q2FEQ2|RS14Z_STAA3	-1.8

590	Aminotransferase, class V OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1579 PE=3 SV=1	Q2FGA4|Q2FGA4_STAA3	-1.8
766	Threonine synthase OS=Staphylococcus aureus (strain USA300) GN=thrC PE=3 SV=1	Q2FHA4|Q2FHA4_STAA3	-1.8
40	1-pyrroline-5-carboxylate dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=rocA PE=3 SV=1	Q2FDV3|ROCA_STAA3	-1.7
62	50S ribosomal protein L2 OS=Staphylococcus aureus (strain USA300) GN=rplB PE=3 SV=1	Q2FEP2|RL2_STAA3	-1.7
104	Aerobic glycerol-3-phosphate dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=glpD PE=3 SV=1	Q2FHD8|GLPD_STAA3	-1.7
105	Ornithine aminotransferase OS=Staphylococcus aureus (strain USA300) GN=rocD PE=3 SV=1	Q2FIB8|Q2FIB8_STAA3	-1.7
133	Prolyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=proS PE=3 SV=1	Q2FHH5|SYP_STAA3	-1.7
137	30S ribosomal protein S12 OS=Staphylococcus aureus (strain USA300) GN=rpsL PE=3 SV=1	Q2FJ95|RS12_STAA3	-1.7
150	Phosphoglucosamine mutase OS=Staphylococcus aureus (strain USA300) GN=glmM PE=3 SV=1	Q2FEX1|GLMM_STAA3	-1.7
152	Protein recA OS=Staphylococcus aureus (strain USA300) GN=recA PE=3 SV=1	Q2FHF3|Q2FHF3_STAA3	-1.7
181	Adenylosuccinate synthetase OS=Staphylococcus aureus (strain USA300) GN=purA PE=3 SV=1	Q2FKN9|Q2FKN9_STAA3	-1.7
187	Translation initiation factor IF-1 OS=Staphylococcus aureus (strain USA300) GN=infA PE=3 SV=1	Q2FER1|IF1_STAA3	-1.7
221	Putative peptidyl-prolyl cis-trans isomerase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0857 PE=3 SV=1	Q2FIC1|PPI1_STAA3	-1.7
255	DNA gyrase subunit B OS=Staphylococcus aureus (strain USA300) GN=gyrB PE=3 SV=3	Q2FKQ1|GYRB_STAA3	-1.7
256	ATP-dependent Clp protease ATP-binding subunit clpX OS=Staphylococcus aureus (strain USA300) GN=clpX PE=3 SV=1	Q2FG62|CLPX_STAA3	-1.7
261	Malate:quinone-oxidoreductase OS=Staphylococcus aureus (strain USA300) GN=mqo PE=3 SV=1	Q2FED1|Q2FED1_STAA3	-1.7
382	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase OS=Staphylococcus aureus (strain USA300) GN=murF PE=3 SV=1	Q2FF44|Q2FF44_STAA3	-1.7
384	2-oxoisovalerate dehydrogenase, E2 component, dihydrolipoamide acetyltransferase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1464 PE=3 SV=1	Q2FGL8|Q2FGL8_STAA3	-1.7
435	Acetyl-coenzyme A synthetase OS=Staphylococcus aureus (strain USA300) GN=acsA PE=4 SV=1	Q2FG05|Q2FG05_STAA3	-1.7
482	Pyrroline-5-carboxylate reductase OS=Staphylococcus aureus (strain USA300) GN=proC PE=4 SV=1	Q2FGN0|Q2FGN0_STAA3	-1.7
519	Conserved virulence factor B OS=Staphylococcus aureus (strain USA300) GN=cvfB PE=3 SV=1	Q2FH47|CVFB_STAA3	-1.7

560	Chromosome segregation protein SMC OS=Staphylococcus aureus (strain USA300) GN=smc PE=4 SV=1	Q2FHK4|Q2FHK4_STAA3	-1.7
574	Uncharacterized protein SAUSA300_1902 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1902 PE=3 SV=1	Q2FFH4|Y1902_STAA3	-1.7
625	2-oxoisovalerate dehydrogenase, E1 component, alpha subunit OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1466 PE=4 SV=1	Q2FGL6|Q2FGL6_STAA3	-1.7
719	RNA methyltransferase, TrmH family, group 3 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0517 PE=4 SV=1	Q2FJA8|Q2FJA8_STAA3	-1.7
727	Na(+)/H(+) antiporter subunit E1 OS=Staphylococcus aureus (strain USA300) GN=mnhE1 PE=3 SV=1	Q2FIC7|MNHE1_STAA3	-1.7
731	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0657 PE=4 SV=1	Q2FIW8|Q2FIW8_STAA3	-1.7
14	Pyruvate kinase OS=Staphylococcus aureus (strain USA300) GN=pyk PE=3 SV=1	Q2FG40|KPYK_STAA3	-1.6
26	Fructose-bisphosphate aldolase class 1 OS=Staphylococcus aureus (strain USA300) GN=fda PE=3 SV=1	Q2FDQ4|ALF1_STAA3	-1.6
63	Acetate kinase OS=Staphylococcus aureus (strain USA300) GN=ackA PE=3 SV=1	Q2FG27|ACKA_STAA3	-1.6
88	Cell division protein ftsA OS=Staphylococcus aureus (strain USA300) GN=ftsA PE=4 SV=1	Q2FHQ2|Q2FHQ2_STAA3	-1.6
96	50S ribosomal protein L13 OS=Staphylococcus aureus (strain USA300) GN=rplM PE=3 SV=1	Q2FES1|RL13_STAA3	-1.6
101	50S ribosomal protein L10 OS=Staphylococcus aureus (strain USA300) GN=rplJ PE=3 SV=1	Q2FJA1|RL10_STAA3	-1.6
108	L-lactate dehydrogenase 1 OS=Staphylococcus aureus (strain USA300) GN=ldh1 PE=3 SV=2	Q2FK29|LDH1_STAA3	-1.6
131	30S ribosomal protein S13 OS=Staphylococcus aureus (strain USA300) GN=rpsM PE=3 SV=1	Q2FER3|RS13_STAA3	-1.6
142	50S ribosomal protein L14 OS=Staphylococcus aureus (strain USA300) GN=rplN PE=3 SV=1	Q2FEP9|RL14_STAA3	-1.6
168	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Staphylococcus aureus (strain USA300) GN=sucD PE=3 SV=1	Q2FHJ2|Q2FHJ2_STAA3	-1.6
184	GTP-binding protein OS=Staphylococcus aureus (strain USA300) GN=typA PE=4 SV=1	Q2FHX1|Q2FHX1_STAA3	-1.6
208	Citrate synthase II OS=Staphylococcus aureus (strain USA300) GN=gltA PE=3 SV=1	Q2FG42|Q2FG42_STAA3	-1.6
241	30S ribosomal protein S6 OS=Staphylococcus aureus (strain USA300) GN=rpsF PE=3 SV=1	Q2FJP8|RS6_STAA3	-1.6
274	30S ribosomal protein S4 OS=Staphylococcus aureus (strain USA300) GN=rpsD PE=3 SV=1	Q2FG18|RS4_STAA3	-1.6
281	D-alanine--D-alanine ligase OS=Staphylococcus aureus (strain USA300) GN=ddl PE=3 SV=1	Q2FF43|DDL_STAA3	-1.6

307	UPF0082 protein SAUSA300_0655 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0655 PE=3 SV=1	Q2FIX0|Y655_STAA3	-1.6
308	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0649 PE=4 SV=1	Q2FIX6|Q2FIX6_STAA3	-1.6
342	GTP pyrophosphokinase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1590 PE=3 SV=1	Q2FG93|Q2FG93_STAA3	-1.6
343	GTP-binding protein era homolog OS=Staphylococcus aureus (strain USA300) GN=era PE=3 SV=1	Q2FGF6|ERA_STAA3	-1.6
381	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2085 PE=4 SV=1	Q2FEZ7|Q2FEZ7_STAA3	-1.6
427	D-3-phosphoglycerate dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=serA PE=3 SV=1	Q2FG14|Q2FG14_STAA3	-1.6
542	D-isomer specific 2-hydroxyacid dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0834 PE=3 SV=1	Q2FIE4|Q2FIE4_STAA3	-1.6
558	Probable DNA-directed RNA polymerase subunit delta OS=Staphylococcus aureus (strain USA300) GN=rpoE PE=3 SV=1	Q2FF00|RPOE_STAA3	-1.6
644	PTS system glucoside-specific EIICBA component OS=Staphylococcus aureus (strain USA300) GN=glcB PE=3 SV=1	Q2FDW8|PTU3C_STAA3	-1.6
682	Putative membrane-associated zinc metalloprotease OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1155 PE=3 SV=1	Q2FHH6|Q2FHH6_STAA3	-1.6
1	Elongation factor Tu OS=Staphylococcus aureus (strain USA300) GN=tuf PE=3 SV=1	Q2FJ92|EFTU_STAA3	-1.5
27	DNA-directed RNA polymerase subunit beta' OS=Staphylococcus aureus (strain USA300) GN=rpoC PE=3 SV=2	Q2FJ97|RPOC_STAA3	-1.5
30	Pyruvate dehydrogenase E1 component, beta subunit OS=Staphylococcus aureus (strain USA300) GN=pdhB PE=4 SV=1	Q2FHY6|Q2FHY6_STAA3	-1.5
54	30S ribosomal protein S5 OS=Staphylococcus aureus (strain USA300) GN=rpsE PE=3 SV=1	Q2FEQ6|RS5_STAA3	-1.5
58	5'-nucleotidase, lipoprotein e(P4) family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0307 PE=4 SV=1	Q2FJV7|Q2FJV7_STAA3	-1.5
72	DNA-directed RNA polymerase subunit beta OS=Staphylococcus aureus (strain USA300) GN=rpoB PE=3 SV=2	Q2FJ98|RPOB_STAA3	-1.5
98	Phosphoenolpyruvate carboxykinase [ATP] OS=Staphylococcus aureus (strain USA300) GN=pckA PE=3 SV=1	Q2FFV5|PCKA_STAA3	-1.5
110	Threonyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=thrS PE=3 SV=1	Q2FG54|SYT_STAA3	-1.5
114	Putative formate dehydrogenase SAUSA300_2258 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2258 PE=3 SV=1	Q2FEI5|FDHL_STAA3	-1.5
115	Septation ring formation regulator ezrA OS=Staphylococcus aureus (strain USA300) GN=ezrA PE=3 SV=1	Q2FG20|EZRA_STAA3	-1.5
118	Pyrimidine-nucleoside phosphorylase OS=Staphylococcus aureus (strain USA300) GN=pdp PE=3 SV=2	Q2FEZ3|PDP_STAA3	-1.5

124	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Staphylococcus aureus (strain USA300) GN=sucC PE=3 SV=1	Q2FHJ3|SUCC_STAA3	-1.5
161	Alkyl hydroperoxide reductase, subunit F OS=Staphylococcus aureus (strain USA300) GN=ahpF PE=3 SV=1	Q2FJN5|Q2FJN5_STAA3	-1.5
162	Putative dipeptidase SAUSA300_1697 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1697 PE=3 SV=1	Q2FFY7|PEPVL_STAA3	-1.5
164	GTP-binding protein YchF OS=Staphylococcus aureus (strain USA300) GN=ychF PE=4 SV=1	Q2FJQ0|Q2FJQ0_STAA3	-1.5
165	UPF0133 protein SAUSA300_0453 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0453 PE=3 SV=1	Q2FJG3|Y453_STAA3	-1.5
180	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1323 PE=4 SV=1	Q2FH08|Q2FH08_STAA3	-1.5
183	Pyruvate carboxylase OS=Staphylococcus aureus (strain USA300) GN=pyc PE=4 SV=1	Q2FHW6|Q2FHW6_STAA3	-1.5
252	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0385 PE=4 SV=1	Q2FJM9|Q2FJM9_STAA3	-1.5
254	Seryl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=serS PE=3 SV=1	Q2FKP7|SYS_STAA3	-1.5
260	50S ribosomal protein L16 OS=Staphylococcus aureus (strain USA300) GN=rplP PE=3 SV=1	Q2FEP6|RL16_STAA3	-1.5
320	Staphylococcal respiratory response protein, SrrA OS=Staphylococcus aureus (strain USA300) GN=srrA PE=4 SV=1	Q2FGP0|Q2FGP0_STAA3	-1.5
321	Glycerophosphoryl diester phosphodiesterase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1020 PE=4 SV=1	Q2FHW0|Q2FHW0_STAA3	-1.5
351	PTS system EIIBC component SAUSA300_0194 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0194 PE=3 SV=1	Q2FK70|PTXBC_STAA3	-1.5
377	Nucleoside diphosphate kinase OS=Staphylococcus aureus (strain USA300) GN=ndk PE=3 SV=2	Q2FGX3|NDK_STAA3	-1.5
400	Carbamoyl-phosphate synthase, small subunit OS=Staphylococcus aureus (strain USA300) GN=carA PE=3 SV=1	Q2FHN6|Q2FHN6_STAA3	-1.5
402	Phosphate starvation-induced protein, PhoH family OS=Staphylococcus aureus (strain USA300) GN=phoH PE=4 SV=1	Q2FGF2|Q2FGF2_STAA3	-1.5
409	Oxidoreductase, aldo/keto reductase family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1728 PE=4 SV=1	Q2FFV8|Q2FFV8_STAA3	-1.5
413	10 kDa chaperonin OS=Staphylococcus aureus (strain USA300) GN=groS PE=3 SV=1	Q2FF94|CH10_STAA3	-1.5
425	Ribonuclease J 1 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0989 PE=3 SV=1	Q2FHZ1|RNJ1_STAA3	-1.5
441	(Dimethylallyl)adenosine tRNA methylthiotransferase miaB OS=Staphylococcus aureus (strain USA300) GN=miaB PE=3 SV=1	Q2FHE6|MIAB_STAA3	-1.5
565	HAD-superfamily hydrolase, subfamily IA, variant 1 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0540 PE=4 SV=1	Q2FJ85|Q2FJ85_STAA3	-1.5

575	Uncharacterized lipoprotein SAUSA300_2315 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2315 PE=4 SV=1	Q2FEC8|Y2315_STAA3	-1.5
601	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0668 PE=4 SV=1	Q2FIV7|Q2FIV7_STAA3	-1.5
637	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1585 PE=4 SV=1	Q2FG98|Q2FG98_STAA3	-1.5
639	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1082 PE=3 SV=1	Q2FHP9|Q2FHP9_STAA3	-1.5
12	Inosine-5'-monophosphate dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=guaB PE=3 SV=1	Q2FJM6|IMDH_STAA3	-1.4
41	Aconitate hydratase OS=Staphylococcus aureus (strain USA300) GN=acnA PE=4 SV=1	Q2FH85|Q2FH85_STAA3	-1.4
50	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Staphylococcus aureus (strain USA300) GN=gatB PE=3 SV=1	Q2FFJ6|GATB_STAA3	-1.4
69	50S ribosomal protein L6 OS=Staphylococcus aureus (strain USA300) GN=rplF PE=3 SV=1	Q2FEQ4|RL6_STAA3	-1.4
74	Immunodominant staphylococcal antigen B OS=Staphylococcus aureus (strain USA300) GN=isaB PE=3 SV=1	Q2FDM1|ISAB_STAA3	-1.4
174	UPF0356 protein SAUSA300_0990 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0990 PE=3 SV=1	Q2FHZ0|Y990_STAA3	-1.4
191	Dehydrogenase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2251 PE=4 SV=1	Q2FEJ2|Q2FEJ2_STAA3	-1.4
234	Aspartyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=aspS PE=3 SV=1	Q2FG97|SYD_STAA3	-1.4
246	Uridylate kinase OS=Staphylococcus aureus (strain USA300) GN=pyrH PE=3 SV=1	Q2FHI0|PYRH_STAA3	-1.4
259	Chaperone protein hchA OS=Staphylococcus aureus (strain USA300) GN=hchA PE=3 SV=1	Q2FJ89|HCHA_STAA3	-1.4
272	CTP synthase OS=Staphylococcus aureus (strain USA300) GN=pyrG PE=3 SV=1	Q2FF01|PYRG_STAA3	-1.4
288	DNA gyrase subunit A OS=Staphylococcus aureus (strain USA300) GN=gyrA PE=3 SV=1	Q2FKQ0|GYRA_STAA3	-1.4
322	Uncharacterized epimerase/dehydratase SAUSA300_0538 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0538 PE=3 SV=1	Q2FJ87|Y538_STAA3	-1.4
360	30S ribosomal protein S17 OS=Staphylococcus aureus (strain USA300) GN=rpsQ PE=3 SV=1	Q2FEP8|RS17_STAA3	-1.4
373	Glycerol kinase OS=Staphylococcus aureus (strain USA300) GN=glpK PE=3 SV=1	Q2FHD9|GLPK_STAA3	-1.4
378	Lipoate-protein ligase A family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0930 PE=4 SV=1	Q2FI50|Q2FI50_STAA3	-1.4
391	Cold shock protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0777 PE=3 SV=1	Q2FIK1|Q2FIK1_STAA3	-1.4

420	Phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase OS=Staphylococcus aureus (strain USA300) GN=coaBC PE=4 SV=1	Q2FHM7|Q2FHM7_STAA3	-1.4
472	Phosphate acyltransferase OS=Staphylococcus aureus (strain USA300) GN=plsX PE=3 SV=1	Q2FHK9|PLSX_STAA3	-1.4
473	ABC transporter, ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0630 PE=4 SV=1	Q2FIZ5|Q2FIZ5_STAA3	-1.4
475	Methicillin resistance protein FemA OS=Staphylococcus aureus (strain USA300) GN=femA PE=4 SV=1	Q2FH62|Q2FH62_STAA3	-1.4
505	Uncharacterized oxidoreductase SAUSA300_2422 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2422 PE=3 SV=1	Q2FE21|Y2422_STAA3	-1.4
515	Decarboxylase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0666 PE=4 SV=1	Q2FIV9|Q2FIV9_STAA3	-1.4
578	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1793 PE=4 SV=1	Q2FFQ2|Q2FFQ2_STAA3	-1.4
669	Menaquinone biosynthesis methyltransferase ubiE OS=Staphylococcus aureus (strain USA300) GN=ubiE PE=4 SV=1	Q2FGX1|Q2FGX1_STAA3	-1.4
687	UvrABC system protein B OS=Staphylococcus aureus (strain USA300) GN=uvrB PE=3 SV=1	Q2FIN5|Q2FIN5_STAA3	-1.4
25	30S ribosomal protein S2 OS=Staphylococcus aureus (strain USA300) GN=rpsB PE=3 SV=1	Q2FHI2|RS2_STAA3	-1.3
33	Immunoglobulin-binding protein sbi OS=Staphylococcus aureus (strain USA300) GN=sbi PE=3 SV=1	Q2FE79|SBI_STAA3	-1.3
49	Pyruvate dehydrogenase E1 component, alpha subunit OS=Staphylococcus aureus (strain USA300) GN=pdhA PE=4 SV=1	Q2FHY7|Q2FHY7_STAA3	-1.3
60	ATP-dependent Clp protease ATP-binding subunit clpL OS=Staphylococcus aureus (strain USA300) GN=clpL PE=3 SV=1	Q2FDV8|CLPL_STAA3	-1.3
95	30S ribosomal protein S7 OS=Staphylococcus aureus (strain USA300) GN=rpsG PE=3 SV=2	Q2FJ94|RS7_STAA3	-1.3
112	50S ribosomal protein L27 OS=Staphylococcus aureus (strain USA300) GN=rpmA PE=3 SV=1	Q2FG82|RL27_STAA3	-1.3
121	Bifunctional protein folD OS=Staphylococcus aureus (strain USA300) GN=folD PE=3 SV=1	Q2FI15|FOLD_STAA3	-1.3
126	50S ribosomal protein L22 OS=Staphylococcus aureus (strain USA300) GN=rplV PE=3 SV=1	Q2FEP4|RL22_STAA3	-1.3
140	Phosphate acetyltransferase OS=Staphylococcus aureus (strain USA300) GN=pta PE=4 SV=1	Q2FJ55|Q2FJ55_STAA3	-1.3
153	Transcription termination factor NusA OS=Staphylococcus aureus (strain USA300) GN=nusA PE=4 SV=1	Q2FHH2|Q2FHH2_STAA3	-1.3
186	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase OS=Staphylococcus aureus (strain USA300) GN=ispD PE=3 SV=1	Q2FK15|ISPD_STAA3	-1.3
195	Immunoglobulin G binding protein A OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0113 PE=3 SV=1	Q2FKE8|Q2FKE8_STAA3	-1.3

243	30S ribosomal protein S10 OS=Staphylococcus aureus (strain USA300) GN=rpsJ PE=3 SV=1	Q2FEN8|RS10_STAA3	-1.3
332	UDP-N-acetylenolpyruvoylglucosamine reductase OS=Staphylococcus aureus (strain USA300) GN=murB PE=3 SV=1	Q2FIQ3|MURB_STAA3	-1.3
350	1-acyl-sn-glycerol-3-phosphate acyltransferases OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1673 PE=4 SV=1	Q2FG11|Q2FG11_STAA3	-1.3
352	Phosphoribosylaminoimidazole carboxylase, catalytic subunit OS=Staphylococcus aureus (strain USA300) GN=purE PE=4 SV=1	Q2FI14|Q2FI14_STAA3	-1.3
379	Ribonucleoside-diphosphate reductase, beta subunit OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0717 PE=4 SV=1	Q2FIQ8|Q2FIQ8_STAA3	-1.3
380	Phosphoribosylglycinamide formyltransferase OS=Staphylococcus aureus (strain USA300) GN=purN PE=4 SV=1	Q2FI06|Q2FI06_STAA3	-1.3
385	Methicillin resistance protein FemB OS=Staphylococcus aureus (strain USA300) GN=femB PE=4 SV=1	Q2FH61|Q2FH61_STAA3	-1.3
408	Sigma-B regulation protein OS=Staphylococcus aureus (strain USA300) GN=rsbU PE=4 SV=1	Q2FF57|Q2FF57_STAA3	-1.3
627	Uncharacterized protein SAUSA300_1248 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1248 PE=3 SV=1	Q2FH83|Y1248_STAA3	-1.3
658	50S ribosomal protein L9 OS=Staphylococcus aureus (strain USA300) GN=rplI PE=3 SV=1	Q2FKP1|RL9_STAA3	-1.3
660	2-dehydropantoate 2-reductase OS=Staphylococcus aureus (strain USA300) GN=panE PE=3 SV=1	Q2FE55|Q2FE55_STAA3	-1.3
20	Enolase OS=Staphylococcus aureus (strain USA300) GN=eno PE=3 SV=1	Q2FIL7|ENO_STAA3	-1.2
122	ABC transporter, ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1911 PE=4 SV=1	Q2FFG5|Q2FFG5_STAA3	-1.2
123	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1804 PE=4 SV=1	Q2FFP1|Q2FFP1_STAA3	-1.2
139	NAD-specific glutamate dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=gudB PE=3 SV=1	Q2FIB7|Q2FIB7_STAA3	-1.2
145	Isoleucyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=ileS PE=3 SV=1	Q2FHP4|SYI_STAA3	-1.2
170	Probable DEAD-box ATP-dependent RNA helicase SAUSA300_2037 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2037 PE=3 SV=1	Q2FF45|Y2037_STAA3	-1.2
175	Adenylosuccinate lyase OS=Staphylococcus aureus (strain USA300) GN=purB PE=3 SV=1	Q2FFI7|PUR8_STAA3	-1.2
182	S-adenosylmethionine synthase OS=Staphylococcus aureus (strain USA300) GN=metK PE=3 SV=1	Q2FFV6|METK_STAA3	-1.2
194	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Staphylococcus aureus (strain USA300) GN=gpmI PE=3 SV=1	Q2FIL8|Q2FIL8_STAA3	-1.2
218	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1792 PE=4 SV=1	Q2FFQ3|Q2FFQ3_STAA3	-1.2

233	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1909 PE=4 SV=1	Q2FFG7|Q2FFG7_STAA3	-1.2
267	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0664 PE=4 SV=1	Q2FIW1|Q2FIW1_STAA3	-1.2
298	30S ribosomal protein S9 OS=Staphylococcus aureus (strain USA300) GN=rpsI PE=3 SV=1	Q2FES2|RS9_STAA3	-1.2
329	DNA polymerase I OS=Staphylococcus aureus (strain USA300) GN=polA PE=3 SV=1	Q2FG47|Q2FG47_STAA3	-1.2
348	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1788 PE=4 SV=1	Q2FFQ7|Q2FFQ7_STAA3	-1.2
375	Putative oxidoreductase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0329 PE=4 SV=1	Q2FJT5|Q2FJT5_STAA3	-1.2
456	Ornithine carbamoyltransferase OS=Staphylococcus aureus (strain USA300) GN=arcB PE=3 SV=1	Q2FDM5|Q2FDM5_STAA3	-1.2
469	UDP-N-acetylglucosamine 1-carboxyvinyltransferase OS=Staphylococcus aureus (strain USA300) GN=murA PE=3 SV=1	Q2FF04|Q2FF04_STAA3	-1.2
476	S-adenosyl-L-methionine-dependent methyltransferase mraW OS=Staphylococcus aureus (strain USA300) GN=mraW PE=3 SV=2	Q2FHQ8|MRAW_STAA3	-1.2
483	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1495 PE=4 SV=1	Q2FGI8|Q2FGI8_STAA3	-1.2
511	Multidrug resistance protein A, drug resistance transporter OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2299 PE=4 SV=1	Q2FEE4|Q2FEE4_STAA3	-1.2
522	UPF0173 metal-dependent hydrolase SAUSA300_1653 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1653 PE=3 SV=1	Q2FG31|Y1653_STAA3	-1.2
531	Penicillin-binding protein 1 OS=Staphylococcus aureus (strain USA300) GN=pbpA PE=4 SV=1	Q2FHQ6|Q2FHQ6_STAA3	-1.2
589	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1720 PE=4 SV=1	Q2FFW5|Q2FFW5_STAA3	-1.2
610	UPF0297 protein SAUSA300_1574 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1574 PE=3 SV=1	Q2FGA9|Y1574_STAA3	-1.2
617	DNA-binding response regulator OS=Staphylococcus aureus (strain USA300) GN=vraR PE=4 SV=1	Q2FFL1|Q2FFL1_STAA3	-1.2
654	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0956 PE=4 SV=1	Q2FI24|Q2FI24_STAA3	-1.2
18	Dihydrolipoyl dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=lpdA PE=3 SV=1	Q2FHY4|Q2FHY4_STAA3	-1.1
56	Glutamyl-tRNA(Gln) amidotransferase subunit A OS=Staphylococcus aureus (strain USA300) GN=gatA PE=3 SV=1	Q2FFJ5|GATA_STAA3	-1.1
100	Triosephosphate isomerase OS=Staphylococcus aureus (strain USA300) GN=tpiA PE=3 SV=1	Q2FIL9|TPIS_STAA3	-1.1
102	Ferritin OS=Staphylococcus aureus (strain USA300) GN=ftnA PE=3 SV=1	Q2FFK2|FTN_STAA3	-1.1

111	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1863 PE=4 SV=1	Q2FFL3|Q2FFL3_STAA3	-1.1
143	30S ribosomal protein S8 OS=Staphylococcus aureus (strain USA300) GN=rpsH PE=3 SV=1	Q2FEQ3|RS8_STAA3	-1.1
149	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2144 PE=4 SV=1	Q2FEU8|Q2FEU8_STAA3	-1.1
202	50S ribosomal protein L23 OS=Staphylococcus aureus (strain USA300) GN=rplW PE=3 SV=1	Q2FEP1|RL23_STAA3	-1.1
213	50S ribosomal protein L21 OS=Staphylococcus aureus (strain USA300) GN=rplU PE=3 SV=1	Q2FG80|RL21_STAA3	-1.1
248	Putative 2-hydroxyacid dehydrogenase SAUSA300_2254 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2254 PE=3 SV=1	Q2FEI9|Y2254_STAA3	-1.1
386	DNA topoisomerase IV, subunit A OS=Staphylococcus aureus (strain USA300) GN=parC PE=4 SV=1	Q2FH80|Q2FH80_STAA3	-1.1
394	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2097 PE=4 SV=1	Q2FEY5|Q2FEY5_STAA3	-1.1
414	Aminotransferase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1916 PE=4 SV=1	Q2FFG0|Q2FFG0_STAA3	-1.1
459	2-oxoisovalerate dehydrogenase, E1 component, beta subunit OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1465 PE=4 SV=1	Q2FGL7|Q2FGL7_STAA3	-1.1
502	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1494 PE=4 SV=1	Q2FGI9|Q2FGI9_STAA3	-1.1
509	RNA polymerase sigma factor OS=Staphylococcus aureus (strain USA300) GN=rpoD PE=3 SV=1	Q2FGG2|Q2FGG2_STAA3	-1.1
545	Preprotein translocase, YajC subunit OS=Staphylococcus aureus (strain USA300) GN=yajC PE=4 SV=1	Q2FG89|Q2FG89_STAA3	-1.1
594	Cardiolipin synthetase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1216 PE=4 SV=1	Q2FHB5|Q2FHB5_STAA3	-1.1
602	UPF0447 protein SAUSA300_0569 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0569 PE=3 SV=1	Q2FJ56|Y569_STAA3	-1.1
714	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1230 PE=4 SV=1	Q2FHA1|Q2FHA1_STAA3	-1.1
17	30S ribosomal protein S1 OS=Staphylococcus aureus (strain USA300) GN=rpsA PE=4 SV=1	Q2FGW6|Q2FGW6_STAA3	-1
59	Uncharacterized protein SAUSA300_0871 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0871 PE=3 SV=1	Q2FIA7|Y871_STAA3	-1
77	GMP synthase [glutamine-hydrolyzing] OS=Staphylococcus aureus (strain USA300) GN=guaA PE=3 SV=1	Q2FJM5|GUAA_STAA3	-1
85	Putative aldehyde dehydrogenase SAUSA300_2076 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2076 PE=3 SV=1	Q2FF06|ALD1_STAA3	-1
87	Probable manganese-dependent inorganic pyrophosphatase OS=Staphylococcus aureus (strain USA300) GN=ppaC PE=3 SV=1	Q2FFH6|PPAC_STAA3	-1

93	Lysyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=lysS PE=3 SV=1	Q2FJC3|SYK_STAA3	-1
120	Polyribonucleotide nucleotidyltransferase OS=Staphylococcus aureus (strain USA300) GN=pnp PE=3 SV=1	Q2FHG4|PNP_STAA3	-1
127	DNA-directed RNA polymerase subunit alpha OS=Staphylococcus aureus (strain USA300) GN=rpoA PE=3 SV=1	Q2FER5|RPOA_STAA3	-1
147	50S ribosomal protein L7/L12 OS=Staphylococcus aureus (strain USA300) GN=rplL PE=3 SV=1	Q2FJA0|RL7_STAA3	-1
163	ATP-dependent Clp protease ATP-binding subunit clpC OS=Staphylococcus aureus (strain USA300) GN=clpC PE=3 SV=1	Q2FJB5|CLPC_STAA3	-1
169	Oligoendopeptidase F OS=Staphylococcus aureus (strain USA300) GN=pepF PE=4 SV=1	Q2FI76|Q2FI76_STAA3	-1
199	6-phosphofructokinase OS=Staphylococcus aureus (strain USA300) GN=pfkA PE=3 SV=1	Q2FG39|Q2FG39_STAA3	-1
253	Putative flavohemoprotein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0234 PE=3 SV=1	Q2FK30|Q2FK30_STAA3	-1
279	Phosphoribosylformylglycinamidine synthase OS=Staphylococcus aureus (strain USA300) GN=purS PE=4 SV=1	Q2FI11|Q2FI11_STAA3	-1
283	ATP-dependent RNA helicase, DEAD/DEAH box family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1518 PE=4 SV=1	Q2FGG5|Q2FGG5_STAA3	-1
345	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1304 PE=4 SV=1	Q2FH27|Q2FH27_STAA3	-1
432	50S ribosomal protein L33 2 OS=Staphylococcus aureus (strain USA300) GN=rpmG2 PE=3 SV=1	Q2FGH2|RL332_STAA3	-1
467	tRNA pseudouridine synthase B OS=Staphylococcus aureus (strain USA300) GN=truB PE=3 SV=1	Q2FHG7|TRUB_STAA3	-1
638	ABC transporter, ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0704 PE=4 SV=1	Q2FIS1|Q2FIS1_STAA3	-1
656	Protein nagD homolog OS=Staphylococcus aureus (strain USA300) GN=nagD PE=3 SV=1	Q2FIE5|NAGD_STAA3	-1
667	Transporter, CorA family OS=Staphylococcus aureus (strain USA300) GN=cobI PE=4 SV=1	Q2FEC0|Q2FEC0_STAA3	-1
717	Peptide deformylase OS=Staphylococcus aureus (strain USA300) GN=def PE=3 SV=1	Q2FHY9|Q2FHY9_STAA3	-1
5	Elongation factor G OS=Staphylococcus aureus (strain USA300) GN=fusA PE=3 SV=3	Q2FJ93|EFG_STAA3	-0.9
13	Cell division protein ftsZ OS=Staphylococcus aureus (strain USA300) GN=ftsZ PE=3 SV=1	Q2FHQ1|Q2FHQ1_STAA3	-0.9
64	Catalase OS=Staphylococcus aureus (strain USA300) GN=katA PE=3 SV=1	Q2FH99|CATA_STAA3	-0.9
83	Penicillin binding protein 2 OS=Staphylococcus aureus (strain USA300) GN=pbp2 PE=4 SV=1	Q2FGZ0|Q2FGZ0_STAA3	-0.9

106	Branched-chain-amino-acid aminotransferase OS=Staphylococcus aureus (strain USA300) GN=ilvE PE=3 SV=1	Q2FJ86|Q2FJ86_STAA3	-0.9
129	Phosphoenolpyruvate-protein phosphotransferase OS=Staphylococcus aureus (strain USA300) GN=ptsI PE=3 SV=1	Q2FHZ6|Q2FHZ6_STAA3	-0.9
178	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 OS=Staphylococcus aureus (strain USA300) GN=murA PE=3 SV=1	Q2FF27|Q2FF27_STAA3	-0.9
198	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1652 PE=4 SV=1	Q2FG32|Q2FG32_STAA3	-0.9
203	3-oxoacyl-(Acyl-carrier-protein) reductase OS=Staphylococcus aureus (strain USA300) GN=fabG PE=3 SV=1	Q2FHK7|Q2FHK7_STAA3	-0.9
219	D-alanine aminotransferase OS=Staphylococcus aureus (strain USA300) GN=dat PE=3 SV=1	Q2FFY8|Q2FFY8_STAA3	-0.9
222	Methionyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=metS PE=3 SV=1	Q2FJF2|Q2FJF2_STAA3	-0.9
258	Arginyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=argS PE=3 SV=1	Q2FJ29|SYR_STAA3	-0.9
275	Orotidine 5'-phosphate decarboxylase OS=Staphylococcus aureus (strain USA300) GN=pyrF PE=3 SV=1	Q2FHN4|PYRF_STAA3	-0.9
290	Putative NAD(P)H nitroreductase SAUSA300_2462 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2462 PE=3 SV=1	Q2FDY2|Y2462_STAA3	-0.9
325	Ribosomal large subunit pseudouridine synthase, RluD subfamily OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1800 PE=4 SV=1	Q2FFP5|Q2FFP5_STAA3	-0.9
326	Putative septation protein spoVG OS=Staphylococcus aureus (strain USA300) GN=spoVG PE=3 SV=1	Q2FJE4|SP5G_STAA3	-0.9
405	Dephospho-CoA kinase OS=Staphylococcus aureus (strain USA300) GN=coaE PE=3 SV=1	Q2FG49|COAE_STAA3	-0.9
433	Redox-sensing transcriptional repressor rex OS=Staphylococcus aureus (strain USA300) GN=rex PE=3 SV=1	Q2FF78|REX_STAA3	-0.9
434	HIT family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1787 PE=4 SV=1	Q2FFQ8|Q2FFQ8_STAA3	-0.9
609	Rod shape-determining protein MreC OS=Staphylococcus aureus (strain USA300) GN=mreC PE=4 SV=1	Q2FG78|Q2FG78_STAA3	-0.9
3	Autolysin OS=Staphylococcus aureus (strain USA300) GN=atl PE=4 SV=1	Q2FI25|Q2FI25_STAA3	-0.8
24	Cysteine synthase OS=Staphylococcus aureus (strain USA300) GN=cysK PE=3 SV=1	Q2FJC8|Q2FJC8_STAA3	-0.8
57	Alkyl hydroperoxide reductase subunit C OS=Staphylococcus aureus (strain USA300) GN=ahpC PE=3 SV=1	Q2FJN4|AHPC_STAA3	-0.8
82	FeS assembly ATPase SufC OS=Staphylococcus aureus (strain USA300) GN=sufC PE=4 SV=1	Q2FIG0|Q2FIG0_STAA3	-0.8
99	60 kDa chaperonin OS=Staphylococcus aureus (strain USA300) GN=groL PE=3 SV=1	Q2FF95|CH60_STAA3	-0.8

135	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0602 PE=4 SV=1	Q2FJ23|Q2FJ23_STAA3	-0.8
177	Glycine cleavage system H protein OS=Staphylococcus aureus (strain USA300) GN=gcvH PE=3 SV=1	Q2FII7|GCSH_STAA3	-0.8
231	Transcription antitermination protein nusG OS=Staphylococcus aureus (strain USA300) GN=nusG PE=3 SV=1	Q2FJA4|Q2FJA4_STAA3	-0.8
295	Peptide methionine sulfoxide reductase regulator MsrR OS=Staphylococcus aureus (strain USA300) GN=msrR PE=4 SV=1	Q2FH74|Q2FH74_STAA3	-0.8
417	Tyrosyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=tyrS PE=3 SV=1	Q2FG09|SYY_STAA3	-0.8
451	Phosphoribosylformylglycinamidine synthase 1 OS=Staphylococcus aureus (strain USA300) GN=purQ PE=3 SV=1	Q2FI10|PURQ_STAA3	-0.8
470	Phenylalanyl-tRNA synthetase (Beta subunit) OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1688 PE=4 SV=1	Q2FFZ6|Q2FFZ6_STAA3	-0.8
480	Uncharacterized peptidase SAUSA300_1654 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1654 PE=3 SV=1	Q2FG30|Y1654_STAA3	-0.8
538	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1333 PE=4 SV=1	Q2FGZ8|Q2FGZ8_STAA3	-0.8
787	Dihydrolipoyl dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=lpdA PE=3 SV=1	Q2FGL5|Q2FGL5_STAA3	-0.8
43	Glycyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=glyQS PE=3 SV=1	Q2FGF8|SYG_STAA3	-0.7
76	Transketolase OS=Staphylococcus aureus (strain USA300) GN=tkt PE=4 SV=1	Q2FH92|Q2FH92_STAA3	-0.7
97	Putative cell division protein FtsH OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0489 PE=4 SV=1	Q2FJD0|Q2FJD0_STAA3	-0.7
117	FeS assembly protein SufD OS=Staphylococcus aureus (strain USA300) GN=sufD PE=4 SV=1	Q2FIF9|Q2FIF9_STAA3	-0.7
119	GTP-sensing transcriptional pleiotropic repressor codY OS=Staphylococcus aureus (strain USA300) GN=codY PE=3 SV=1	Q2FHI3|CODY_STAA3	-0.7
128	6-phosphogluconate dehydrogenase, decarboxylating OS=Staphylococcus aureus (strain USA300) GN=gnd PE=3 SV=1	Q2FGM3|Q2FGM3_STAA3	-0.7
158	2-oxoglutarate dehydrogenase E1 component OS=Staphylococcus aureus (strain USA300) GN=odhA PE=3 SV=1	Q2FH25|ODO1_STAA3	-0.7
193	Transaldolase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1725 PE=3 SV=1	Q2FFW0|Q2FFW0_STAA3	-0.7
211	Uncharacterized protein SAUSA300_0736 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0736 PE=3 SV=1	Q2FIN9|Y736_STAA3	-0.7
238	50S ribosomal protein L30 OS=Staphylococcus aureus (strain USA300) GN=rpmD PE=3 SV=1	Q2FEQ7|RL30_STAA3	-0.7
245	Valyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=valS PE=3 SV=1	Q2FG72|SYV_STAA3	-0.7

265	Alanyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=alaS PE=3 SV=1	Q2FGA8|SYA_STAA3	-0.7
335	Acetyltransferase, GNAT family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1070 PE=4 SV=1	Q2FHR1|Q2FHR1_STAA3	-0.7
353	Alcohol dehydrogenase, zinc-containing OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2147 PE=4 SV=1	Q2FEU5|Q2FEU5_STAA3	-0.7
356	Aspartate semialdehyde dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=asd PE=3 SV=1	Q2FH44|Q2FH44_STAA3	-0.7
376	Acetyltransferase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2460 PE=4 SV=1	Q2FDY4|Q2FDY4_STAA3	-0.7
422	ATP-dependent Clp protease proteolytic subunit OS=Staphylococcus aureus (strain USA300) GN=clpP PE=3 SV=1	Q2FIM5|CLPP_STAA3	-0.7
500	Epimerase family protein SAUSA300_0753 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0753 PE=3 SV=1	Q2FIM4|Y753_STAA3	-0.7
563	Molybdopterin converting factor, subunit 1 OS=Staphylococcus aureus (strain USA300) GN=moaD PE=4 SV=1	Q2FEM2|Q2FEM2_STAA3	-0.7
631	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0874 PE=4 SV=1	Q2FIA4|Q2FIA4_STAA3	-0.7
701	GMP reductase OS=Staphylococcus aureus (strain USA300) GN=guaC PE=3 SV=1	Q2FH96|GUAC_STAA3	-0.7
79	Glucose-6-phosphate isomerase OS=Staphylococcus aureus (strain USA300) GN=pgi PE=3 SV=1	Q2FIB3|G6PI_STAA3	-0.6
86	UPF0457 protein SAUSA300_2132 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2132 PE=3 SV=1	Q2FEV9|Y2132_STAA3	-0.6
166	Uncharacterized hydrolase SAUSA300_2518 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2518 PE=3 SV=1	Q2FDS6|Y2518_STAA3	-0.6
197	Putative lipoprotein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0372 PE=4 SV=1	Q2FJP2|Q2FJP2_STAA3	-0.6
224	Alcohol dehydrogenase, zinc-containing OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0250 PE=4 SV=1	Q2FK14|Q2FK14_STAA3	-0.6
236	Chaperone clpB OS=Staphylococcus aureus (strain USA300) GN=clpB PE=3 SV=1	Q2FIA1|Q2FIA1_STAA3	-0.6
250	Fibrinogen-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1052 PE=4 SV=1	Q2FHS8|Q2FHS8_STAA3	-0.6
287	2',3'-cyclic-nucleotide 2'-phosphodiesterase OS=Staphylococcus aureus (strain USA300) GN=cvfA PE=3 SV=1	Q2FHF2|CNPD_STAA3	-0.6
364	30S ribosomal protein S19 OS=Staphylococcus aureus (strain USA300) GN=rpsS PE=3 SV=1	Q2FEP3|RS19_STAA3	-0.6
370	Probable uridylyltransferase SAUSA300_2130 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2130 PE=3 SV=1	Q2FEW1|URTF_STAA3	-0.6
444	PTS system, mannitol specific IIA component OS=Staphylococcus aureus (strain USA300) GN=mtlA PE=4 SV=1	Q2FEX5|Q2FEX5_STAA3	-0.6

460	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2418 PE=4 SV=1	Q2FE25|Q2FE25_STAA3	-0.6
498	Glutathione peroxidase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1197 PE=3 SV=1	Q2FHD4|Q2FHD4_STAA3	-0.6
566	Putative lipoprotein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0992 PE=4 SV=1	Q2FHY8|Q2FHY8_STAA3	-0.6
583	Bifunctional protein glmU OS=Staphylococcus aureus (strain USA300) GN=glmU PE=3 SV=1	Q2FJE2|GLMU_STAA3	-0.6
592	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1351 PE=4 SV=1	Q2FGY0|Q2FGY0_STAA3	-0.6
606	Competence/damage-inducible protein cinA OS=Staphylococcus aureus (strain USA300) GN=cinA PE=4 SV=1	Q2FHF4|Q2FHF4_STAA3	-0.6
36	Phosphoglycerate kinase OS=Staphylococcus aureus (strain USA300) GN=pgk PE=3 SV=1	Q2FIM0|PGK_STAA3	-0.5
51	Dihydrolipoamide acetyltransferase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0995 PE=3 SV=1	Q2FHY5|Q2FHY5_STAA3	-0.5
90	Trigger factor OS=Staphylococcus aureus (strain USA300) GN=tig PE=3 SV=1	Q2FG61|TIG_STAA3	-0.5
289	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C OS=Staphylococcus aureus (strain USA300) GN=gatC PE=3 SV=1	Q2FFJ4|GATC_STAA3	-0.5
415	Excinuclease ABC, A subunit OS=Staphylococcus aureus (strain USA300) GN=uvrA PE=3 SV=1	Q2FIN4|Q2FIN4_STAA3	-0.5
431	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0373 PE=4 SV=1	Q2FJP1|Q2FJP1_STAA3	-0.5
443	Cystathionine gamma-synthase OS=Staphylococcus aureus (strain USA300) GN=metB PE=3 SV=1	Q2FJI1|Q2FJI1_STAA3	-0.5
477	Lytic regulatory protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2100 PE=4 SV=1	Q2FEY2|Q2FEY2_STAA3	-0.5
501	30S ribosomal protein S20 OS=Staphylococcus aureus (strain USA300) GN=rpsT PE=3 SV=1	Q2FGD8|RS20_STAA3	-0.5
754	Sulfite reductase flavoprotein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2554 PE=3 SV=1	Q2FDP0|Q2FDP0_STAA3	-0.5
22	Glyceraldehyde-3-phosphate dehydrogenase, type I OS=Staphylococcus aureus (strain USA300) GN=gap PE=3 SV=1	Q2FIM1|Q2FIM1_STAA3	-0.4
132	Foldase protein prsA OS=Staphylococcus aureus (strain USA300) GN=prsA PE=3 SV=1	Q2FFQ5|PRSA_STAA3	-0.4
151	Serine hydroxymethyltransferase OS=Staphylococcus aureus (strain USA300) GN=glyA PE=3 SV=1	Q2FF15|GLYA_STAA3	-0.4
214	Glutamyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=gltX PE=3 SV=1	Q2FJB2|SYE_STAA3	-0.4
229	D-alanine--poly(phosphoribitol) ligase subunit 1 OS=Staphylococcus aureus (strain USA300) GN=dltA PE=3 SV=1	Q2FIE3|DLTA_STAA3	-0.4

239	3-oxoacyl-(Acyl-carrier-protein) synthase II OS=Staphylococcus aureus (strain USA300) GN=fabF PE=3 SV=1	Q2FI92|Q2FI92_STAA3	-0.4
240	Glycerol phosphate lipoteichoic acid synthase OS=Staphylococcus aureus (strain USA300) GN=ltaS PE=3 SV=1	Q2FIS2|LTAS_STAA3	-0.4
277	Thioredoxin reductase OS=Staphylococcus aureus (strain USA300) GN=trxB PE=3 SV=1	Q2FIM9|Q2FIM9_STAA3	-0.4
313	Ribosome-recycling factor OS=Staphylococcus aureus (strain USA300) GN=frr PE=3 SV=1	Q2FHH9|RRF_STAA3	-0.4
318	Iron compound ABC transporter, iron compound-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2235 PE=4 SV=1	Q2FEK8|Q2FEK8_STAA3	-0.4
323	50S ribosomal protein L29 OS=Staphylococcus aureus (strain USA300) GN=rpmC PE=4 SV=1	Q2FEP7|Q2FEP7_STAA3	-0.4
337	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--L-lysine ligase OS=Staphylococcus aureus (strain USA300) GN=murE PE=3 SV=1	Q2FI59|MURE_STAA3	-0.4
421	Putative thioredoxin OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1690 PE=4 SV=1	Q2FFZ4|Q2FFZ4_STAA3	-0.4
535	Nitroreductase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1986 PE=4 SV=1	Q2FF91|Q2FF91_STAA3	-0.4
544	50S ribosomal protein L28 OS=Staphylococcus aureus (strain USA300) GN=rpmB PE=3 SV=1	Q2FHL4|RL28_STAA3	-0.4
596	Putative transcriptional regulator OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2259 PE=4 SV=1	Q2FEI4|Q2FEI4_STAA3	-0.4
599	Fibrinogen-binding protein OS=Staphylococcus aureus (strain USA300) GN=efb PE=4 SV=1	Q2FHS5|Q2FHS5_STAA3	-0.4
607	Arginine deiminase OS=Staphylococcus aureus (strain USA300) GN=arcA PE=3 SV=1	Q2FDM4|Q2FDM4_STAA3	-0.4
44	Acyl carrier protein OS=Staphylococcus aureus (strain USA300) GN=acpP PE=3 SV=1	Q2FHK6|ACP_STAA3	-0.3
189	Cell cycle protein gpsB OS=Staphylococcus aureus (strain USA300) GN=gpsB PE=3 SV=1	Q2FGZ4|GPSB_STAA3	-0.3
445	HTH-type transcriptional regulator rot OS=Staphylococcus aureus (strain USA300) GN=rot PE=3 SV=1	Q2FFX6|Q2FFX6_STAA3	-0.3
448	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1803 PE=4 SV=1	Q2FFP2|Q2FFP2_STAA3	-0.3
464	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1904 PE=4 SV=1	Q2FFH2|Q2FFH2_STAA3	-0.3
546	Cold shock protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2639 PE=3 SV=1	Q2FDF5|Q2FDF5_STAA3	-0.3
550	Cmp-binding-factor 1 OS=Staphylococcus aureus (strain USA300) GN=cbf1 PE=4 SV=1	Q2FFQ4|Q2FFQ4_STAA3	-0.3
564	N utilization substance protein B homolog OS=Staphylococcus aureus (strain USA300) GN=nusB PE=3 SV=1	Q2FGK9|NUSB_STAA3	-0.3

626	Dihydrofolate reductase OS=Staphylococcus aureus (strain USA300) GN=folA PE=3 SV=1	Q2FH12|Q2FH12_STAA3	-0.3
80	Glutamine synthetase OS=Staphylococcus aureus (strain USA300) GN=glnA PE=3 SV=1	Q2FHD0|Q2FHD0_STAA3	-0.2
144	Naphthoate synthase OS=Staphylococcus aureus (strain USA300) GN=menB PE=4 SV=1	Q2FI32|Q2FI32_STAA3	-0.2
173	Putative aldehyde dehydrogenase AldA OS=Staphylococcus aureus (strain USA300) GN=aldA PE=3 SV=1	Q2FK94|ALDA_STAA3	-0.2
190	3-hexulose-6-phosphate synthase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0555 PE=3 SV=1	Q2FJ70|HPS_STAA3	-0.2
192	50S ribosomal protein L18 OS=Staphylococcus aureus (strain USA300) GN=rplR PE=3 SV=1	Q2FEQ5|RL18_STAA3	-0.2
299	Transcription elongation factor greA OS=Staphylococcus aureus (strain USA300) GN=greA PE=3 SV=1	Q2FGB6|GREA_STAA3	-0.2
302	30S ribosomal protein S18 OS=Staphylococcus aureus (strain USA300) GN=rpsR PE=3 SV=1	Q2FJP6|RS18_STAA3	-0.2
312	Probable glycine dehydrogenase [decarboxylating] subunit 1 OS=Staphylococcus aureus (strain USA300) GN=gcvPA PE=3 SV=1	Q2FGI6|GCSPA_STAA3	-0.2
314	50S ribosomal protein L17 OS=Staphylococcus aureus (strain USA300) GN=rplQ PE=3 SV=1	Q2FER6|RL17_STAA3	-0.2
347	ABC transporter, substrate-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0798 PE=4 SV=1	Q2FII0|Q2FII0_STAA3	-0.2
368	Amino acid ABC transporter, amino acid-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2359 PE=4 SV=1	Q2FE84|Q2FE84_STAA3	-0.2
424	Homoserine dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1226 PE=3 SV=1	Q2FHA5|Q2FHA5_STAA3	-0.2
430	Peptide methionine sulfoxide reductase msrB OS=Staphylococcus aureus (strain USA300) GN=msrB PE=3 SV=1	Q2FH15|MSRB_STAA3	-0.2
447	PTS system, glucose-specific IIA component OS=Staphylococcus aureus (strain USA300) GN=crr PE=4 SV=1	Q2FH16|Q2FH16_STAA3	-0.2
479	Argininosuccinate synthase OS=Staphylococcus aureus (strain USA300) GN=argG PE=3 SV=1	Q2FIB4|ASSY_STAA3	-0.2
484	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1303 PE=4 SV=1	Q2FH28|Q2FH28_STAA3	-0.2
495	Organic hydroperoxide resistance protein-like OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0786 PE=3 SV=1	Q2FIJ2|OHRL_STAA3	-0.2
52	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1581 PE=4 SV=1	Q2FGA2|Q2FGA2_STAA3	-0.1
113	Pyruvate oxidase OS=Staphylococcus aureus (strain USA300) GN=cidC PE=3 SV=1	Q2FDW7|Q2FDW7_STAA3	-0.1
207	Molybdenum ABC transporter, molybdenum-binding protein ModA OS=Staphylococcus aureus (strain USA300) GN=modA PE=4 SV=1	Q2FEL3|Q2FEL3_STAA3	-0.1

212	Iron compound ABC transporter, iron compound-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2136 PE=4 SV=1	Q2FEV5|Q2FEV5_STAA3	-0.1
366	Elongation factor P OS=Staphylococcus aureus (strain USA300) GN=efp PE=3 SV=1	Q2FGJ3|EFP_STAA3	-0.1
406	Anti-sigma factor antagonist OS=Staphylococcus aureus (strain USA300) GN=rsbV PE=3 SV=1	Q2FF58|Q2FF58_STAA3	-0.1
461	Fructose specific permease OS=Staphylococcus aureus (strain USA300) GN=fruA PE=4 SV=1	Q2FIU0|Q2FIU0_STAA3	-0.1
466	Leucyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=leuS PE=3 SV=1	Q2FFY0|SYL_STAA3	-0.1
487	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0985 PE=4 SV=1	Q2FHZ5|Q2FHZ5_STAA3	-0.1
562	Penicillin-binding protein 4 OS=Staphylococcus aureus (strain USA300) GN=pbp4 PE=3 SV=1	Q2FIZ6|Q2FIZ6_STAA3	-0.1
629	50S ribosomal protein L32 OS=Staphylococcus aureus (strain USA300) GN=rpmF PE=3 SV=1	Q2FHV3|RL32_STAA3	-0.1
7	DNA-binding protein HU OS=Staphylococcus aureus (strain USA300) GN=hup PE=3 SV=1	Q2FGW9|Q2FGW9_STAA3	0
84	Fructose bisphosphate aldolase OS=Staphylococcus aureus (strain USA300) GN=fba PE=4 SV=1	Q2FF03|Q2FF03_STAA3	0
226	Adenylate kinase OS=Staphylococcus aureus (strain USA300) GN=adk PE=3 SV=1	Q2FER0|Q2FER0_STAA3	0
303	50S ribosomal protein L31 type B OS=Staphylococcus aureus (strain USA300) GN=rpmE2 PE=3 SV=1	Q2FF08|RL31B_STAA3	0
309	Signal transduction protein TRAP OS=Staphylococcus aureus (strain USA300) GN=traP PE=3 SV=1	Q2FFR1|TRAP_STAA3	0
481	Staphylococcal accessory regulator OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0114 PE=4 SV=1	Q2FKE7|Q2FKE7_STAA3	0
541	Phenylalanyl-tRNA synthetase beta chain OS=Staphylococcus aureus (strain USA300) GN=pheT PE=3 SV=1	Q2FHU2|SYFB_STAA3	0
580	Penicillin-binding protein 3 OS=Staphylococcus aureus (strain USA300) GN=pbp3 PE=4 SV=1	Q2FGH1|Q2FGH1_STAA3	0
615	Iron compound ABC transporter, iron compound-binding protein SirA OS=Staphylococcus aureus (strain USA300) GN=sirA PE=4 SV=1	Q2FKE4|Q2FKE4_STAA3	0
711	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2378 PE=4 SV=1	Q2FE65|Q2FE65_STAA3	0
6	UPF0337 protein SAUSA300_0816 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0816 PE=3 SV=1	Q2FIG2|Y816_STAA3	0.1
21	Chaperone protein dnaK OS=Staphylococcus aureus (strain USA300) GN=dnaK PE=2 SV=1	Q2FGE3|DNAK_STAA3	0.1
107	UPF0342 protein SAUSA300_1795 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1795 PE=3 SV=1	Q2FFQ0|Y1795_STAA3	0.1

157	Copper chaperone copZ OS=Staphylococcus aureus (strain USA300) GN=copZ PE=3 SV=1	Q2FDU9|COPZ_STAA3	0.1
227	Thiol peroxidase OS=Staphylococcus aureus (strain USA300) GN=tpx PE=4 SV=1	Q2FG25|Q2FG25_STAA3	0.1
268	FMN-dependent NADH-azoreductase OS=Staphylococcus aureus (strain USA300) GN=azoR PE=3 SV=1	Q2FK58|AZOR_STAA3	0.1
293	Glucokinase OS=Staphylococcus aureus (strain USA300) GN=glk PE=4 SV=1	Q2FGH6|Q2FGH6_STAA3	0.1
419	50S ribosomal protein L24 OS=Staphylococcus aureus (strain USA300) GN=rplX PE=3 SV=1	Q2FEQ0|RL24_STAA3	0.1
458	Putative cell-division initiation protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1086 PE=4 SV=1	Q2FHP5|Q2FHP5_STAA3	0.1
647	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2246 PE=4 SV=1	Q2FEJ7|Q2FEJ7_STAA3	0.1
722	(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase OS=Staphylococcus aureus (strain USA300) GN=fabZ PE=3 SV=1	Q2FF28|FABZ_STAA3	0.1
34	N-acetylmuramoyl-L-alanine amidase domain protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2579 PE=4 SV=1	Q2FDL5|Q2FDL5_STAA3	0.2
185	50S ribosomal protein L11 OS=Staphylococcus aureus (strain USA300) GN=rplK PE=3 SV=3	Q2FJA3|RL11_STAA3	0.2
215	50S ribosomal protein L25 OS=Staphylococcus aureus (strain USA300) GN=rplY PE=3 SV=1	Q2FJE0|RL25_STAA3	0.2
389	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1215 PE=4 SV=1	Q2FHB6|Q2FHB6_STAA3	0.2
492	Chorismate mutase/phospho-2-dehydro-3-deoxyheptonate aldolase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1683 PE=4 SV=1	Q2FG01|Q2FG01_STAA3	0.2
507	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0931 PE=4 SV=1	Q2FI49|Q2FI49_STAA3	0.2
683	Putative GTP-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1136 PE=4 SV=1	Q2FHJ5|Q2FHJ5_STAA3	0.2
771	NADPH-dependent oxidoreductase OS=Staphylococcus aureus (strain USA300) GN=nfrA PE=3 SV=1	Q2FJN3|NFRA_STAA3	0.2
10	Alkaline shock protein 23 OS=Staphylococcus aureus (strain USA300) GN=asp23 PE=3 SV=1	Q2FEV0|ASP23_STAA3	0.3
172	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1698 PE=4 SV=1	Q2FFY6|Q2FFY6_STAA3	0.3
286	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Staphylococcus aureus (strain USA300) GN=odhB PE=3 SV=1	Q2FH26|ODO2_STAA3	0.3
401	30S ribosomal protein S16 OS=Staphylococcus aureus (strain USA300) GN=rpsP PE=3 SV=1	Q2FHK0|RS16_STAA3	0.3
768	SUF system FeS assembly protein, NifU family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0821 PE=4 SV=1	Q2FIF7|Q2FIF7_STAA3	0.3

28	Secretory antigen SsaA OS=Staphylococcus aureus (strain USA300) GN=ssaA PE=4 SV=1	Q2FEJ4|Q2FEJ4_STAA3	0.4
141	N-acetylmuramoyl-L-alanine amidase sle1 OS=Staphylococcus aureus (strain USA300) GN=sle1 PE=3 SV=1	Q2FJH7|SLE1_STAA3	0.4
324	6,7-dimethyl-8-ribityllumazine synthase OS=Staphylococcus aureus (strain USA300) GN=ribH PE=3 SV=1	Q2FFX3|RISB_STAA3	0.4
393	Mannitol-1-phosphate 5-dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=mtlD PE=3 SV=1	Q2FEX4|MTLD_STAA3	0.4
398	Translation initiation factor IF-3 OS=Staphylococcus aureus (strain USA300) GN=infC PE=3 SV=1	Q2FG56|IF3_STAA3	0.4
407	D-alanine--poly(phosphoribitol) ligase subunit 2 OS=Staphylococcus aureus (strain USA300) GN=dltC PE=3 SV=1	Q2FIE1|DLTC_STAA3	0.4
489	Triacylglycerol lipase OS=Staphylococcus aureus (strain USA300) GN=lip PE=4 SV=1	Q2FDJ1|Q2FDJ1_STAA3	0.4
618	NLPA lipoprotein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0437 PE=4 SV=1	Q2FJH8|Q2FJH8_STAA3	0.4
38	Thioredoxin OS=Staphylococcus aureus (strain USA300) GN=trxA PE=3 SV=1	Q2FHT6|THIO_STAA3	0.5
396	NH(3)-dependent NAD(+) synthetase OS=Staphylococcus aureus (strain USA300) GN=nadE PE=3 SV=1	Q2FFI3|NADE_STAA3	0.5
571	Putative lipoprotein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0724 PE=4 SV=1	Q2FIQ1|Q2FIQ1_STAA3	0.5
75	Phosphocarrier protein HPr OS=Staphylococcus aureus (strain USA300) GN=ptsH PE=4 SV=1	Q2FHZ7|Q2FHZ7_STAA3	0.6
134	Transcriptional regulator sarA OS=Staphylococcus aureus (strain USA300) GN=sarA PE=3 SV=1	Q2FJ20|SARA_STAA3	0.6
310	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Staphylococcus aureus (strain USA300) GN=accA PE=1 SV=1	Q2FG38|ACCA_STAA3	0.6
624	Probable transglycosylase sceD OS=Staphylococcus aureus (strain USA300) GN=sceD PE=2 SV=1	Q2FF31|SCED_STAA3	0.6
296	Malonyl CoA-acyl carrier protein transacylase OS=Staphylococcus aureus (strain USA300) GN=fabD PE=4 SV=1	Q2FHK8|Q2FHK8_STAA3	0.7
540	tRNA uridine 5-carboxymethylaminomethyl modification enzyme mnmG OS=Staphylococcus aureus (strain USA300) GN=mnmG PE=3 SV=2	Q2FDE9|MNMG_STAA3	0.7
372	Methionine-S-sulfoxide reductase OS=Staphylococcus aureus (strain USA300) GN=msrA PE=3 SV=1	Q2FH14|Q2FH14_STAA3	0.8
503	Methionine aminopeptidase OS=Staphylococcus aureus (strain USA300) GN=map PE=3 SV=1	Q2FFK7|Q2FFK7_STAA3	0.8
619	Clumping factor A OS=Staphylococcus aureus (strain USA300) GN=clfA PE=3 SV=1	Q2FIK6|Q2FIK6_STAA3	0.8
23	Probable transglycosylase isaA OS=Staphylococcus aureus (strain USA300) GN=isaA PE=3 SV=1	Q2FDT8|ISAA_STAA3	0.9

45	D-lactate dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=ddh PE=3 SV=1	Q2FDY1|Q2FDY1_STAA3	0.9
263	UPF0435 protein SAUSA300_1861 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1861 PE=3 SV=2	Q2FFL5|Y1861_STAA3	0.9
349	S-ribosylhomocysteine lyase OS=Staphylococcus aureus (strain USA300) GN=luxS PE=3 SV=1	Q2FEZ4|LUXS_STAA3	0.9
478	Carboxyl-terminal protease OS=Staphylococcus aureus (strain USA300) GN=ctpA PE=3 SV=1	Q2FH18|Q2FH18_STAA3	0.9
659	Membrane-associated protein tcaA OS=Staphylococcus aureus (strain USA300) GN=tcaA PE=3 SV=1	Q2FEE1|TCAA_STAA3	0.9
358	Transferrin receptor OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0721 PE=4 SV=1	Q2FIQ4|Q2FIQ4_STAA3	1
418	Probable glycine dehydrogenase [decarboxylating] subunit 2 OS=Staphylococcus aureus (strain USA300) GN=gcvPB PE=3 SV=1	Q2FGI7|GCSPB_STAA3	1
525	Glutamine amidotransferase subunit pdxT OS=Staphylococcus aureus (strain USA300) GN=pdxT PE=3 SV=1	Q2FJC0|PDXT_STAA3	1
713	Aminopeptidase PepS OS=Staphylococcus aureus (strain USA300) GN=pepS PE=4 SV=1	Q2FFL6|Q2FFL6_STAA3	1
66	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2473 PE=4 SV=1	Q2FDX1|Q2FDX1_STAA3	1.1
266	UDP-N-acetylmuramoylalanine--D-glutamate ligase OS=Staphylococcus aureus (strain USA300) GN=murD PE=3 SV=1	Q2FHQ4|MURD_STAA3	1.1
206	General stress protein 20U OS=Staphylococcus aureus (strain USA300) GN=dps PE=3 SV=1	Q2FEZ0|Q2FEZ0_STAA3	1.3
363	Imidazolonepropionase OS=Staphylococcus aureus (strain USA300) GN=hutI PE=3 SV=1	Q2FEG6|HUTI_STAA3	1.5
16	Elongation factor Ts OS=Staphylococcus aureus (strain USA300) GN=tsf PE=3 SV=1	Q2FHI1|EFTS_STAA3	1.6
284	Superoxide dismutase [Mn/Fe] 1 OS=Staphylococcus aureus (strain USA300) GN=sodA PE=3 SV=1	Q2FGH0|SODM1_STAA3	1.6
513	Arginase OS=Staphylococcus aureus (strain USA300) GN=rocF PE=3 SV=1	Q2FEW8|Q2FEW8_STAA3	1.7
374	GTP cyclohydrolase folE2 OS=Staphylococcus aureus (strain USA300) GN=folE2 PE=3 SV=1	Q2FJ74|GCH4_STAA3	1.8
462	Cysteinyl-tRNA synthetase OS=Staphylococcus aureus (strain USA300) GN=cysS PE=3 SV=1	Q2FJB0|SYC_STAA3	1.8
2	Antibacterial protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1067 PE=4 SV=1	Q2FHR4|Q2FHR4_STAA3	2.2
280	Superoxide dismutase [Mn/Fe] 2 OS=Staphylococcus aureus (strain USA300) GN=sodM PE=3 SV=1	Q2FKC6|SODM2_STAA3	2.2
4	Antibacterial protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1068 PE=4 SV=1	Q2FHR3|Q2FHR3_STAA3	2.7

257	UPF0337 protein SAUSA300_1582 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1582 PE=3 SV=1	Q2FGA1|Y1582_STAA3	2.7
438	Phi77 ORF014-like protein, phage anti-repressor protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1966 PE=4 SV=1	Q2FFB1|Q2FFB1_STAA3	2.9
176	Deoxyribose-phosphate aldolase OS=Staphylococcus aureus (strain USA300) GN=deoC PE=3 SV=1	Q2FKC1|Q2FKC1_STAA3	No Values
291	UDP-N-acetylmuramate--L-alanine ligase OS=Staphylococcus aureus (strain USA300) GN=murC PE=3 SV=1	Q2FFZ8|MURC_STAA3	No Values
331	Pseudouridine synthase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1090 PE=3 SV=1	Q2FHP1|Q2FHP1_STAA3	No Values
397	Fumarate hydratase, class II OS=Staphylococcus aureus (strain USA300) GN=fumC PE=4 SV=1	Q2FFP4|Q2FFP4_STAA3	No Values
410	Cytosol aminopeptidase OS=Staphylococcus aureus (strain USA300) GN=ampA PE=3 SV=1	Q2FID3|Q2FID3_STAA3	No Values
446	Exodeoxyribonuclease 7 small subunit OS=Staphylococcus aureus (strain USA300) GN=xseB PE=3 SV=1	Q2FGL1|EX7S_STAA3	No Values
449	Protein grpE OS=Staphylococcus aureus (strain USA300) GN=grpE PE=3 SV=1	Q2FGE2|GRPE_STAA3	No Values
454	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1336 PE=4 SV=1	Q2FGZ5|Q2FGZ5_STAA3	No Values
463	50S ribosomal protein L15 OS=Staphylococcus aureus (strain USA300) GN=rplO PE=3 SV=1	Q2FEQ8|RL15_STAA3	No Values
465	30S ribosomal protein S15 OS=Staphylococcus aureus (strain USA300) GN=rpsO PE=3 SV=1	Q2FHG5|RS15_STAA3	No Values
474	Serine-aspartate repeat-containing protein D OS=Staphylococcus aureus (strain USA300) GN=sdrD PE=3 SV=1	Q2FJ78|SDRD_STAA3	No Values
488	L-lactate permease OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2313 PE=4 SV=1	Q2FED0|Q2FED0_STAA3	No Values
494	Putative zinc-binding dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2317 PE=4 SV=1	Q2FEC6|Q2FEC6_STAA3	No Values
512	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1684 PE=4 SV=1	Q2FG00|Q2FG00_STAA3	No Values
518	Esterase-like protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2296 PE=4 SV=1	Q2FEE7|Q2FEE7_STAA3	No Values
520	3-methyl-2-oxobutanoate hydroxymethyltransferase OS=Staphylococcus aureus (strain USA300) GN=panB PE=3 SV=2	Q2FDR0|PANB_STAA3	No Values
526	ATP synthase epsilon chain OS=Staphylococcus aureus (strain USA300) GN=atpC PE=3 SV=1	Q2FF25|ATPE_STAA3	No Values
528	D-isomer specific 2-hydroxyacid dehydrogenase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2496 PE=3 SV=1	Q2FDU8|Q2FDU8_STAA3	No Values
529	Coenzyme A disulfide reductase OS=Staphylococcus aureus (strain USA300) GN=cdr PE=3 SV=1	Q2FIA5|CDR_STAA3	No Values

530	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0383 PE=4 SV=1	Q2FJN1|Q2FJN1_STAA3	No Values
532	Molybdopterin biosynthesis protein A OS=Staphylococcus aureus (strain USA300) GN=moeA PE=4 SV=1	Q2FEL9|Q2FEL9_STAA3	No Values
533	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1171 PE=3 SV=1	Q2FHG0|Q2FHG0_STAA3	No Values
536	Adenine phosphoribosyltransferase OS=Staphylococcus aureus (strain USA300) GN=apt PE=3 SV=1	Q2FG92|APT_STAA3	No Values
543	Methionine import ATP-binding protein MetN 2 OS=Staphylococcus aureus (strain USA300) GN=metN2 PE=3 SV=1	Q2FII2|METN2_STAA3	No Values
547	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2482 PE=4 SV=1	Q2FDW2|Q2FDW2_STAA3	No Values
549	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase OS=Staphylococcus aureus (strain USA300) GN=dapH PE=3 SV=1	Q2FH41|DAPH_STAA3	No Values
554	TelA-like protein SAUSA300_1299 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1299 PE=3 SV=1	Q2FH32|TELL_STAA3	No Values
561	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0749 PE=4 SV=1	Q2FIM7|Q2FIM7_STAA3	No Values
572	DNA topoisomerase 1 OS=Staphylococcus aureus (strain USA300) GN=topA PE=3 SV=2	Q2FHI8|TOP1_STAA3	No Values
573	ABC transporter, ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2357 PE=4 SV=1	Q2FE86|Q2FE86_STAA3	No Values
576	Putative N-acetyltransferase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2631 PE=3 SV=1	Q2FDG3|Q2FDG3_STAA3	No Values
581	DNA mismatch repair protein mutL OS=Staphylococcus aureus (strain USA300) GN=mutL PE=3 SV=1	Q2FHE2|MUTL_STAA3	No Values
588	Purine nucleoside phosphorylase OS=Staphylococcus aureus (strain USA300) GN=deoD PE=3 SV=1	Q2FEZ1|Q2FEZ1_STAA3	No Values
591	UPF0473 protein SAUSA300_1572 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1572 PE=3 SV=1	Q2FGB1|Y1572_STAA3	No Values
593	Glycolytic operon regulator OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0755 PE=4 SV=1	Q2FIM2|Q2FIM2_STAA3	No Values
598	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1536 PE=4 SV=1	Q2FGE7|Q2FGE7_STAA3	No Values
600	Sensor protein OS=Staphylococcus aureus (strain USA300) GN=srrB PE=3 SV=1	Q2FGP1|Q2FGP1_STAA3	No Values
614	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0173 PE=4 SV=1	Q2FK91|Q2FK91_STAA3	No Values
616	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1180 PE=4 SV=1	Q2FHF1|Q2FHF1_STAA3	No Values
620	Putative teichoic acid biosynthesis protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0251 PE=4 SV=1	Q2FK13|Q2FK13_STAA3	No Values

628	Glycine betaine transporter opuD OS=Staphylococcus aureus (strain USA300) GN=opuD PE=4 SV=1	Q2FH86|Q2FH86_STAA3	No Values
632	UPF0349 protein SAUSA300_0842 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0842 PE=3 SV=1	Q2FID6|Y842_STAA3	No Values
635	Glutamate racemase OS=Staphylococcus aureus (strain USA300) GN=murI PE=3 SV=1	Q2FHT1|MURI_STAA3	No Values
636	PhiPVL ORF41-like protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1961 PE=4 SV=1	Q2FFB6|Q2FFB6_STAA3	No Values
640	DNA ligase OS=Staphylococcus aureus (strain USA300) GN=ligA PE=3 SV=1	Q2FFJ1|DNLJ_STAA3	No Values
643	Putative chromosome partioning protein, ParB family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2643 PE=4 SV=1	Q2FDF1|Q2FDF1_STAA3	No Values
648	Glutamyl-aminopeptidase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1691 PE=4 SV=1	Q2FFZ3|Q2FFZ3_STAA3	No Values
650	Bacterial luciferase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1580 PE=4 SV=1	Q2FGA3|Q2FGA3_STAA3	No Values
652	Alpha glucosidase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1456 PE=3 SV=1	Q2FGM6|Q2FGM6_STAA3	No Values
653	Oligoendopeptidase F OS=Staphylococcus aureus (strain USA300) GN=pepF PE=4 SV=1	Q2FH53|Q2FH53_STAA3	No Values
674	ABC transporter, substrate-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0231 PE=4 SV=1	Q2FK33|Q2FK33_STAA3	No Values
675	PTS system, trehalose-specific IIBC component OS=Staphylococcus aureus (strain USA300) GN=treP PE=4 SV=1	Q2FJG8|Q2FJG8_STAA3	No Values
679	Transcription-repair-coupling factor OS=Staphylococcus aureus (strain USA300) GN=mfd PE=3 SV=1	Q2FJD8|MFD_STAA3	No Values
680	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2327 PE=4 SV=1	Q2FEB6|Q2FEB6_STAA3	No Values
681	Phosphoglucomutase OS=Staphylococcus aureus (strain USA300) GN=pgcA PE=3 SV=2	Q2FE11|PGCA_STAA3	No Values
684	Putative osmoprotectant ABC transporter, ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0706 PE=4 SV=1	Q2FIR9|Q2FIR9_STAA3	No Values
685	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2404 PE=4 SV=1	Q2FE39|Q2FE39_STAA3	No Values
686	UDP-N-acetylglucosamine 2-epimerase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2065 PE=3 SV=1	Q2FF17|Q2FF17_STAA3	No Values
688	Para-nitrobenzyl esterase OS=Staphylococcus aureus (strain USA300) GN=pnbA PE=3 SV=1	Q2FE47|Q2FE47_STAA3	No Values
689	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2112 PE=4 SV=1	Q2FEX0|Q2FEX0_STAA3	No Values
690	Transcriptional repressor nrdR OS=Staphylococcus aureus (strain USA300) GN=nrdR PE=3 SV=1	Q2FG51|NRDR_STAA3	No Values

691	UTP--glucose-1-phosphate uridylyltransferase OS=Staphylococcus aureus (strain USA300) GN=gtaB PE=3 SV=2	Q2FE05|GTAB_STAA3	No Values
692	Uroporphyrinogen decarboxylase OS=Staphylococcus aureus (strain USA300) GN=hemE PE=3 SV=1	Q2FFR2|DCUP_STAA3	No Values
693	Aminotransferase, class I OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0952 PE=3 SV=1	Q2FI28|Q2FI28_STAA3	No Values
694	Indole-3-pyruvate decarboxylase OS=Staphylococcus aureus (strain USA300) GN=ipdC PE=3 SV=1	Q2FK74|Q2FK74_STAA3	No Values
695	Monooxygenase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2255 PE=4 SV=1	Q2FEI8|Q2FEI8_STAA3	No Values
703	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0814 PE=4 SV=1	Q2FIG4|Q2FIG4_STAA3	No Values
704	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0740 PE=4 SV=1	Q2FIN6|Q2FIN6_STAA3	No Values
706	DHH subfamily 1 protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0014 PE=4 SV=1	Q2FKP2|Q2FKP2_STAA3	No Values
707	Acetyltransferase, GNAT family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0451 PE=4 SV=1	Q2FJG5|Q2FJG5_STAA3	No Values
709	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1010 PE=4 SV=1	Q2FHX0|Q2FHX0_STAA3	No Values
710	Acetyl-CoA carboxylase, biotin carboxylase OS=Staphylococcus aureus (strain USA300) GN=accC PE=4 SV=1	Q2FGC0|Q2FGC0_STAA3	No Values
712	Formimidoylglutamase OS=Staphylococcus aureus (strain USA300) GN=hutG PE=3 SV=1	Q2FEG2|HUTG_STAA3	No Values
715	Probable GTP-binding protein engB OS=Staphylococcus aureus (strain USA300) GN=engB PE=3 SV=1	Q2FG63|ENGB_STAA3	No Values
716	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2447 PE=4 SV=1	Q2FDZ7|Q2FDZ7_STAA3	No Values
718	NADH-dependent flavin oxidoreductase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0859 PE=4 SV=1	Q2FIB9|Q2FIB9_STAA3	No Values
720	Putative phage infection protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2578 PE=4 SV=1	Q2FDL6|Q2FDL6_STAA3	No Values
723	Diacylglycerol kinase OS=Staphylococcus aureus (strain USA300) GN=dagK PE=3 SV=1	Q2FFJ7|DAGK_STAA3	No Values
724	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1671 PE=4 SV=1	Q2FG13|Q2FG13_STAA3	No Values
725	Delta-aminolevulinic acid dehydratase OS=Staphylococcus aureus (strain USA300) GN=hemB PE=3 SV=1	Q2FG68|Q2FG68_STAA3	No Values
726	Glycosyl transferase, group 1 family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1349 PE=4 SV=1	Q2FGY2|Q2FGY2_STAA3	No Values
728	Ribonuclease R OS=Staphylococcus aureus (strain USA300) GN=rnr PE=3 SV=1	Q2FIL3|Q2FIL3_STAA3	No Values

732	Iron-dependent repressor OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0621 PE=4 SV=1	Q2FJ04|Q2FJ04_STAA3	No Values
733	SIS domain protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0556 PE=4 SV=1	Q2FJ69|Q2FJ69_STAA3	No Values
734	Serine acetyltransferase OS=Staphylococcus aureus (strain USA300) GN=cysE PE=4 SV=1	Q2FJB1|Q2FJB1_STAA3	No Values
735	Putative membrane protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0279 PE=4 SV=1	Q2FJY5|Q2FJY5_STAA3	No Values
738	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0466 PE=4 SV=1	Q2FJF3|Q2FJF3_STAA3	No Values
739	UPF0403 protein SAUSA300_1321 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1321 PE=3 SV=1	Q2FH10|Y1321_STAA3	No Values
741	DNA polymerase III polC-type OS=Staphylococcus aureus (strain USA300) GN=polC PE=3 SV=1	Q2FHH4|DPO3_STAA3	No Values
742	Putative peptidase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2087 PE=4 SV=1	Q2FEZ5|Q2FEZ5_STAA3	No Values
743	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2394 PE=4 SV=1	Q2FE49|Q2FE49_STAA3	No Values
744	Queuine tRNA-ribosyltransferase OS=Staphylococcus aureus (strain USA300) GN=tgt PE=3 SV=1	Q2FG88|TGT_STAA3	No Values
745	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2527 PE=4 SV=1	Q2FDR7|Q2FDR7_STAA3	No Values
746	Glycine betaine/carnitine/choline ABC transporter OS=Staphylococcus aureus (strain USA300) GN=opuCc PE=4 SV=1	Q2FE52|Q2FE52_STAA3	No Values
747	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2381 PE=4 SV=1	Q2FE62|Q2FE62_STAA3	No Values
748	tRNA (guanine-N(7)-)-methyltransferase OS=Staphylococcus aureus (strain USA300) GN=trmB PE=3 SV=1	Q2FFZ0|TRMB_STAA3	No Values
749	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1534 PE=4 SV=1	Q2FGE9|Q2FGE9_STAA3	No Values
753	HAD-superfamily hydrolase, subfamily IA, variant 1 OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0557 PE=4 SV=1	Q2FJ68|Q2FJ68_STAA3	No Values
755	Ribosomal RNA small subunit methyltransferase G OS=Staphylococcus aureus (strain USA300) GN=rsmG PE=3 SV=1	Q2FDF0|RSMG_STAA3	No Values
757	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta OS=Staphylococcus aureus (strain USA300) GN=accD PE=3 SV=1	Q2FG37|ACCD_STAA3	No Values
758	Porphobilinogen deaminase OS=Staphylococcus aureus (strain USA300) GN=hemC PE=3 SV=1	Q2FG66|HEM3_STAA3	No Values
760	Thymidylate synthase OS=Staphylococcus aureus (strain USA300) GN=thyA PE=3 SV=1	Q2FH11|TYSY_STAA3	No Values
761	Glycine betaine aldehyde dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=betB PE=3 SV=1	Q2FDP8|Q2FDP8_STAA3	No Values

762	Preprotein translocase subunit secY OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2184 PE=3 SV=1	Q2FEQ9|Q2FEQ9_STAA3	No Values
763	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2143 PE=4 SV=1	Q2FEU9|Q2FEU9_STAA3	No Values
765	Peptide methionine sulfoxide reductase MsrA OS=Staphylococcus aureus (strain USA300) GN=msrA PE=3 SV=1	Q2FH75|Q2FH75_STAA3	No Values
767	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1069 PE=4 SV=1	Q2FHR2|Q2FHR2_STAA3	No Values
770	Serine-aspartate repeat-containing protein E OS=Staphylococcus aureus (strain USA300) GN=sdrE PE=3 SV=1	Q2FJ77|SDRE_STAA3	No Values
772	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1650 PE=4 SV=1	Q2FG34|Q2FG34_STAA3	No Values
773	Peptidase T OS=Staphylococcus aureus (strain USA300) GN=pepT PE=3 SV=1	Q2FIP8|PEPT_STAA3	No Values
774	DNA topoisomerase 3 OS=Staphylococcus aureus (strain USA300) GN=topB PE=3 SV=1	Q2FEN5|TOP3_STAA3	No Values
775	Oligopeptide ABC transporter, substrate-binding protein OS=Staphylococcus aureus (strain USA300) GN=oppA PE=4 SV=1	Q2FI87|Q2FI87_STAA3	No Values
776	Putative lipoprotein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0079 PE=4 SV=1	Q2FKI1|Q2FKI1_STAA3	No Values
777	Ferredoxin--NADP reductase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2319 PE=3 SV=1	Q2FEC4|FENR_STAA3	No Values
778	Urea amidolyase-related protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0702 PE=4 SV=1	Q2FIS3|Q2FIS3_STAA3	No Values
779	Guanylate kinase OS=Staphylococcus aureus (strain USA300) GN=gmk PE=3 SV=1	Q2FHM9|KGUA_STAA3	No Values
780	Glycerol uptake facilitator OS=Staphylococcus aureus (strain USA300) GN=glpF PE=3 SV=1	Q2FHE0|Q2FHE0_STAA3	No Values
781	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1011 PE=4 SV=1	Q2FHW9|Q2FHW9_STAA3	No Values
782	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1908 PE=4 SV=1	Q2FFG8|Q2FFG8_STAA3	No Values
783	FtsK/SpoIIIE family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1687 PE=4 SV=1	Q2FFZ7|Q2FFZ7_STAA3	No Values
784	MutS2 protein OS=Staphylococcus aureus (strain USA300) GN=mutS2 PE=3 SV=1	Q2FHT7|MUTS2_STAA3	No Values
785	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase OS=Staphylococcus aureus (strain USA300) GN=menD PE=3 SV=1	Q2FI34|MEND_STAA3	No Values
786	Sensor protein kinase walK OS=Staphylococcus aureus (strain USA300) GN=walK PE=3 SV=1	Q2FKN7|WALK_STAA3	No Values
789	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1081 PE=4 SV=1	Q2FHQ0|Q2FHQ0_STAA3	No Values

790	DNA polymerase III, gamma and tau subunits OS=Staphylococcus aureus (strain USA300) GN=dnaX PE=4 SV=1	Q2FJG4|Q2FJG4_STAA3	No Values
791	Pantothenate synthetase OS=Staphylococcus aureus (strain USA300) GN=panC PE=3 SV=1	Q2FDR1|PANC_STAA3	No Values
346	Cysteine desulfurases, SufS subfamily subfamily OS=Staphylococcus aureus (strain USA300) GN=sufS PE=3 SV=1	Q2FIF8|Q2FIF8_STAA3	Reference Missing
395	Aldehyde dehydrogenase OS=Staphylococcus aureus (strain USA300) GN=aldA2 PE=3 SV=1	Q2FFH5|Q2FFH5_STAA3	Reference Missing
455	Transcriptional regulator OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0958 PE=4 SV=1	Q2FI22|Q2FI22_STAA3	Reference Missing
499	HPr kinase/phosphorylase OS=Staphylococcus aureus (strain USA300) GN=hprK PE=3 SV=1	Q2FIN3|HPRK_STAA3	Reference Missing
524	FMN-dependent NADPH-azoreductase OS=Staphylococcus aureus (strain USA300) GN=azo1 PE=3 SV=1	Q2FJ80|AZO1_STAA3	Reference Missing
605	Transcriptional regulator, Fur family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1448 PE=4 SV=1	Q2FGN4|Q2FGN4_STAA3	Reference Missing
630	Oligopeptide ABC transporter, ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=oppD PE=4 SV=1	Q2FI89|Q2FI89_STAA3	Reference Missing
663	Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase trmFO OS=Staphylococcus aureus (strain USA300) GN=trmFO PE=3 SV=1	Q2FHI7|TRMFO_STAA3	Reference Missing
672	Putative iron compound ABC transporter, iron compound-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0598 PE=4 SV=1	Q2FJ27|Q2FJ27_STAA3	Reference Missing
677	Ribosome-binding factor A OS=Staphylococcus aureus (strain USA300) GN=rbfA PE=3 SV=1	Q2FHG8|RBFA_STAA3	Reference Missing
708	Peptidase, M20/M25/M40 family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1460 PE=4 SV=1	Q2FGM2|Q2FGM2_STAA3	Reference Missing
730	Undecaprenyl-diphosphatase OS=Staphylococcus aureus (strain USA300) GN=uppP PE=3 SV=1	Q2FIV6|UPPP_STAA3	Reference Missing
201	Alpha-hemolysin OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1058 PE=4 SV=1	Q2FHS2|Q2FHS2_STAA3	Value Missing
242	Transcriptional regulatory protein walR OS=Staphylococcus aureus (strain USA300) GN=walR PE=3 SV=1	Q2FKN8|WALR_STAA3	Value Missing
328	S1 RNA binding domain protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2021 PE=4 SV=1	Q2FF61|Q2FF61_STAA3	Value Missing
362	Probable acetyl-CoA acyltransferase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0355 PE=3 SV=1	Q2FJQ9|THLA_STAA3	Value Missing
365	Ferrochelatase OS=Staphylococcus aureus (strain USA300) GN=hemH PE=3 SV=1	Q2FFR3|Q2FFR3_STAA3	Value Missing
369	Alpha-acetolactate synthase OS=Staphylococcus aureus (strain USA300) GN=alsS PE=3 SV=1	Q2FES6|Q2FES6_STAA3	Value Missing
416	Proline dipeptidase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1491 PE=3 SV=1	Q2FGJ2|Q2FGJ2_STAA3	Value Missing

423	Type I restriction-modification system, M subunit OS=Staphylococcus aureus (strain USA300) GN=hsdM PE=4 SV=1	Q2FFT5|Q2FFT5_STAA3 (+1)	Value Missing
439	Peptide chain release factor 3 OS=Staphylococcus aureus (strain USA300) GN=prfC PE=3 SV=1	Q2FI57|RF3_STAA3	Value Missing
457	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2446 PE=4 SV=1	Q2FDZ8|Q2FDZ8_STAA3	Value Missing
468	Alkaline phosphatase synthesis transcriptional regulatory protein PhoP OS=Staphylococcus aureus (strain USA300) GN=phoP PE=4 SV=1	Q2FG44|Q2FG44_STAA3	Value Missing
493	Chorismate synthase OS=Staphylococcus aureus (strain USA300) GN=aroC PE=3 SV=1	Q2FGX4|AROC_STAA3	Value Missing
510	DNA topoisomerase IV, subunit B OS=Staphylococcus aureus (strain USA300) GN=parE PE=3 SV=1	Q2FH81|Q2FH81_STAA3	Value Missing
514	Protein kinase OS=Staphylococcus aureus (strain USA300) GN=pknB PE=4 SV=1	Q2FHL8|Q2FHL8_STAA3	Value Missing
527	Low molecular weight protein-tyrosine-phosphatase ptpA OS=Staphylococcus aureus (strain USA300) GN=ptpA PE=3 SV=1	Q2FFL4|PTPA_STAA3	Value Missing
537	Pyridine nucleotide-disulfide oxidoreductase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1369 PE=4 SV=1	Q2FGW2|Q2FGW2_STAA3	Value Missing
539	Phosphotransferase system, fructose-specific IIABC component OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2576 PE=4 SV=1	Q2FDL8|Q2FDL8_STAA3	Value Missing
553	Hydrolase, HAD-superfamily, subfamily IIIA OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1557 PE=4 SV=1	Q2FGC6|Q2FGC6_STAA3	Value Missing
555	Panton-Valentine leukocidin, LukF-PV OS=Staphylococcus aureus (strain USA300) GN=lukF-PV PE=4 SV=1	Q2FGV0|Q2FGV0_STAA3	Value Missing
556	Tributyrin esterase OS=Staphylococcus aureus (strain USA300) GN=estA PE=4 SV=1	Q2FDN0|Q2FDN0_STAA3	Value Missing
569	Aldo/keto reductase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0589 PE=4 SV=1	Q2FJ36|Q2FJ36_STAA3	Value Missing
570	Pur operon repressor OS=Staphylococcus aureus (strain USA300) GN=purR PE=4 SV=1	Q2FJE6|Q2FJE6_STAA3	Value Missing
577	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2525 PE=4 SV=1	Q2FDR9|Q2FDR9_STAA3	Value Missing
584	Thymidylate kinase OS=Staphylococcus aureus (strain USA300) GN=tmk PE=3 SV=1	Q2FJG0|KTHY_STAA3	Value Missing
595	4,4'-diaponeurosporene oxidase OS=Staphylococcus aureus (strain USA300) GN=crtP PE=3 SV=1	Q2FDU3|CRTP_STAA3	Value Missing
597	Protoporphyrinogen oxidase OS=Staphylococcus aureus (strain USA300) GN=hemG PE=4 SV=1	Q2FFR4|Q2FFR4_STAA3	Value Missing
604	ABC transporter, ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2399 PE=4 SV=1	Q2FE44|Q2FE44_STAA3	Value Missing
608	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1857 PE=4 SV=1	Q2FFL9|Q2FFL9_STAA3	Value Missing

611	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0812 PE=4 SV=1	Q2FIG6|Q2FIG6_STAA3	Value Missing
612	Hydrolase, TatD family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0468 PE=4 SV=1	Q2FJF1|Q2FJF1_STAA3	Value Missing
613	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Staphylococcus aureus (strain USA300) GN=metE PE=3 SV=1	Q2FJQ7|METE_STAA3	Value Missing
622	Hydroxymethylglutaryl-CoA reductase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2483 PE=3 SV=1	Q2FDW1|Q2FDW1_STAA3	Value Missing
623	Glutamyl-aminopeptidase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2400 PE=4 SV=1	Q2FE43|Q2FE43_STAA3	Value Missing
633	Carboxylesterase OS=Staphylococcus aureus (strain USA300) GN=est PE=4 SV=1	Q2FIL4|Q2FIL4_STAA3	Value Missing
634	Transcriptional regulator ctsR OS=Staphylococcus aureus (strain USA300) GN=ctsR PE=3 SV=1	Q2FJB8|CTSR_STAA3	Value Missing
642	Universal stress protein family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0067 PE=4 SV=1	Q2FKJ2|Q2FKJ2_STAA3	Value Missing
645	ABC transporter, ATP-binding protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2288 PE=4 SV=1	Q2FEF5|Q2FEF5_STAA3	Value Missing
646	Ribose 5-phosphate isomerase A OS=Staphylococcus aureus (strain USA300) GN=rpiA PE=3 SV=1	Q2FEG0|Q2FEG0_STAA3	Value Missing
649	Alanine dehydrogenase 2 OS=Staphylococcus aureus (strain USA300) GN=ald2 PE=3 SV=1	Q2FG29|DHA2_STAA3	Value Missing
651	Aminomethyltransferase OS=Staphylococcus aureus (strain USA300) GN=gcvT PE=3 SV=1	Q2FGI5|GCST_STAA3	Value Missing
655	Isochorismate synthase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0945 PE=4 SV=1	Q2FI35|Q2FI35_STAA3	Value Missing
657	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0725 PE=4 SV=1	Q2FIQ0|Q2FIQ0_STAA3	Value Missing
661	Primosomal protein DnaI OS=Staphylococcus aureus (strain USA300) GN=dnaI PE=4 SV=1	Q2FG53|Q2FG53_STAA3	Value Missing
664	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0192 PE=4 SV=1	Q2FK72|Q2FK72_STAA3	Value Missing
665	Gamma-hemolysin component B OS=Staphylococcus aureus (strain USA300) GN=hlgB PE=4 SV=1	Q2FE76|Q2FE76_STAA3	Value Missing
673	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0593 PE=4 SV=1	Q2FJ32|Q2FJ32_STAA3	Value Missing
676	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1003 PE=4 SV=1	Q2FHX7|Q2FHX7_STAA3	Value Missing
678	Peptide chain release factor 1 OS=Staphylococcus aureus (strain USA300) GN=prfA PE=3 SV=1	Q2FF10|RF1_STAA3	Value Missing
698	ATPase, AAA family OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1584 PE=4 SV=1	Q2FG99|Q2FG99_STAA3	Value Missing

700	Pseudouridine synthase OS=Staphylococcus aureus (strain USA300) GN=rluB PE=3 SV=1	Q2FGN9|Q2FGN9_STAA3	Value Missing
702	Inositol monophosphatase family protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1007 PE=4 SV=1	Q2FHX3|Q2FHX3_STAA3	Value Missing
705	ABC transporter, permease protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0308 PE=4 SV=1	Q2FJV6|Q2FJV6_STAA3	Value Missing
721	Carbamate kinase 2 OS=Staphylococcus aureus (strain USA300) GN=arcC2 PE=3 SV=1	Q2FDM7|ARCC2_STAA3	Value Missing
736	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0042 PE=4 SV=1	Q2FKL6|Q2FKL6_STAA3	Value Missing
740	Urease accessory protein ureG OS=Staphylococcus aureus (strain USA300) GN=ureG PE=3 SV=1	Q2FEK0|UREG_STAA3	Value Missing
756	Putative membrane protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_1864 PE=3 SV=1	Q2FFL2|Q2FFL2_STAA3	Value Missing
764	Haloacid dehalogenase-like hydrolase OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_2102 PE=4 SV=1	Q2FEY0|Q2FEY0_STAA3	Value Missing
769	Putative uncharacterized protein OS=Staphylococcus aureus (strain USA300) GN=SAUSA300_0632 PE=3 SV=1	Q2FIZ3|Q2FIZ3_STAA3	Value Missing

Table A13. Complete list of intracellular proteins identified from the USA 300 adaptive mutant at 15 hours.

Appendix C. Phyre results.

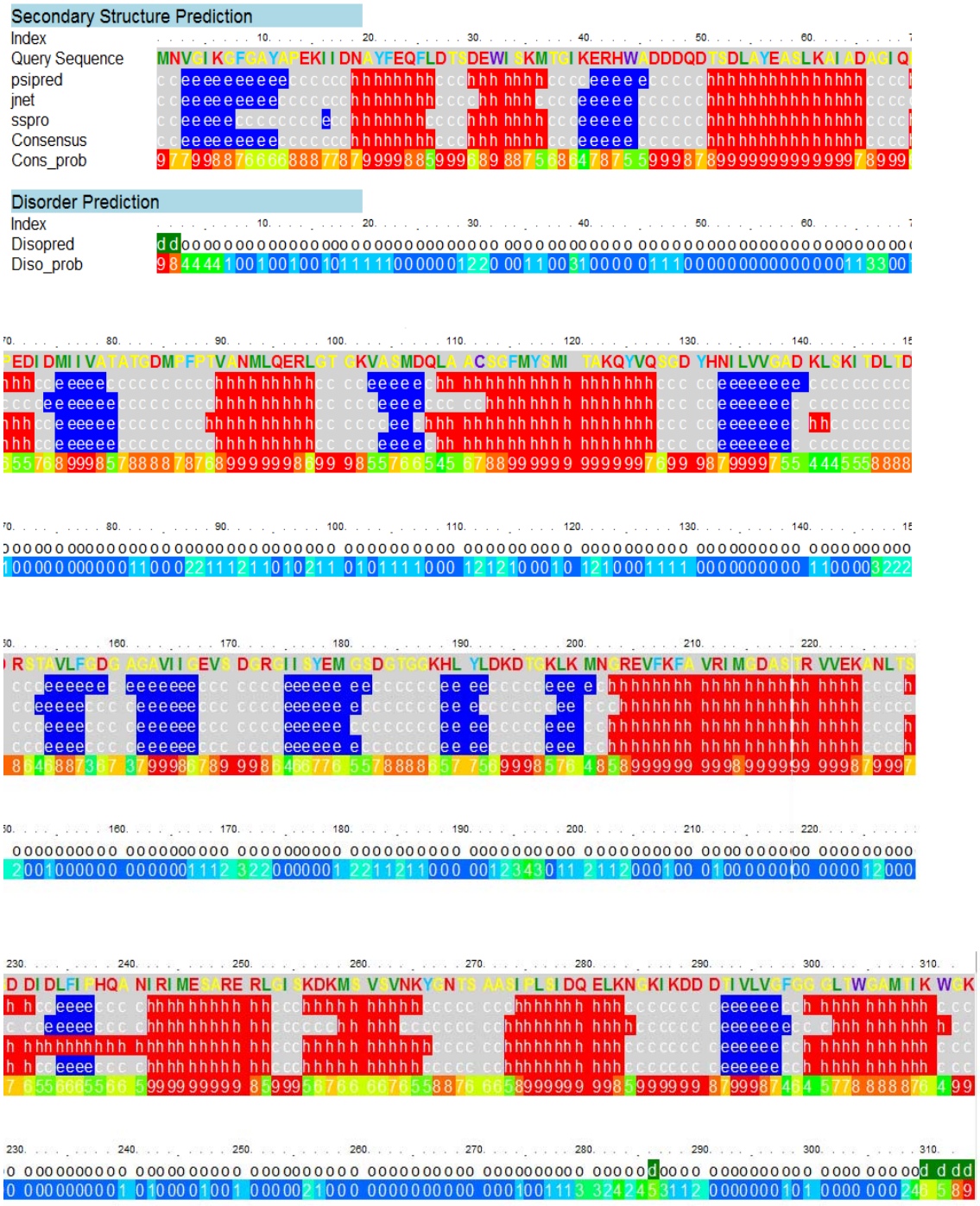

Figure A1. Results of QuickPhyre analysis of COL (top) and USA 100 635 (bottom) amino acid sequences and predicted structures. Red = predicted α-helix. Blue = predicted β-pleated sheet.