黄色ブドウ球菌の糖代謝系の薬剤感受性に及ぼす影響についての研究

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黄色ブドウ球菌は種々の化膿性疾患、腸炎、食中毒等を引き起こす病原性細菌の一つである。また、院内感染原因菌として特にメチシリン耐性黄色ブドウ球菌（MRSA）は時として治療を困難なものにする。近年、MRSA の有効な治療薬の一つであるバンコマイシンなどのグリコペプチド系の抗生剤にも低感受性あるいは耐性を示す菌の出現が報告されている。

本研究では MRSA のβ-ラクタム剤およびグリコペプチド系剤の低感受性機序の解明を目的としてペプチドグリカンの主要構成成分である糖の代謝系と薬剤感受性との関連性について検討を行った。

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研究発表

（１）学会誌等

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小松澤均、藤原環、菅井基行
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第８０回日本細菌学会総会　平成１９年３月２６日－２８日

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「黄色ブドウ球菌の糖代謝系の薬剤感受性に及ぼす影響についての研究」

研究成果

（１）GlmS リボザイムの解析

黄色ブドウ球菌の細胞壁主要成分であるペプチドグリカンは細胞内に取り込まれた糖を出発材料として種々の過程を経て合成される（図１）。その中で GlmS は菌体内に取り込んだ種々の糖を解糖系とペプチドグリカン合成系に分配する key module である（図２）。特に、黄色ブドウ球菌の場合 NagB の活性が非常に弱いため（Komatsuzawa et al. Mol. Microbiol. 2004, 53: 1221-1231）、糖の分配はこの GlmS のみで行われていると考える。また、以前の研究により *glmS* 欠損株においては N-アセチルグルコサミンなどのアミノ糖非存在化では生育できないこと、メチシリンやバンコマイシンの感受性が大幅に増大することを報告している。そこで、本研究では GlmS の転写調節について中心に検討を行った。

１）リポーターシステムによる解析

以前の研究により GlmS の発現は N-アセチルグルコサミンにより減少することを見出していたため（Komatsuzawa et al. Mol. Microbiol. 2004, 53: 1221-1231）、*glmS orf* 上流域のどの部分までが転写調節に関与しているか XylE をレポータータンパクとしてカテコール分解活性について検討を行った。

方法：
pCL15 ベクターを用いプロモーター活性を検討した。方法は小松澤らの方法に準じて行った（Komatsuzawa et al. Antimicrob. Agents Chemother. 1999, 43:2121—2125）。プロモーター領域を欠損した xylE の上流に種々の DNA フラグメントを挿入したプラスミドを作製した。得られたプラスミドを *S. aureus* RN4220 に導入した株を作製した。対数増殖期後期まで菌を培養後，菌を lysostaphin により破壊し遠心後の上清画分を粗酵素画分として使用した。カテコール分解活性を指標としてプロモーター活性を測定した。

結果：
結果を図３に示す。種々の truncated DNA fragment を用いた結果、プロモーター領域は glmS orf の 400 bp 以上上流域に存在することが明らかになった。また、N-アセチルグルコサミン（50mM）添加により転写活性が減少するには orf 上流 180 bp から 300 bp の領域が必要であることが示された。N-アセチルグルコサミン非添加時においても、180 から 300 bp 上流域の欠損によりプロモーター活性は上昇したことから，intact な状態ではプロモーター活性は抑制されていることが考えられた。

また、プロモーターを黄色ブドウ球菌の細胞壁合成系に関与する因子である *fmt* 遺伝子のプロモーターを用い、N-アセチルグルコサミン添加による転写調節に関与する遺伝子領域を組込んだ系でも N—アセチルグルコサミン添加によりプロモーター活性は減少した。

２）*glmS* リボザイムの推定構造

Bucillus sutilis で *glmS* の N-アセチルグルコサミンによる転写活性の抑制は DNA 結合タンパク等のトランスに働く因子によるものではなく *glmS*-mRNA レベルでの調節がなされていることが報告された（Winkleret al. Nature. 2004, 428: 281-286）。そこで、黄色ブドウ球菌の *glmS* 遺伝子上領域について塩基配列での相同性解析を行った結果、*B. subtilis* と同様に黄色ブドウ球菌もリボザイムコア

領域を有していることが明らかになった（図４）。また、グルコサミン６リン酸による予想されるリボザイム活性を図４右に示す。リボザイムコア部分にグルコサミン６リン酸が結合することでglmS-mRNAの5'末端部分がself cleavageを起こすことで転写活性が抑制される。

３）定量性PCRを用いたリボザイム活性の検出

方法：

図４に示すリボザイム活性を実際に黄色ブドウ球菌が示すかどうかについて検討するため、図５に示すようにプライマーを設計し、Real-Time PCRを行った。予想されるcleavage siteを挟むような形で２つのプライマーセット（glmS-50 + glmS-29, glmS-28 + glmS-29）を作製し、併せてglmS orf内に一つのプライマーセット（SA1959-F + SA1959-R）を作製した。それぞれのプライマーセットを用いて、glmS遺伝子を含むプラスミドDNAの１０倍系列希釈液を鋳型に定量性PCRを行い、定量性の確認を行った。定量性の確認が得られたため本実験を行った。Overnight cultureを少量新しいN-アセチルグルコサミン添加（50 mM）および非添加のTrypticase Soy Brothに接種し対数増殖期後期まで培養後，全RNAを抽出した。cDNAを合成し、それを鋳型として定量性PCRを行った。

また、もう一つの実験として対数増殖期中期まで培養した菌液にN-アセチルグルコサミンを添加し経時的に菌を回収し、RNAを抽出し同様の実験を行った。

結果：

S. aureus COL株およびBB270株について検討した結果を図５に示す。いずれの株においてもN-アセチルグルコサミン添加培地で培養した場合、glmS-50とglmS-29のプライマーセットによるPCR産物は大幅に減少した。また、glmS28とglmS29のプライマーセットによる産物も減少した。

経時的変化の結果を図６に示す。N-アセチルグルコサミン添加５分後から急激にリボザイム切断活性が認められた。また、プライマーセットのglmS28 +glmS-29による産物も急激な減少傾向を示したことから、切断活性外にもglmS-mRNAそのものも著しい分解を受けていることが考えられた。また、ウェスタン解析によりGlmSタンパクの発現量もN-アセチルグルコサミン添加３０分後から著名な減少を示した。

４）変異株を用いた解析

これまでの研究成果により、N-アセチルグルコサミン添加による糖の分配がGlmSの転写量により調節されていることが明らかになったため、*glmS*リボザイムの変異体を作製し*glmS*転写調節の異常による薬剤感受性への影響について検討した。

方法：

IPTGによるタンパク発現調節可能なプラスミドpCL15を用い、種々の変異glmS遺伝子を挿入したプラスミドを作製した（図７）。その後、プラスミドを*S. aureus* RN4220に導入した株を得た。また、バクテリオファージ８０αを用いた形質導入により、それぞれのプラスミドをBB270株に移入した。得られた株を用いて、ウェスタン解析によるGlmSの発現量について検討を行い，併せてオキサシリンの最小発育阻止濃度（MIC）を測定した。

結果：

リボザイムコアを取り除いた*glmS*はN-アセチルグルコサミン添加した場合でもタンパクの発現抑制は認められず恒常的な発現性を示した（図８）。切断部位を置換した*glmS*でもN-アセチルグルコサミン添加による発現抑制が著名には認められなかった。

オキサシリン感受性については、特にリボザイムコア領域を欠失させた株では大幅なMIC値の低下が認められた（表１）。しかし、切断部位を置換した株ではMICの変動は著名には認められなかった。

（２）PTS変異株の解析

細菌は細胞外に存在する種々の糖を取り込み、エネルギー代謝や細胞壁ペプチドグリカン合成などに利用している。糖の取り込みには糖をリン酸化し細胞内に取り込むシステム（phosphotransferase system: PTS）とPTSシステムを利用しない（non-PTS）と２つあるが主要なものはPTSである。PTSは特異性が高く個々の糖により異なるPTSが存在する。黄色ブドウ球菌のゲノム解析の結果により推定されるPTSを表２に示す。グルコース、フルクトースなど多種のPTSの存在が考えられる。そこで本研究では実際にどのPTSがどの糖を特異的に取り込むかを同定し、また種々のPTS欠損株を作製し糖の取込み阻害による抗菌剤の感受性の変化について明らかにする。

１）PTS欠損株の作製および薬剤感受性試験

方法：
PTS欠損株の作製は温度感受性プラスミドpCL52.1を用い、個々のPTSをコードするorf内のフラグメントをベクターに組込んだプラスミドを作製した。その後、黄色ブドウ球菌MW2株にプラスミドを導入し，４２℃で培養することで目的の遺伝子にプラスミドを挿入させる１点組み換え法により変異株を作製した。遺伝子の破壊はPCR法にて確認を行った。

結果：
計１７のPTSおよびPTSのリン酸化に関与する統括的な酵素ptsIの変異株を得た。抗菌剤のMICの結果を表３に示す。β-ラクタム剤およびテイコプラニンの感受性に大きな変化は認められなかった。

２）種々の糖源を用いたPTS欠損株の増殖能について

方法：
１）で得られた変異株を用いて、合成培地の糖源を変えることにより増殖能について検討を行った。合成培地の組成は以前用いたもの（Komatsuzawa et al. Mol. Microbiol. 2004, 53: 1221-1231）を使用した。グルコース（10% wt/vol）の代わりにフルクトース，ラクトース、スクロース、マルトース、ラフィノース、N-アセチルグルコサミン、グルコサミンを同様の濃度で培地に添加した。９６ウェルプレートを用いて、作製した種々の糖を含む培地を糖非含有の培地で系列２倍希釈を行った後、菌液を少量（10^5/well）添加し、２４時間および４８時間後の菌の増殖を肉眼で確認した。

結果：
結果を表４に示す。*ptsI*の欠損株においてはラクトース、ラフィノース、スクロース、N-アセチルグルコサミン、グルコサミン単独の培地では菌の増殖が認められなかった。*gatC, treP*変異株においてはN-アセチルグルコサミン添加培地での増殖が認められる濃度範囲が親株および他の変異株に比べて非常に狭いことが示された。しかし、その他の変異株においては著名な増殖能に変化を及ぼすことは認められなかった。

（３）CcpA変異株の解析

種々の糖源の中でグルコースは細菌の主要な糖源である。細菌はこのグルコース存在下、非存在下に

おいてその代謝過程において異なる因子が関与している。したがって、グルコースによるグローバルな調節性因子が存在することが明らかになっており Catabolite control protein (CcpA)が種々の細菌種でゲノム解析により同定されている。黄色ブドウ球菌にも CcpA の存在はゲノム上で確認されている。そこで、CcpA 欠損株を作製し薬剤感受性について検討を行い，糖代謝系と薬剤感受性の関連性について検討を行った。

１）CcpA 欠損株の作製および性状解析

方法：

ccpA 欠損株の作製は（２）の１）に準じて行った。最終的に PCR 法にて ccpA 遺伝子の破壊を確認した。この変異株を用いてグルコースの取込み能について検討を行った。放射活性を有するグルコースを培地中に添加し一定時間培養後菌体を回収し、その放射活性について検討した。また、菌体を 4% SDS で加熱処理し細胞質成分を除去後、細胞壁画分の放射活性についても検討した。

また、得られた変異株および親株について種々の薬剤感受性試験を行った。

結果：

ccpA 欠損株をメチシリン感受性株(RN4220 株)およびメチシリン耐性株（BB270 株）で得た。

グルコースの取込み能について検討した結果，親株に比べてグルコースの取込み量は著名に減少傾向を示した（図９)。また、同様の方法で N-アセチルグルコサミンについての取り込み実験を行った結果、グルコースと同様に取込み量の減少が認められた。細胞壁への移行する割合はグルコース，N-アセチルグルコサミンともに親株と大きな変化は認められなかった。

薬剤感受性については CcpA 変異株において著名なβ—ラクタム剤の MIC の減少が認められた。また、バンコマイシンの感受性も増加傾向を示した（表５)。

２）CcpA 変異株におけるマイクロアレイ解析

方法：

CcpA 変異株と親株について対数増殖期後期まで培養後、全 RNA を抽出し cDNA を合成後 Alexa Flour 555 and 647（Invitrogen）でラベリングを行い、S. aureus N315, MW2, Mu50 株の全 ORF を網羅したスライドガラス（九州大学農学部久原研との共同研究により作製）を用い２株についての発現比較解析を行った。

結果：

CcpA 変異株において種々の因子の発現の変動が認められた（表６)。特に carbohydrate metabolism のいくつかの因子が CcpA 変異株において発現増大傾向を示した。また、アミノ酸代謝系や核酸代謝系の因子についても一部変動が認められた。しかし、ペニシリン結合タンパクを含む細胞壁合成系の因子については両株間で大きな変動は認められなかった。CcpA の認識部位である cre 配列が黄色ブドウ球菌では９０個認められたが実際に変動を示したものは２０個程度であった。

（４）種々の糖源を用いた網羅的遺伝子発現解析

黄色ブドウ球菌のメチシリンの薬剤感受性が培地中の糖源の種類により変化を生じるのか、また種々の糖存在化での遺伝子発現パターンに変化を生じるのかを検討した。

１）薬剤感受性試験

方法：

培地には（２）－２）で用いた合成培地を使用した。すなわち、種々の糖源が 50mM になるように培地中に添加し微量液体希釈法により MIC を測定した。N-アセチルグルコサミンは最終濃度 10mM になるように他の糖源とともに添加した。菌株は MRSA 株である COL, MW2, BB270 を用いた。

結果：

結果を表７に示す。フルクトースのみの添加培地では COL, BB270 株は薬剤非添加時においても増殖が認められなかった。高度耐性の COL 株においてはフルクトース以外の糖源の添加培地を用いた場合、グルコース添加培地のものと MIC 値とほぼ同じ値を示した。しかし、MW2, BB270 株においてはトレハロース添加培地でグルコース添加培地の時の約４倍高い MIC 値を示した。また、MW2 株についてはラクトース、N-アセチルグルコサミン両添加培地でも MIC 値の上昇が認められた。

３）マイクロアレイ解析による検討

方法：

種々の糖を添加した合成培地を用いて検討した。使用した菌株は MW2 で、種々の培地で対数増殖期後期まで培養後、全 RNA を抽出し（３）－２）と同様の方法で解析を行った。グルコース添加時の発現とそれぞれの糖添加時の発現との比較解析を行った。

結果：

種々の糖源添加により遺伝子発現パターンが変化することが明らかになった（表８）。特に，糖源特異的な PTS が明らかになった。また、グルコースの発現パターンと近似するものとかなりパターンが異なるものが認められた。しかし、細胞壁の代謝に関与する因子についてはあまり大きな変動は示さなかった。

総括

黄色ブドウ球菌のメチシリンおよびバンコマイシン感受性と糖の代謝系との関連性について明らかにするため、以下の点について検討を行った。

1）PTS システム欠損株の作製および薬剤感受性：黄色ブドウ球菌ゲノム上に存在するグルコース、グルコサミン等の PTS システム１７個欠損株の作製を行った。種々の薬剤に対する感受性について検討した結果、著名に感受性が変化した株は認められなかった。

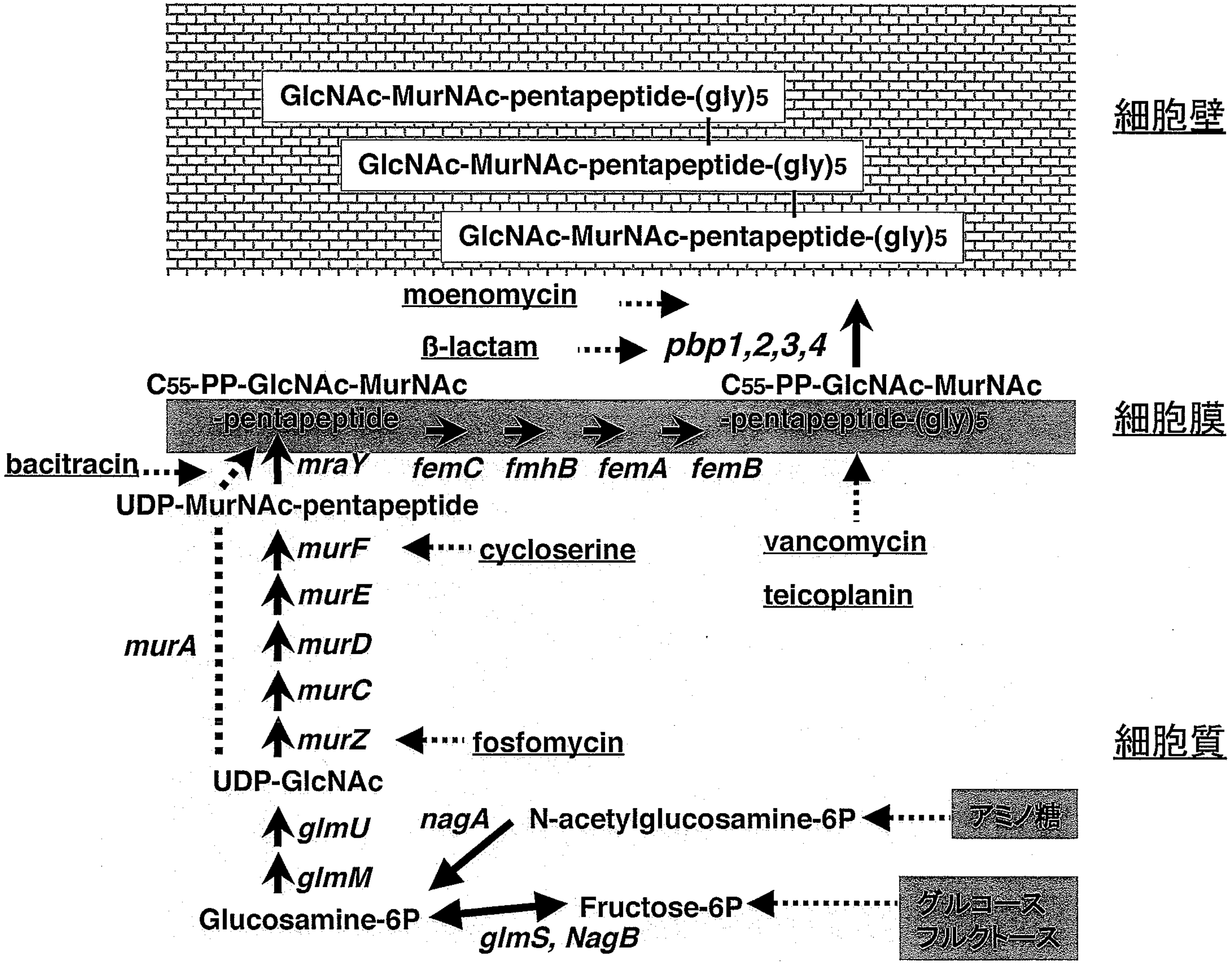
2）CcpA 変異株の作製および発現解析：グルコース代謝のグローバル調節性因子の CcpA の変異株を作製し、薬剤感受性試験を行った。結果、メチシリンの耐性度の減少が認められた。また、マイクロアレイ解析により CcpA の結合配列（Cre 配列）を有する遺伝子の中で実際に CcpA により発現に変化を及ぼす因子が同定できた。また、CcpA の欠損により影響を受ける遺伝子群の同定ができた。

3）GlmS リボザイムの解析：mRNA レベルでどの部分が分解活性に必要かを検討するため、orf 上流域における種々の長さのプロモーター領域を作製し、XylE リポーターシステムベクターに組込みこんだ株を作製し検討した結果、プロモーターと orf 開始点の間およそ 300bp の領域が重要である事が判明した。また、N-アセチルグルコサミン添加による glmS-mRNA のリボザイム活性による特異的部位切断活性について定量性 PCR 法で検討した結果、N-アセチルグルコサミン添加により切断活性は増大したが、*glmS*-mRNA そのものの分解能も増大していることが明らかになった。

4）種々の糖添加によるマイクロアレイ解析：グルコース、フルクトース、ラクトース等の種々の糖を添加した際の発現解析をマイクロアレイにより検討し、それぞれの糖に関与する PTS を明らかにした。また、種々の糖存在下での特異的に変化する因子についてもスクリーニングが行えた。

図１

細胞壁ペプチドグリカン合成系



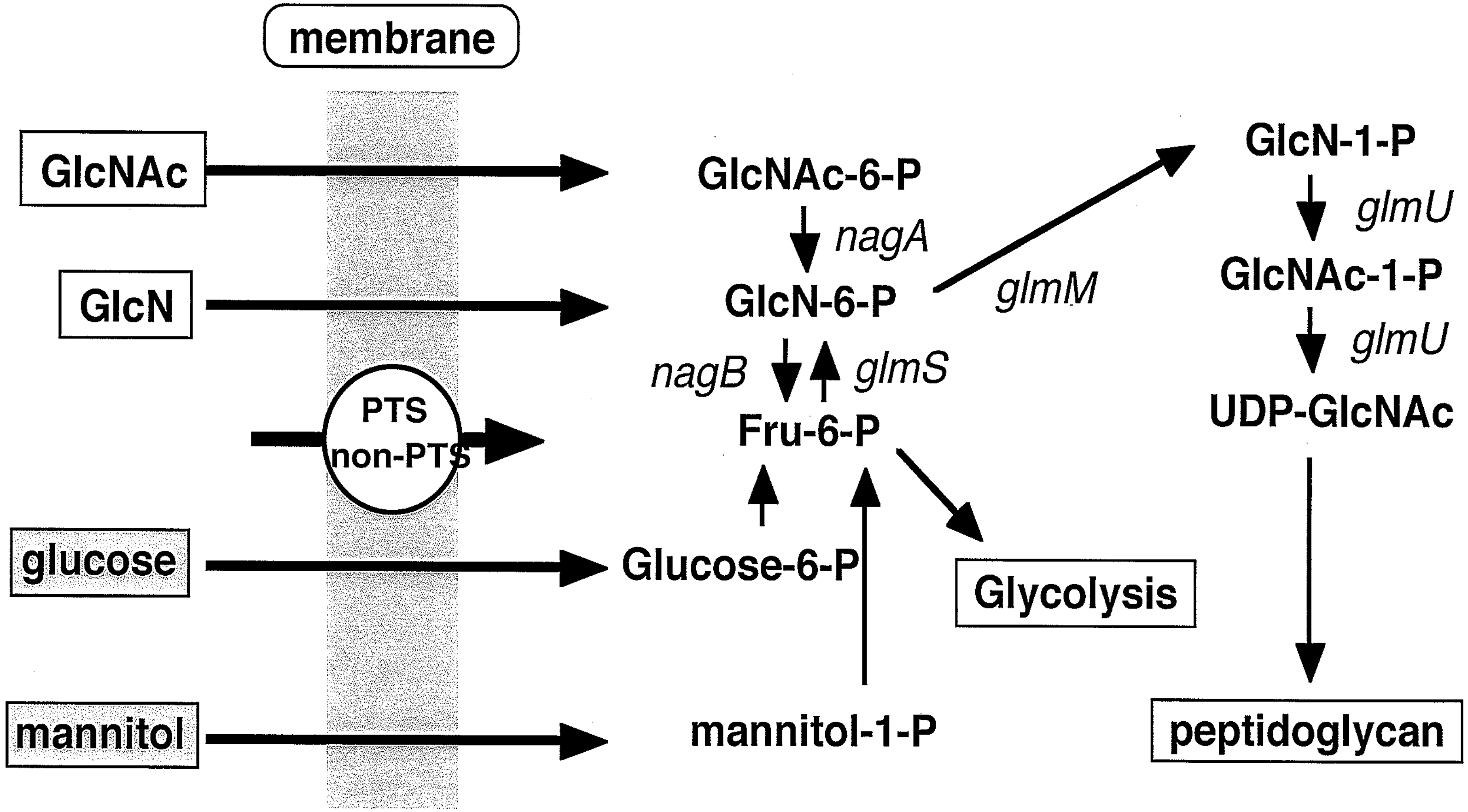


図２　糖の代謝経路（モデル図）

菌対外の糖はPTSあるいはnon-PTSにより菌体内に取り込まれ、種々の反応を経て解糖系、細胞壁合成系等に分配される。

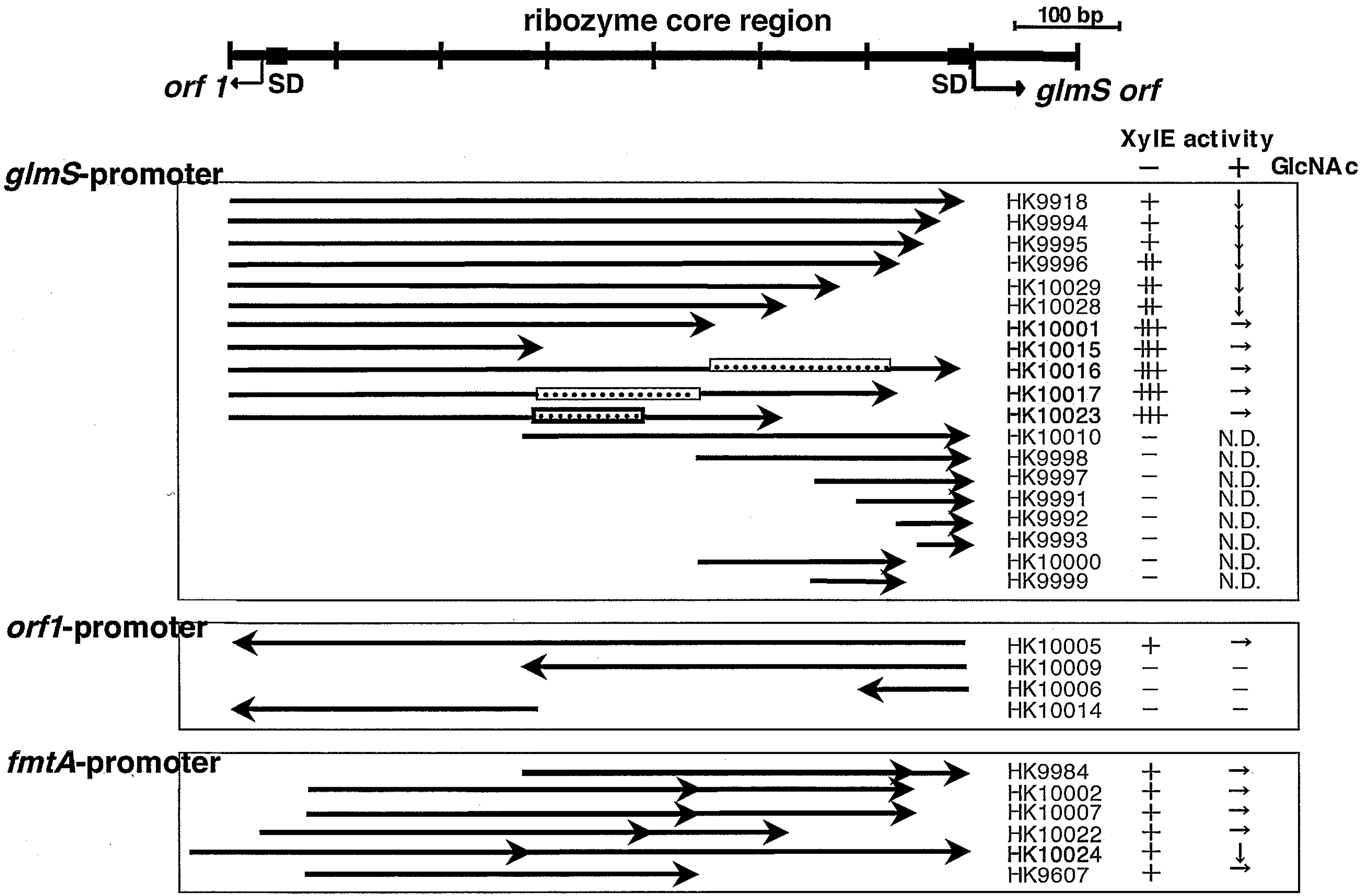


図３　Reporter systemによる*glmS* promoter活性検討

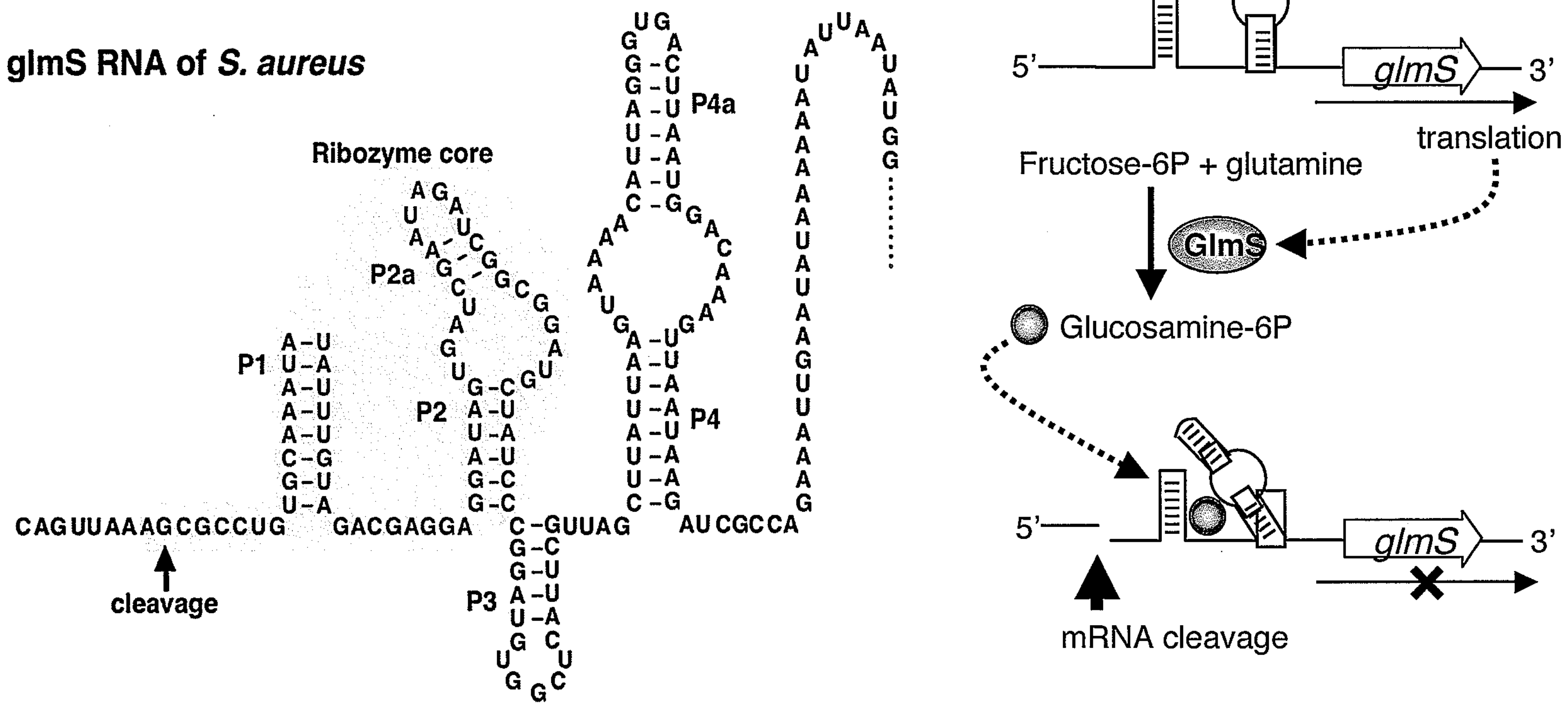


図４　mRNA-*glmS*の構造および ribozymeモデル

推定される*S. aureus*のmRNA-*glmS*の５’側の構造（左）およびribozyme活性の予想モデルを示す（右）。

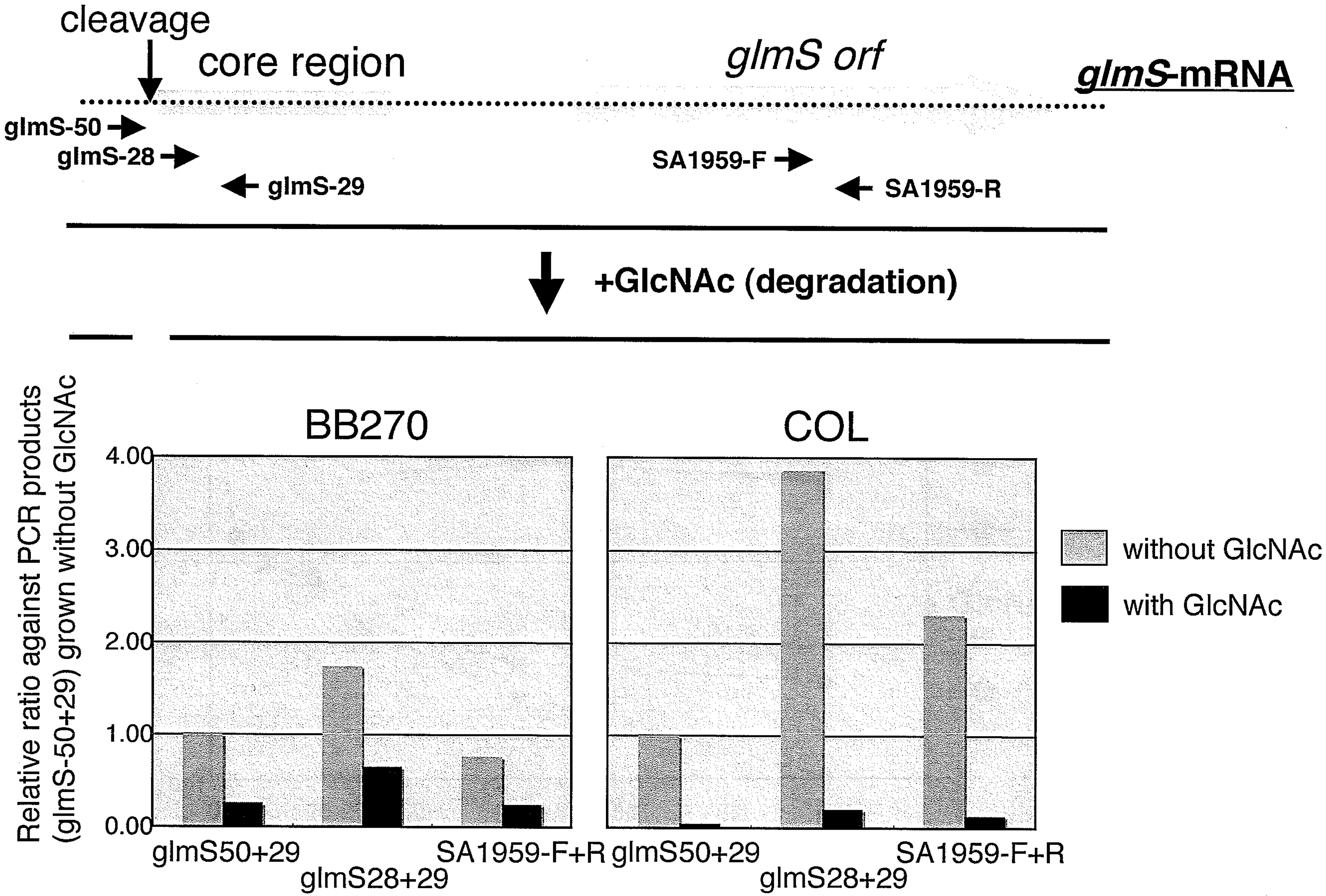


図５　定量性PCR法によるmRNA-*glmS*の転写量の検討

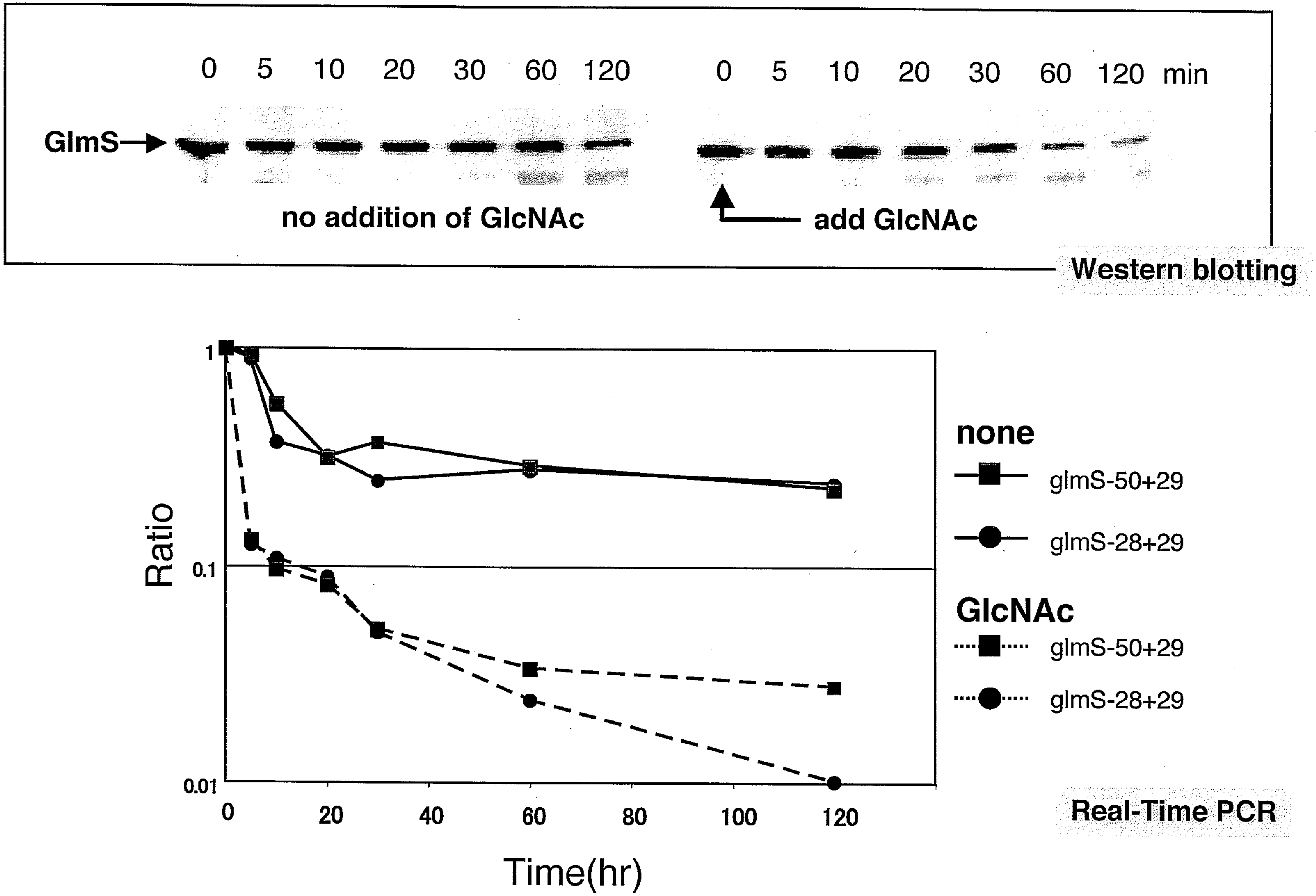
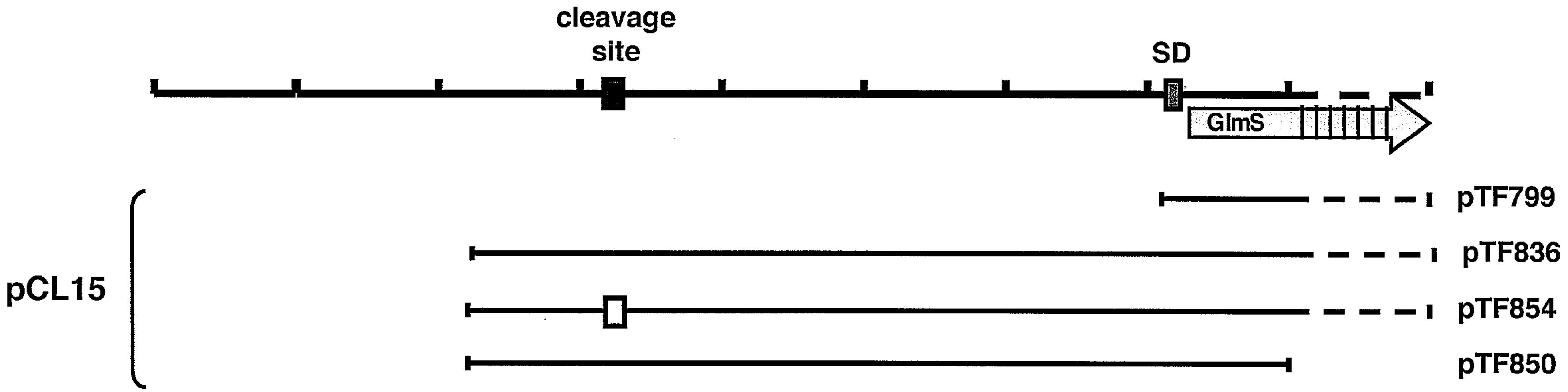
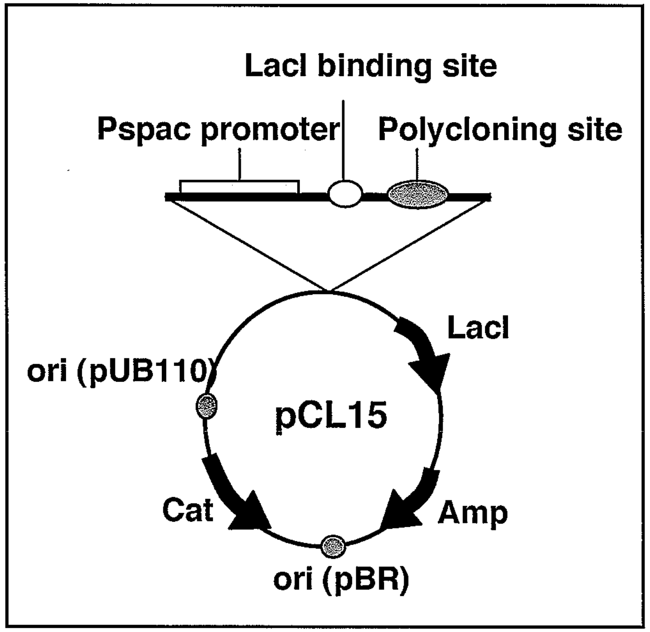


図 6　定量性PCR法によるGlcNAc添加時のmRNA-*glmS*の分解活性の検討





Strains constructed

	pCL15	pTF779	pTF836	pTF854	pTF850
RN4220 (MSSA)	TF5421	TF5390	TF5407	TF5427	TF5426
BB270 (MRSA)	TF5391	TF5394	TF5417	TF5442	-

図７　glmS-発現変異株の作製

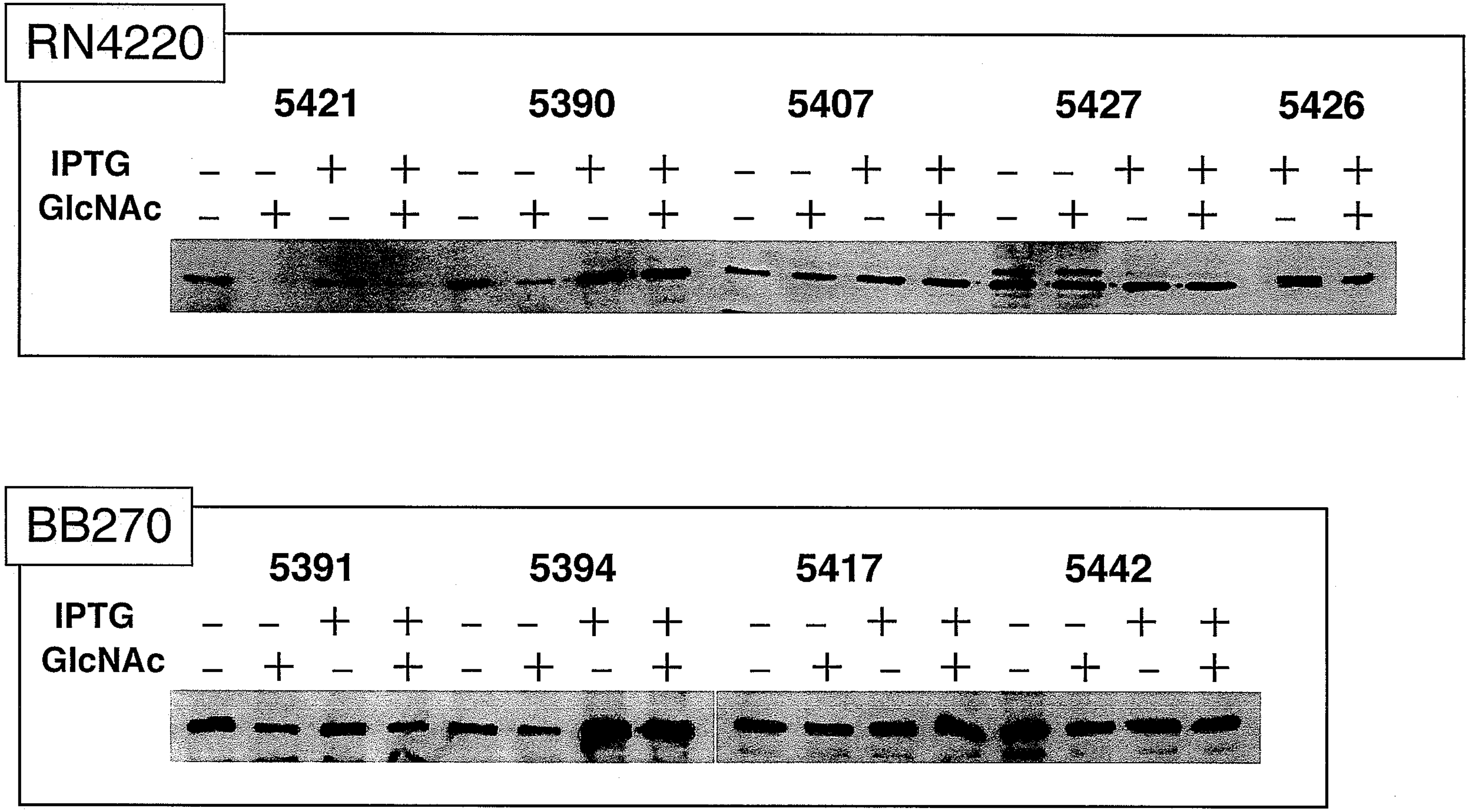


図８　glmS-発現変異株におけるGlmS発現量（Western Blotting）

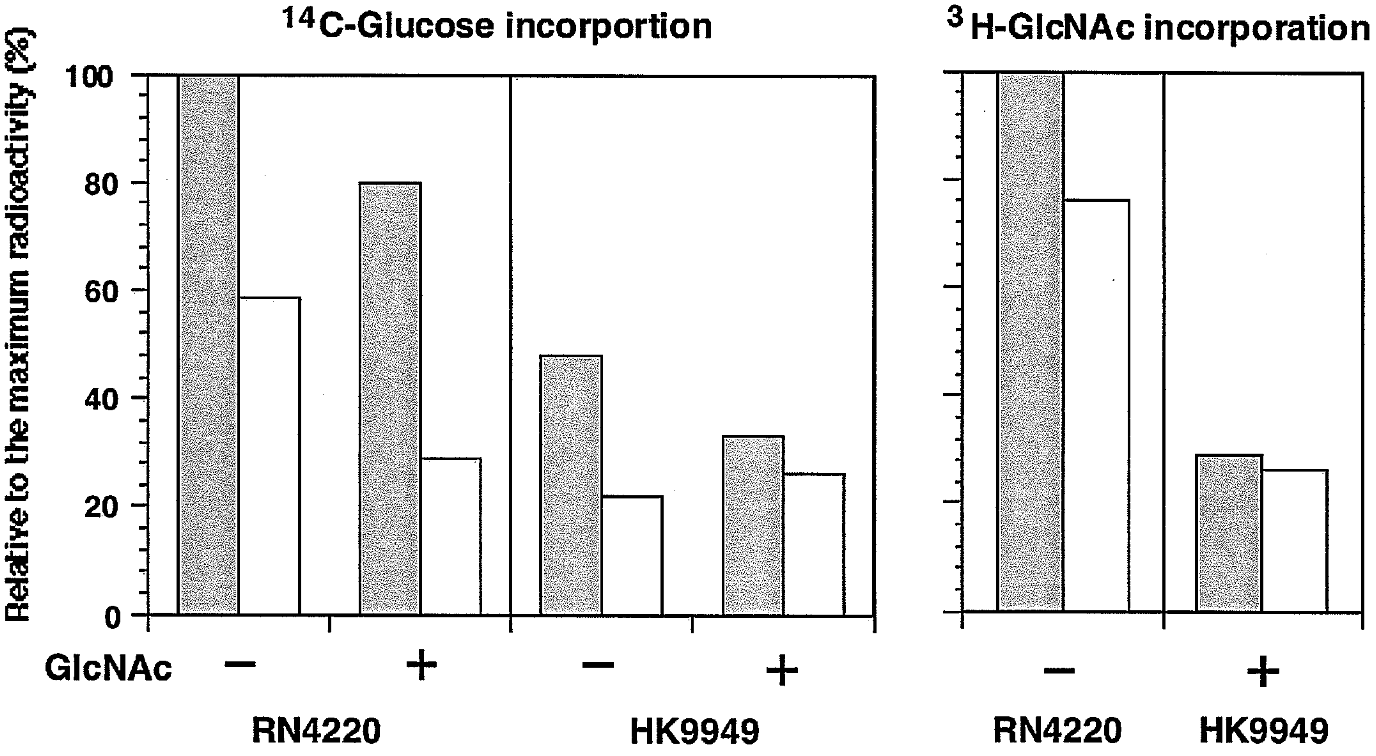


図9　*ccpA*変異株におけるグルコース、N-アセチルグルコサミンの取込み

表１　*glmS* 変異株のオキサシリンのMIC

（単位：μg／ml）

	chemically defined medium				TSB	
	Glu		Glu+GlcNAc			
IPTG	-	+	-	+	+	+
TF5391	128	128	64	64	64	64
TF5394	2	1	> 0.5	> 0.5	4	4
TF5417	32	32	32	32	16	16
TF5442	32	32	16	16	32	32

Glu: glucose (10%) GlcNAc: N-acetylglucosamine (2%)

表2　黄色ブドウ球菌のPTSおよび作製した変異株

gene ID	name	operon	ORF length	character	mutant constructed
SA0183	*glcA*		2046	PTS enzyme II (EC 2.7.1.69), glucose-specific, factor IIA homologue	○
SA0186		SA0184-187	5	hypothetical protein, similar to sucrose phophotransferase enzyme II	○
SA0208		SA0207-0209	1269	maltose/maltodextrin transport permease homologue	○
SA0209		SA0207-0209	840	maltose/maltodextrin transport permease homologue	
SA0233			1530	PTS enzyme II (EC 2.7.1.69), glucose-specific, factor II homologue	○
SA0236		SA0235-0237	468	hypothetical protein, similar toPTS fructose-specific, factor IIBC homologue	
SA0237		SA0235-0237	279	hypothetical protein, similar toPTS galacitol-specific, factor IIB homologue	
SA0238	*gatA*		1260	hypothetical protein, similar toPTS galacitol-specific, factor IIC homologue	○
SA0255			792	hypothetical protein, similar toPTS bata-glucoside-specific enzyme II, ABC component	○
SA0320			444	hypothetical protein, similar toPTS fructose-specific enzyme IIBC component	
SA0432	*treP*		1428	PTS enzyme II, phosphoenolpyruvate-dependent, trehalose specific	○
SA0655	*fruA*		1959	PTS system, fructose specific permease, enzyme IIA	○
SA0935	*ptsI*		1719	phosphoenolpyruvate-protein phosphatase	○
SA1255			501	PTS system, glucose specific enzyme IIA component	
SA1547	*ptaA*		1467	PTS system, N-acetylglucosamine -specific enzyme IIABC component	○
SA1960	*mtlF*	SA1960-1963	1539	PTS system, manitol-specific enzyme IIBC component	○
SA1962	*mtlA*	SA1960-1963	435	PTS system, manitol-specific enzyme IIA component	
SA1992	*lacE*	SA1997-1991	1713	PTS system, lactose-specific enzyme IIBC component	○
SA1993	*lacF*	SA1997-1991	312	PTS system, lactose-specific enzyme IIA component	
SA2053			864	glucose uptake protein homologue	○
SA2114	*glvC*		1605	PTS system, arbutin-like enzyme IIBC component	○
SA2167	*scrA*		1443	PTS system, sucrose-specific enzyme IIBC component	○
SA2326	*ptsG*		2067	PTS system, glucose-specific enzyme IIABC component	○
SA2434		SA2433-2435	1953	fructose PTS enzyme fruA homologue	○

表3　PTS変異株のメチシリン、テイコプラニンのMIC

mutated gene	name	character	メチシリン	テイコプラニン
none		Wild type (MW2)	16	0.5
SA0183	*glcA*	PTS enzyme II (EC 2.7.1.69), glucose-specific, factor IIA homologue	16	0.5
SA0186		hypothetical protein, similar to sucrose phophotransferase enzyme II	16	0.5
SA0208		maltose/maltodextrin transport permease homologue	8	0.5
SA0233		PTS enzyme II (EC 2.7.1.69), glucose-specific, factor II homologue	8	0.5
SA0238	*gatA*	hypothetical protein, similar toPTS galacitol-specific, factor IIC homologue	16	1
SA0255		hypothetical protein, similar toPTS bata-glucoside-specific enzyme II, ABC component	16	0.5
SA0432	*treP*	PTS enzyme II, phosphoenolpyruvate-dependent, trehalose specific	16	0.5
SA0655	*fruA*	PTS system, fructose specific permease, enzyme IIA	32	0.5
SA0935	*ptsI*	phosphoenolpyruvate-protein phosphatase	32	1
SA1547	*ptaA*	PTS system, N-acetylglucosamine -specific enzyme IIABC component	32	1
SA1960	*mtlF*	PTS system, manitol-specific enzyme IIBC component	8	1
SA1992	*lacE*	PTS system, lactose-specific enzyme IIBC component	16	1
SA2053		glucose uptake protein homologue	16	1
SA2114	*glvC*	PTS system, arbutin-like enzyme IIBC component	8	1
SA2167	*scrA*	PTS system, sucrose-specific enzyme IIBC component	32	0.5
SA2326	*ptsG*	PTS system, glucose-specific enzyme IIABC component	16	0.5
SA2434		fructose PTS enzyme fruA homologue	16	0.5

（単位:μg／ml）

表4　PTS変異株の種々の糖源による増殖能

mutated gene	name	character	glucose	fructose	galactose	maltose	lactose	raffinose
none		Wild type (MW2)	0.04	0.08	0.04	0.04	0.04	0.04
SA0183	*glcA*	PTS enzyme II (EC 2.7.1.69), glucose-specific, factor IIA homologue	0.04	0.08	0.04	0.04	0.04	0.04
SA0186		hypothetical protein, similar to sucrose phophotransferase enzyme II	0.08	0.08	0.04	0.08	0.04	0.04
SA0208		maltose/maltodextrin transport permease homologue	0.08	0.08	0.04	0.08	0.04	0.04
SA0233		PTS enzyme II (EC 2.7.1.69), glucose-specific, factor II homologue	0.08	0.16	0.04	0.08	0.08	0.08
SA0238	*gatA*	hypothetical protein, similar toPTS galacitol-specific, factor IIC homologue	0.08	0.04	0.04	0.04	0.04	0.16
SA0255		hypothetical protein, similar toPTS bata-glucoside-specific enzyme II, ABC component	0.08	0.08	0.04	0.08	0.04	0.04
SA0432	*treP*	PTS enzyme II, phosphoenolpyruvate-dependent, trehalose specific	0.16	0.16	0.32	0.08	0.08	0.16
SA0655	*fruA*	PTS system, fructose specific permease, enzyme IIA	0.08	0.16	0.08	0.16	0.08	0.08
SA0935	*ptsI*	phosphoenolpyruvate-protein phosphatase	0.16	1.25-0.63	no growth	0.63	no growth	no growth
SA1547	*ptaA*	PTS system, N-acetylglucosamine -specific enzyme IIABC component	0.08	0.16	0.08	0.08	0.08	0.08
SA1960	*mtlF*	PTS system, manitol-specific enzyme IIBC component	0.08	0.08	0.08	0.08	0.08	0.08
SA1992	*lacE*	PTS system, lactose-specific enzyme IIBC component	0.08	0.08	0.04	0.08	0.04	0.04
SA2053		glucose uptake protein homologue	0.08	0.08	0.04	0.08	0.04	0.04
SA2114	*glvC*	PTS system, arbutin-like enzyme IIBC component	0.08	0.08	0.04	0.04	0.04	0.04
SA2167	*scrA*	PTS system, sucrose-specific enzyme IIBC component	0.08	0.08	0.04	0.08	0.04	0.04
SA2326	*ptsG*	PTS system, glucose-specific enzyme IIABC component	0.08	0.08	0.04	0.08	0.08	0.08
SA2434		fructose PTS enzyme fruA homologue	0.08	0.08	0.32	0.08	0.08	0.16
none		COL (wild type)	0.04	0.32	1.25	0.02	0.04	0.16-0.04
none		BB270 (wild type)	0.08	1.25-0.08	0.32	0.08	0.08	0.63

数値が単独の場合には10%からの増殖可能範囲を示す

（単位：%〔wt/vol〕）

表5　*ccpA*変異株の薬剤感受性

strain	GlcNAc (mM)	oxacillin		methicillin		teicoplanin		vancomycin		fosfomycin		bacitracin		moenomycin	
		24 h	48 h	24 h	48 h	24 h	48 h	24 h	48 h	24 h	48 h	24 h	48 h	24 h	48 h
BB270	0	256	512	512	512	0.125	0.25	0.25	0.5	32	64	64	256	0.06	0.125
	10	8	512	32	512	<0.06	0.25	0.25	0.5	32	64	32	128	0.015	0.06
HK9949 (ccpA)	0	N.D.	256	N.D.	256	N.D.	0.06	N.D.	0.5	N.D.	32	N.D.	64	N.D.	0.015
	10	N.D.	<1	N.D.	<4	N.D.	<0.03	N.D.	<0.03	N.D.	16	N.D.	<1	N.D.	<0.001

表6 アレイ解析(RN4220 vs. RN4220 ccpA)

TSB	CDM	GENE ID	cre配列	gene name	characteristic	function	category
ratio(mutant/parent)	ratio(mutant/parent)	N315株				(DOGAN)	
0.89	1.00	SA0001		dnaA	chromosomal replication initiator protein	DNA replication	Information pathway
0.85	1.04	SA0002		dnaN	DNA polymerase III, beta chain	DNA replication	Information pathway
0.85	0.92	SA0003	cre		conserved hypothetical protein		
0.75	0.92	SA0004		recF	DNA repair and genetic recombination protein	DNA repair or modify	Information pathway
0.56	0.77	SA0005		gyrB	DNA gyrase subunit B	DNA packaging	Information pathway
0.51	0.72	SA0006		gyrA	DNA gyrase subunit A	DNA packaging	Information pathway
1.36	1.19	SA0007			conserved hypothetical protein		
1.17	0.76	SA0008	cre	hutH	histidine ammonia-lyase	aminoacid metabolism	Intermediary metabolism
0.83	1.18	SA0009	cre	serS	seryl-tRNA synthetase	protein synthesis	Information pathway
1.20	0.76	SA0010			hypothetical protein, similar to amino acid permease	transport/binding	cell envelop and process
1.33	0.91	SA0011			hypothetical protein, similar to homoserine-o-acetyltransferase	aminoacid metabolism	Intermediary metabolism
0.87	0.78	SA0012			conserved hypothetical protein		
0.73	0.87	SA0013			conserved hypothetical protein		
0.94	0.91	SA0014		rplI	50S ribosomal protein L9	protein synthesis	Information pathway
0.79	0.80	SA0015		dnaC	replicative DNA helicase	DNA replication	Information pathway
0.90	0.90	SA0016		purA	adenylosuccinate synthase	nucleic acid metabolism	Intermediary metabolism
1.01	0.74	SA0017		vicR	response regulator	RNA synthesis	Information pathway
0.92	0.79	SA0018		vicK	two-component sensor histidine kinase	sensor	cell envelop and process
0.86	0.82	SA0019			conserved hypothetical protein		
0.84	0.98	SA0020			conserved hypothetical protein		
0.80	0.91	SA0021			conserved hypothetical protein		
0.81	0.68	SA0022			hypothetical protein, similar to 5'-nucleotidase	nucleic acid metabolism	Intermediary metabolism
1.56	1.07	SA0023		orfX	conserved hypothetical protein orfX		
1.27	1.12	SA0080			conserved hypothetical protein		
1.06	0.93	SA0081			conserved hypothetical protein		
1.22	0.82	SA0082			conserved hypothetical protein		
0.89	0.98	SA0083			conserved hypothetical protein		
1.00	0.74	SA0084			hypothetical protein, similar to homo sapiens CGI-44 protein, PRO1975 protein	miscellaneous	other function
0.91	0.98	SA0085			conserved hypothetical protein		
0.97	1.07	SA0086			hypothetical protein		
0.85	0.94	SA0087			hypothetical protein		
1.26	0.88	SA0088			hypothetical protein		
1.36	1.08	SA0090			hypothetical protein		
1.50	1.04	SA0091		plc	1-phosphatidylinositol phosphodiesterase precurosr	pathogenic factor	other function
1.00	1.02	SA0092			hypothetical protein		
0.93	0.96	SA0095			hypothetical protein		
1.01	0.96	SA0096			hypothetical protein		
0.88	0.69	SA0097			hypothetical protein, similar to transcription regulator AraC/XylS family	RNA synthesis	Information pathway
1.13	0.88	SA0098			hypothetical protein, similar to aminoacylase	aminoacid metabolism	Intermediary metabolism
1.02	0.69	SA0099			hypothetical protein, similar to transmembrane efflux pump protein	transport/binding	cell envelop and process
0.57	0.80	SA0100			conserved hypothetical protein		
1.69	1.19	SA0100a			conserved hypothetical protein		
1.04	0.70	SA0102			67 kDa Myosin-crossreactive streptococcal antigen homologue	pathogenic factor	other function
1.02	0.70	SA0103			conserved hypothetical protein		
0.71	0.65	SA0104			hypothetical protein, similar to transcription regulator GntR family	RNA synthesis	Information pathway
0.90	0.95	SA0105			hypothetical protein		
0.86	1.02	SA0106	cre	lctP	L-lactate permease homologue	transport/binding	cell envelop and process
0.76	1.12	SA0107		spa	Immunoglobulin G binding protein A precursor	pathogenic factor	other function
1.28	1.32	SA0108		sarH1(sarS)	staphylococcal accessory regulator A homologue	RNA synthesis	Information pathway
0.97	0.89	SA0109		sirC	lipoprotein	transport/binding	cell envelop and process
0.67	0.53	SA0110		sirB	lipoprotein	transport/binding	cell envelop and process
0.82	0.86	SA0111		sirA	lipoprotein	transport/binding	cell envelop and process
0.94	0.79	SA0112			hypothetical protein, similar to cysteine synthase	aminoacid metabolism	Intermediary metabolism
0.95	0.88	SA0113			hypothetical protein, similar to ornithine cyclodeaminase	aminoacid metabolism	Intermediary metabolism
0.90	0.84	SA0114			conserved hypothetical protein		
1.23	0.96	SA0115			hypothetical protein, similar to multi-drug resistance efflux pump	transport/binding	cell envelop and process
0.57	0.52	SA0116			hypothetical protein, similar to rhizobactin siderophore biosynthesisprotein Rhs	miscellaneous	other function
0.80	0.82	SA0117			hypothetical protein, similar to rhizobactin siderophore biosynthesisprotein Rhs	miscellaneous	other function
1.12	0.85	SA0118			hypothetical protein, similar to various aldolase	aminoacid metabolism	Intermediary metabolism
1.10	0.76	SA0119			hypothetical protein, similar to diaminopimelate decarboxylase	aminoacid metabolism	Intermediary metabolism
1.00	0.90	SA0120			hypothetical protein		
1.00	0.91	SA0121			hypothetical protein		
3.05	0.98	SA0122		butA	acetoinreductase	carbohydrate metabolism	Intermediary metabolism
1.05	0.88	SA0123			hypothetical protein, similar to UDP-glucose 4-epimerase (gale-1)	carbohydrate metabolism	Intermediary metabolism
1.25	0.86	SA0124			hypothetical protein, similar to glycosyltransferase TuaA	cell wall	cell envelop and process
1.07	0.87	SA0125			hypothetical protein, similar to Eps(Exopolysaccharide)G	cell wall	cell envelop and process
1.15	0.85	SA0126			hypothetical protein, similar to capsular polysaccharide synthesis protein 14H	transport/binding	cell envelop and process
0.83	0.74	SA0127			hypothetical protein, similar to capsular polysaccharide synthesis protein 14L	transport/binding	cell envelop and process
0.62	0.94	SA0128		sodM	superoxide dismutase	detoxification	other function
0.68	1.91	SA0129			hypothetical protein		
1.25	1.49	SA0130			hypothetical protein, similar to trehalose operon transcriptional repressor	RNA synthesis	Information pathway
3.36	4.09	SA0131		pnp	purine nucleoside phosphorylase	nucleic acid metabolism	Intermediary metabolism
3.58	4.06	SA0132			hypothetical protein, similar to tetracyclin resistance protein	detoxification	other function
2.42	2.39	SA0133		dra	deoxyribose-phosphate aldolase	[illegible]	Intermediary metabolism
0.73	1.43	SA0134		drm	phosphopentomutase	[illegible]	Intermediary metabolism
1.19	1.07	SA0135			hypothetical protein, similar to phosphonates transport permease	transport/binding	cell envelop and process
1.14	0.92	SA0136			hypothetical protein, similar to phosphonates transport permease	transport/binding	cell envelop and process
0.87	0.76	SA0137			hypothetical protein, similar to transport system protein	transport/binding	cell envelop and process
1.12	0.91	SA0138			hypothetical protein, similar to alkylphosphonate ABC tranporter	transport/binding	cell envelop and process
1.15	0.86	SA0139			hypothetical protein		
0.91	0.70	SA0140			hypothetical protein, similar to lactococcal phosphatase homologue	phosphate metabolism	Intermediary metabolism
1.89	0.98	SA0142			hypothetical protein, similar to DNA-binding protein	RNA synthesis	Information pathway
3.77	1.03	SA0143		adhE	alcohol-acetaldehyde dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.13	0.85	SA0144		capA	capsular polysaccharide synthesis enzyme Cap5A	adaptation to atypical	other function
0.92	0.79	SA0145		capB	capsular polysaccharide synthesis enzyme Cap5B	adaptation to atypical	other function
0.87	0.75	SA0146		capC	capsular polysaccharide synthesis enzyme Cap8C	adaptation to atypical	other function
0.78	0.53	SA0147		capD	capsular polysaccharide synthesis enzyme Cap5D	adaptation to atypical	other function
1.00	0.77	SA0148		capE	capsular polysaccharide synthesis enzyme Cap8E	adaptation to atypical	other function
1.08	0.66	SA0149		capF	capsular polysaccharide synthesis enzyme Cap5F	adaptation to atypical	other function
1.02	0.70	SA0150		capG	capsular polysaccharide synthesis enzyme Cap5G	adaptation to atypical	other function
0.94	0.77	SA0151		capH	capsular polysaccharide synthesis enzyme O-acetyl transferase Cap5H	adaptation to atypical	other function
0.89	0.76	SA0152		capI	capsular polysaccharide synthesis enzyme Cap5I	adaptation to atypical	other function
0.82	0.70	SA0153		capJ	capsular polysaccharide synthesis enzyme Cap5J	adaptation to atypical	other function
0.61	0.51	SA0154		capK	capsular polysaccharide synthesis enzyme Cap5K	adaptation to atypical	other function
1.05	0.91	SA0155		capL	capsular polysaccharide synthesis enzyme Cap5L	adaptation to atypical	other function
1.00	0.96	SA0156		capM	capsular polysaccharide synthesis enzyme Cap5M	adaptation to atypical	other function
0.95	1.00	SA0157		capN	capsular polysaccharide synthesis enzyme Cap5N	adaptation to atypical	other function
1.16	0.94	SA0158		capO	capsular polysaccharide synthesis enzyme Cap8O	adaptation to atypical	other function

0.97	0.96	SA0159		capP	capsular polysaccharide synthesis enzyme Cap5P	adaptation to atypical	other function
0.78	0.92	SA0160			conserved hypothetical protein		
1.35	1.34	SA0161			conserved hypothetical protein		
6.24	4.01	SA0162	cre	aldA	aldehyde dehydrogenase homologue	carbohydrate metabolism	Intermediary metabolism
1.26	1.11	SA0163			hypothetical protein, similar to cation-efflux system membrane protein CzcD	transport/binding	cell envelop and process
1.17	1.11	SA0164			hypothetical protein		
0.26	0.75	SA0165			hypothetical protein, similar to alpha-helical coiled-coil protein SrpF		
0.40	0.93	SA0166			hypothetical protein, similar to nitrate transporter	transport/binding	cell envelop and process
0.61	0.85	SA0167			hypothetical protein, similar to membrane lipoprotein SrpL	transport/binding	cell envelop and process
0.43	0.85	SA0168			hypothetical protein, similar to probable permease of ABC transporter	transport/binding	cell envelop and process
0.48	0.91	SA0169			hypothetical protein, similar to acyl-CoA dehydrogenase family protein	aminoacid metabolism	Intermediary metabolism
0.58	1.00	SA0170			conserved hypothetical protein		
0.70	0.75	SA0171		fdh	NAD-dependent formate dehydrogenase	carbohydrate metabolism	Intermediary metabolism
0.81	1.14	SA0172			hypothetical protein, similar to integral membrane protein LmrP	transport/binding	cell envelop and process
0.90	0.65	SA0173			hypothetical protein, similar to surfactin synthetase	antibiotic production	other function
1.14	0.87	SA0174			conserved hypothetical protein		
0.87	0.51	SA0175			conserved hypothetical protein		
0.99	0.87	SA0176			hypothetical protein, similar to N-acetylglutamate 5-phosphotransferase	aminoacid metabolism	Intermediary metabolism
0.72	0.59	SA0177		argJ	arginine biosynthesis bifunctional protein homologue	aminoacid metabolism	Intermediary metabolism
0.97	0.76	SA0178		argC	N-acetylglutamate gamma-semialdehyde dehydrogenase	aminoacid metabolism	Intermediary metabolism
1.12	0.75	SA0179	cre		ornithine aminotransferase	aminoacid metabolism	Intermediary metabolism
0.95	0.59	SA0180			hypothetical protein, similar to branched-chain amino acid transport system carrier protein	aminoacid metabolism	Intermediary metabolism
1.59	1.20	SA0181			hypothetical protein, similar to isochorismatase	coenzyme metabolism	Intermediary metabolism
1.64	1.50	SA0182			hypothetical protein, similar to indole-3-pyruvate decarboxylas	carbohydrate metabolism	Intermediary metabolism
0.65	0.94	SA0183	cre	glcA	PTS enzyme II (EC 2.7.1.69), glucose-specific, factor IIA homologue	transport/binding	cell envelop and process
16.94	6.21	SA0184	cre		conserved hypothetical protein		
15.81	3.75	SA0185			conserved hypothetical protein		
25.06	4.61	SA0186			hypothetical protein, similar to sucrose phosphotransferase enzyme II	transport/binding	cell envelop and process
15.92	4.81	SA0187			hypothetical protein, similar to transcription regulator	RNA synthesis	Information pathway
1.26	1.50	SA0189		hsdR	probable type I restriction enzyme restriction chain	DNA repair or modify	Information pathway
1.42	1.14	SA0189a		hsdR	probable type I restriction enzyme restriction chain	DNA repair or modify	Information pathway
1.39	1.07	SA0198		oppF	oligopeptide transport ATP-binding protein	transport/binding	cell envelop and process
0.85	0.80	SA0199		oppB#truncat	runcated hypothetical protein, similar to oligopeptide ABC transporter permeas	transport/binding	cell envelop and process
0.70	0.56	SA0200			hypothetical protein, similar to dipeptide transporter protein dppC	transport/binding	cell envelop and process
0.83	0.84	SA0201		rlp	RGD-containing lipoprotein	transport/binding	cell envelop and process
1.44	1.09	SA0202	cre		hypothetical protein, similar to gamma-glutamyltranspeptidase precursor	aminoacid metabolism	Intermediary metabolism
1.05	0.99	SA0203			hypothetical protein		
1.41	1.07	SA0204			NAD(P)H dehydrogenase homologue	membrane bioenergetics	cell envelop and process
0.84	1.06	SA0205			hypothetical protein, similar to lysostaphin precursor	cell wall	cell envelop and process
1.34	1.12	SA0206	cre	msmX	multiple sugar-binding transport ATP-binding protein	transport/binding	cell envelop and process
2.51	1.55	SA0207a			hypothetical protein, similar to maltose/maltodextrin-binding protein	transport/binding	cell envelop and process
1.98	1.51	SA0207b			hypothetical protein, similar to maltose/maltodextrin-binding protein	transport/binding	cell envelop and process
2.83	1.67	SA0208			maltose/maltodextrin transport permease homologue	transport/binding	cell envelop and process
2.83	1.83	SA0209			maltose/maltodextrin transport permease homologu	transport/binding	cell envelop and process
2.94	1.68	SA0210			hypothetical protein, similar to NADH-dependent dehydrogenase	membrane bioenergetics	cell envelop and process
2.36	1.56	SA0211			hypothetical protein, similar to NADH-dependent dehydrogenase	membrane bioenergetics	cell envelop and process
3.01	1.70	SA0212			conserved hypothetical protein		
0.82	1.20	SA0213			conserved hypothetical protein		
4.37	1.31	SA0214		uhpT	hexose phosphate transport protein	transport/binding	cell envelop and process
1.47	1.16	SA0215			hypothetical protein, similar to two-component response regulator	RNA synthesis	Information pathway
0.98	0.81	SA0216			hypothetical protein, similar to two-component sensor histidine kinase	sensor	cell envelop and process
1.50	1.22	SA0217			hypothetical protein, similar to periplasmic-iron-binding protein BitC	transport/binding	cell envelop and process
5.41	5.50	SA0218	cre	pflB	formate acetyltransferase	carbohydrate metabolism	Intermediary metabolism
6.65	5.70	SA0219		pflA	formate acetyltransferase activating enzyme	carbohydrate metabolism	Intermediary metabolism
2.36	1.36	SA0220			hypothetical protein, similar to glycerophosphodiester phosphodiesterase	lipid metabolism	Intermediary metabolism
1.02	1.25	SA0221			hypothetical protein		
1.08	1.26	SA0222		coa	staphylocoagulase precursor	pathogenic factor	other function
1.50	1.68	SA0223			acetyl-CoA acetyltransferase homologue	carbohydrate metabolism	Intermediary metabolism
1.83	1.64	SA0224			hypothetical protein, similar to 3-hydroxyacyl-CoA dehydrogenase	lipid metabolism	Intermediary metabolism
1.84	1.39	SA0225	cre		hypothetical protein, similar to glutaryl-CoA dehydrogenase	lipid metabolism	Intermediary metabolism
1.58	1.56	SA0226			hypothetical protein, similar to acid-CoA ligase	lipid metabolism	Intermediary metabolism
1.66	1.41	SA0227			conserved hypothetical protein		
0.64	0.76	SA0228			hypothetical protein		
0.99	0.82	SA0229			hypothetical protein, similar to nickel ABC transporter nickel-binding protein	transport/binding	cell envelop and process
0.94	0.87	SA0230			conserved hypothetical protein		
0.86	0.84	SA0231			hypothetical protein, similar to flavohemoprotein	miscellaneous	other function
0.65	0.37	SA0232	cre	lctE	L-lactate dehydrogenase	carbohydrate metabolism	Intermediary metabolism
4.21	0.83	SA0233			PTS enzyme (EC 2.7.1.69), maltose- and glucose-specific, factor II homologue	transport/binding	cell envelop and process
0.96	0.80	SA0234			hypothetical protein, similar to inosine-uridine preferring nucleoside hydrolase	nucleic acid metabolism	Intermediary metabolism
0.91	0.71	SA0235			hypothetical protein, similar to BglG antiterminator family	RNA synthesis	Information pathway
1.39	1.02	SA0236			hypothetical protein, similar to PTS fructose-specific enzyme IIBC component	transport/binding	cell envelop and process
1.11	0.91	SA0236a			hypothetical protein, similar to PTS fructose-specific enzyme IIBC component	transport/binding	cell envelop and process
0.97	0.96	SA0237			hypothetical protein, similar to PTS, galactitol-specific IIB component	transport/binding	cell envelop and process
1.09	0.69	SA0238		gatC	probable PTS galactitol-specific enzyme IIC component	transport/binding	cell envelop and process
1.21	0.89	SA0239			sorbitol dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.01	0.71	SA0240			sorbitol dehydrogenase homologue	carbohydrate metabolism	Intermediary metabolism
0.76	1.00	SA0241			hypothetical protein, similar to 4-diphosphocytidyl-2C-methyl-D-erythritol syntha	coenzyme metabolism	Intermediary metabolism
0.83	0.86	SA0242			hypothetical protein, similar to xylitol dehydrogenase	carbohydrate metabolism	Intermediary metabolism
0.71	0.82	SA0243			hypothetical protein, similar to teichoic acid biosynthesis protein B	cell wall	cell envelop and process
0.86	1.11	SA0244			hypothetical protein, similar to teichoic acid biosynthesis protein F	cell wall	cell envelop and process
0.94	1.10	SA0245			conserved hypotheticl protein		
0.87	1.07	SA0246			hypotheticl protein, similar to D-xylulose reductase	carbohydrate metabolism	Intermediary metabolism
0.89	0.95	SA0247			hypothetical protein, similar to teichoic acid biosynthesis protein B	cell wall	cell envelop and process
0.80	0.78	SA0248			hypothetical protein, similar to beta-glycosyltransferase	cell wall	cell envelop and process
1.85	0.93	SA0249		scdA	cell division and morphogenesis-related protein	cell division	cell envelop and process
1.53	0.92	SA0250		lytS	two-component sensor histidine kinase	sensor	cell envelop and process
1.57	0.95	SA0251		lytR	two-component response regulator	RNA synthesis	Information pathway
1.92	0.95	SA0252		lrgA	holin-like protein LrgA	phage-related	other function
2.34	0.95	SA0253		lrgB	holin-like protein LrgB	phage-related	other function
1.21	0.94	SA0254			hypothetical protein, similar to transcription regulator GntR family	RNA synthesis	Information pathway
0.84	0.84	SA0255	cre		hypothetical protein, similar to PTS beta-glucoside-specific enzyme II, ABC compon	transport/binding	cell envelop and process
1.04	0.84	SA0256		bglA	6-phospho-beta-glucosidase	carbohydrate metabolism	Intermediary metabolism
2.07	1.15	SA0257			conserved hypothetical protein		
1.61	1.32	SA0258		rbsK	probable ribokinase	carbohydrate metabolism	Intermediary metabolism
1.58	1.35	SA0259		rbsD	ribose permease	transport/binding	cell envelop and process
0.42	0.68	SA0260	cre		hypothetical protein, similar to ribose transporter RbsU	transport/binding	cell envelop and process
1.28	0.94	SA0261			hypothetical protein, similar to rbs operon repressor RbsR	RNA synthesis	Information pathway
1.20	0.95	SA0263			hypothetical protein, similar to proton antiporter efflux pump	transport/binding	cell envelop and process
1.26	0.91	SA0264			hypothetical protein, similar to penicillin amidase (EC 3.5.1.11) V	detoxification	other function
0.90	0.86	SA0265	cre	lytM	peptidoglycan hydrolase	cell wall	cell envelop and process

1.06	0.79	SA0266			conserved hypothetical protein		
1.07	0.84	SA0267			hypothetical protein		
1.00	0.86	SA0268			hypothetical protein		
0.85	0.68	SA0269			hypothetical protein		
0.68	0.65	SA0270		ssaA	hypothetical protein, similar to secretory antigen precursor SsaA	pathogenic factor	other function
0.58	0.43	SA0271			conserved hypothetical protein		
0.62	0.59	SA0272			hypothetical protein, similar to transmembrane protein Tmp7	transport/binding	cell envelop and process
0.90	0.78	SA0273			hypothetical protein		
0.93	0.90	SA0274			conserved hypothetical protein		
0.95	0.77	SA0275			conserved hypothetical protein		
0.41	0.70	SA0276			conserved hypothetical protein, similar to diarrheal toxin	pathogenic factor	other function
0.92	0.88	SA0277			hypothetical protein		
0.88	0.82	SA0278			hypothetical protein		
0.84	0.77	SA0279			hypothetical protein		
1.10	0.79	SA0280			hypothetical protein		
0.87	1.05	SA0283			hypothetical protein		
0.83	0.99	SA0284			hypothetical protein		
0.80	0.88	SA0285			hypothetical protein		
0.22	0.35	SA0287			conserved hypothetical protein		
0.91	0.84	SA0291			hypothetical protein		
0.86	0.79	SA0292			hypothetical protein		
1.24	0.92	SA0293			hypothetical protein, similar to formate transporter NirC	transport/binding	cell envelop and process
0.99	0.76	SA0294			hypothetical protein, similar to branched-chain amino acid uptake carrier	transport/binding	cell envelop and process
0.85	0.46	SA0295			hypothetical protein, similar to outer membrane protein precursor	transport/binding	cell envelop and process
1.55	0.98	SA0296			conserved hypothetical protein		
0.40	0.35	SA0297			hypothetical protein, similar to ABC transporter ATP-binding protein	transport/binding	cell envelop and process
1.02	1.00	SA0298			hypothetical protein, similar to regulatory protein PfoR	RNA synthesis	Information pathway
4.04	2.00	SA0299	cre		hypothetical protein, similar to carbohydrate kinase, PfkB family	carbohydrate metabolism	Intermediary metabolism
5.38	2.34	SA0301			conserved hypothetical protein		
4.76	2.25	SA0302			probable pyrimidine nucleoside transport protein	transport/binding	cell envelop and process
6.70	2.13	SA0303			hypothetical protein, similar to sodium-coupled permease	transport/binding	cell envelop and process
5.35	1.36	SA0304		nanA	N-acetylneuraminate lyase subunit	carbohydrate metabolism	Intermediary metabolism
2.65	1.32	SA0305	cre		hypothetical protein, similar to glucokinase	carbohydrate metabolism	Intermediary metabolism
1.82	1.26	SA0306			conserved hypothetical protein		
1.46	1.10	SA0307			conserved hypothetical protein		
0.91	0.80	SA0308			conserved hypothetical protein		
0.80	0.87	SA0309		geh	glycerol ester hydrolase	pathogenic factor	other function
0.90	0.87	SA0310			hypothetical protein		
0.98	0.85	SA0311			hypothetical protein, similar to trimethylamine dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.08	0.92	SA0312			hypothetical protein, similar to alkanal monooxygenase alpha chain	detoxification	other function
1.11	0.98	SA0313			hypothetical protein, similar to glycine cleavage system H protein	aminoacid metabolism	Intermediary metabolism
0.71	0.78	SA0314			conserved hypothetical protein		
0.80	0.99	SA0315			hypothetical protein		
0.29	0.36	SA0316			hypothetical protein, similar to lipoate-protein ligase	protein modification	Information pathway
1.06	0.92	SA0317			hypothetical protein, similar to dihydroflavonol-4-reductase	coenzyme metabolism	Intermediary metabolism
0.32	0.28	SA0318			hypothetical protein, similar to transport protein SgaT	transport/binding	cell envelop and process
1.29	1.03	SA0319			conserved hypothetical protein		
0.99	1.01	SA0320			hypothetical protein, similar to PTS fructose-specific enzyme IIBC component	transport/binding	cell envelop and process
1.16	0.93	SA0321			hypothetical protein, similar to transcription antiterminator BglG family	RNA synthesis	Information pathway
0.76	0.79	SA0322	cre		hypothetical protein, similar to transcription regulator	RNA synthesis	Information pathway
0.92	1.02	SA0323		svrA	conserved hypothetical protein	RNA synthesis	Information pathway
1.22	1.18	SA0324			hypothetical protein		
10.54	4.15	SA0325		glpT	glycerol-3-phosphate transporter	transport/binding	cell envelop and process
1.24	1.00	SA0326	cre		conserved hypothetical protein		
1.34	1.03	SA0327			conserved hypothetical protein		
0.77	0.85	SA0328			hypothetical protein, similar to NADH-dependent FMN reductase	coenzyme metabolism	Intermediary metabolism
1.30	0.92	SA0329			conserved hypothetical protein		
2.39	0.90	SA0330			hypothetical protein, similar to ribosomal-protein-serine N-acetyltransferase	protein modification	Information pathway
1.30	0.81	SA0331			conserved hypothetical protein		
1.31	0.92	SA0332			conserved hypothetical protein		
1.16	1.35	SA0333			conserved hypothetical protein		
0.45	0.67	SA0334			conserved hypothetical protein		
0.58	0.99	SA0335			conserved hypothetical protein		
0.42	0.89	SA0336			hypothetical protein		
1.21	1.23	SA0337			hypothetical protein, similar to transcriptional repressor	RNA synthesis	Information pathway
1.15	1.18	SA0339			hypothetical protein, similar to ABC transporter ATP-binding protein	transport/binding	cell envelop and process
1.02	1.09	SA0340			conserved hypothetical protein		
0.42	0.68	SA0341			hypothetical protein, similar to low temperature requirement A protein		
1.23	1.40	SA0342			acetyl-CoA C-acetyltransferase homologue	carbohydrate metabolism	Intermediary metabolism
0.99	0.81	SA0343			conserved hypothetical protein		
0.90	0.70	SA0344		metE	5-methyltetrahydropteroyltriglutamate-homocystei ne methyltransferase	aminoacid metabolism	Intermediary metabolism
0.53	0.27	SA0345			conserved hypothetical protein		
1.11	0.83	SA0346			hypothetical protein, similar to cystathionine beta-lyase	aminoacid metabolism	Intermediary metabolism
0.99	0.91	SA0347	cre		hypothetical protein, similar to cystathionine gamma-synthase	aminoacid metabolism	Intermediary metabolism
0.72	0.69	SA0348			hypothetical protein, similar to transcription terminator	RNA synthesis	Information pathway
1.06	1.18	SA0349			conserved hypothetical protein		
0.86	1.05	SA0350			conserved hypothetical protein		
0.97	0.92	SA0351			hypothetical protein, similar to GTP-binding protein		
0.66	0.63	SA0352		rpsF	30S ribosomal protein S6	protein synthesis	Information pathway
0.46	0.47	SA0353		ssb	single-strand DNA-binding protein of phage phi PVL	phage-related	other function
0.79	0.80	SA0354		rpsR	30S ribosomal protein S18	protein synthesis	Information pathway
1.04	0.93	SA0355			hypothetical protein, similar to hypothetical protein virulence plasmid pXO1-38		
1.19	0.94	SA0357			hypothetical protein, similar to exotoxin 2	pathogenic factor	other function
1.12	0.98	SA0358			conserved hypothetical protein		
1.15	0.97	SA0359			conserved hypothetical protein		
1.18	0.95	SA0360			conserved hypothetical protein		
1.00	0.92	SA0361			truncated hypothetical protein, similar to phosphoglycerate mutase; Gpm3p	carbohydrate metabolism	Intermediary metabolism
1.31	0.86	SA0362			conserved hypothetical protein		
0.94	0.93	SA0363			hypothetical protein		
0.93	1.09	SA0364			hypothetical protein		
0.98	1.37	SA0365		ahpF	alkyl hydroperoxide reductase subunit F	membrane bioenergetics	cell envelop and process
1.27	1.44	SA0366		ahpC	alkyl hydroperoxide reductase subunit C	membrane bioenergetics	cell envelop and process
1.01	0.91	SA0367			hypothetical protein, similar to nitro/flavin reductase	membrane bioenergetics	cell envelop and process
0.31	0.82	SA0368			hypothetical protein, similar to proton/sodium-glutamate symport protein	transport/binding	cell envelop and process
0.66	0.70	SA0370			conserved hypothetical protein		
2.06	1.51	SA0371			hypothetical protein		
2.55	2.12	SA0372			hypothetical protein		

0.77	0.56	SA0373		xprT	xanthine phosphoribosyltransferase	nucleic acid metabolism	Intermediary metabolism
0.73	0.53	SA0374		pbuX	xanthine permease	transport/binding	cell envelop and process
0.70	0.58	SA0375		guaB	inositol-monophosphate dehydrogenase	nucleic acid metabolism	Intermediary metabolism
0.68	0.56	SA0376		guaA	GMP synthase(quaA)	nucleic acid metabolism	Intermediary metabolism
0.94	0.88	SA0377			hypothetical protein		
1.05	0.87	SA0378			hypothetical protein		
0.85	1.03	SA0379	cre		probable transposase	transposon and IS	other function
1.10	0.96	SA0380			conserved hypothetical protein		
1.03	1.03	SA0381			conserved hypothetical protein		
0.71	0.79	SA0382		set6	exotoxin 6	pathogenic factor	other function
0.95	0.93	SA0383		set7	exotoxin 7	pathogenic factor	other function
0.94	0.86	SA0384		set8	exotoxin 8	pathogenic factor	other function
1.08	0.86	SA0385		set9	exotoxin 9	pathogenic factor	other function
1.25	1.03	SA0386		set10	exotoxin 10	pathogenic factor	other function
1.10	0.78	SA0387		set11	exotoxin 11	pathogenic factor	other function
0.85	1.04	SA0388		set12	exotoxin 12	pathogenic factor	other function
0.71	0.82	SA0389		set13	exotoxin 13	pathogenic factor	other function
0.90	1.12	SA0390	cre	set14	exotoxin 14	pathogenic factor	other function
1.05	0.66	SA0391		hsdM	probable type I site-specific deoxyribonuclease LldI chain hsdM	DNA repair or modify	Information pathway
0.87	0.84	SA0392		hsdS	probable restriction modification system specificity subunit	DNA repair or modify	Information pathway
0.76	0.97	SA0393		set15	exotoxin 15	pathogenic factor	other function
0.56	0.72	SA0394			hypothetical protein		
0.82	0.47	SA0395			hypothetical protein		
1.10	1.09	SA0397		lpl2	hypothetical protein		
0.88	1.10	SA0403		lpl7	hypothetical protein (Pathogenicity island SaPIn2)		
1.21	1.28	SA0404		lpl8	hypothetical protein		
0.87	1.01	SA0406			hypothetical protein		
1.00	1.03	SA0407			conserved hypothetical protein		
0.92	0.90	SA0408			hypothetical protein		
0.83	1.04	SA0409			hypothetical protein		
1.31	0.86	SA0410			conserved hypothetical protein		
0.55	0.45	SA0411		ndhF	NADH dehydrogenase subunit 5	membrane bioenergetics	cell envelop and process
0.91	0.60	SA0412			conserved hypothetical protein		
1.25	0.92	SA0413			conserved hypothetical protein		
1.19	1.04	SA0414			hypothetical protein		
0.99	0.99	SA0415			conserved hypothetical protein		
0.91	0.86	SA0416			hypothetical protein, similar to carboxylesterase	aminoacid metabolism	Intermediary metabolism
0.83	0.93	SA0417			hypothetical protein, similar to sodium-dependent transporter	transport/binding	cell envelop and process
0.62	1.01	SA0418		cysM	cysteine synthase homologue	aminoacid metabolism	Intermediary metabolism
1.06	0.88	SA0419		metB	cystathionine gamma-synthase	aminoacid metabolism	Intermediary metabolism
1.38	0.93	SA0420			hypothetical protein, similar to ABC transporter ATP-binding protein	transport/binding	cell envelop and process
1.33	0.79	SA0421			hypothetical protein, similar to ABC transporter permease protein	transport/binding	cell envelop and process
1.57	0.93	SA0422			hypothetical protein, similar to lactococcal lipoprotein	transport/binding	cell envelop and process
1.23	0.49	SA0423			hypothetical protein, similar to autolysin (N-acetylmuramoyl-L-alanine amidase	cell wall	cell envelop and process
0.90	0.84	SA0424			hypothetical protein		
0.91	1.03	SA0425			conserved hypothetical protein		
0.97	0.93	SA0426			conserved hypothetical protein		
0.47	0.61	SA0427			conserved hypothetical protein		
1.07	0.67	SA0429		gltC	transcription activator of glutamate synthase operon	RNA synthesis	Information pathway
0.65	0.42	SA0430		gltB	glutamate synthase large subunit	aminoacid metabolism	Intermediary metabolism
0.71	0.68	SA0431		gltD	NADH-glutamate synthase small subunit	aminoacid metabolism	Intermediary metabolism
1.97	1.50	SA0432		treP	PTS enzyme II, phosphoenolpyruvate-dependent, trehalose-specific	transport/binding	cell envelop and process
4.03	1.48	SA0433		treC	alpha-glucosidase	carbohydrate metabolism	Intermediary metabolism
0.74	0.73	SA0434			hypothetical protein, similar to trehalose operon transcriptional repressor	RNA synthesis	Information pathway
1.03	0.99	SA0435			conserved hypothetical protein		
0.74	0.73	SA0436		dnaX	DNA polymerase III gamma and tau subunits	DNA replication	Information pathway
0.70	0.79	SA0437			conserved hypothetical protein		
0.56	0.64	SA0438		recR	recombination protein	DNA recombination	Information pathway
0.95	0.69	SA0439			hypothetical protein, similar to lysine decarboxylase	aminoacid metabolism	Intermediary metabolism
1.23	0.89	SA0440		tmk	putative thymidylate kinase	nucleic acid metabolism	Intermediary metabolism
1.12	0.94	SA0441			conserved hypothetical protein		
1.09	0.81	SA0442		holB	probable DNA polymerase III, delta prime subunit	DNA replication	Information pathway
1.00	0.80	SA0443			hypothetical protein, similar to signal peptidase II homologue	protein secretion	cell envelop and process
0.98	0.89	SA0444			conserved hypothetical protein		
0.94	0.77	SA0445			conserved hypothetical protein		
0.83	0.95	SA0446			conserved hypothetical protein		
0.69	0.68	SA0447			conserved hypothetical protein		
0.88	0.82	SA0448		metS	methionyl-tRNA synthetase	protein synthesis	Information pathway
0.79	0.90	SA0449			conserved hypothetical protein		
0.81	0.97	SA0450	cre		conserved hypothetical protein		
0.95	0.93	SA0451		ksgA	dimethyladenosine transferase(16S rRNA dimethylase) homologue	RNA modification	Information pathway
3.85	0.66	SA0452		veg	VEG protein homologue		
1.15	0.76	SA0453			hypothetical protein, similar to 4-diphosphocytidyl-2-C-methyl-D-erythritol kinas	nucleic acid metabolism	Intermediary metabolism
1.01	0.81	SA0454		purR	pur operon repressor homologue	RNA synthesis	Information pathway
1.08	0.78	SA0455			translation initiation inhibitor homologue	protein synthesis	Information pathway
1.12	0.96	SA0456		spoVG	stage V sporulation protein G homologue	cell division	cell envelop and process
1.01	0.96	SA0457		gcaD	UDP-N-acetylglucosamine pyrophosphorylase homologue	cell wall	cell envelop and process
0.82	0.93	SA0458		prs	ribose-phosphate pyrophosphokinase	nucleic acid metabolism	Intermediary metabolism
0.67	0.89	SA0459		rplY	50S ribosomal protein L25	protein synthesis	Information pathway
0.82	0.86	SA0460		pth	peptidyl-tRNA hydrolase	protein synthesis	Information pathway
0.64	0.94	SA0461		mfd	transcription-repair coupling factor	RNA synthesis	Information pathway
0.67	0.86	SA0462			hypothetical protein, similar to low temperature requirement B protein	adaptation to atypical	other function
0.82	0.93	SA0463			conserved hypothetical protein		
0.82	1.02	SA0464			conserved hypothetical protein		
0.74	0.88	SA0465			hypothetical protein, similar to cell-division initiation protein	cell division	cell envelop and process
0.60	0.74	SA0466			hypothetical protein, similar to polyribonucleotide nucleotidyltransferase	nucleic acid metabolism	Intermediary metabolism
0.92	0.82	SA0467			conserved hypothetical protein		
0.70	0.96	SA0468			hypoxanthine-guanine phosphoribosyltransferase homologue	nucleic acid metabolism	Intermediary metabolism
0.75	0.81	SA0469		ftsH	cell-division protein	cell division	cell envelop and process
0.93	0.99	SA0469a		ftsH	cell-division protein	cell division	cell envelop and process
0.53	0.92	SA0470			heat-shock protein HSP33 homologue	adaptation to atypical	other function
0.51	1.06	SA0471		cysK	cysteine synthase (o-acetylserine sulfhydrylase) homologue	aminoacid metabolism	Intermediary metabolism
0.63	0.90	SA0472		folP	dihydropteroate synthase chain A synthetase	coenzyme metabolism	Intermediary metabolism
0.69	1.17	SA0473		folB	7,8-dihydroneopterin aldolase	coenzyme metabolism	Intermediary metabolism
0.73	0.99	SA0474		folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridin e pyrophosphokinase	coenzyme metabolism	Intermediary metabolism
0.61	0.71	SA0475		lysS	lysyl-tRNA synthetase	protein synthesis	Information pathway
0.92	0.74	SA0476			hypothetical protein, similar to transcription regulator GntR family	RNA synthesis	Information pathway

1.06	0.80	SA0477			conserved hypothetical protein		
1.12	0.92	SA0478			conserved hypothetical protein		
1.39	1.15	SA0479		nupC	pyrimidine nucleoside transport protein	transport/binding	cell envelop and process
0.95	1.35	SA0480		ctsR	transcription repressor of class III stress genes homologue	RNA synthesis	Information pathway
1.14	1.59	SA0481			conserved hypothetical protein		
1.21	1.30	SA0482			hypothetical protein, similar to creatine kinase	miscellaneous	other function
1.13	1.46	SA0483		clpC	endopeptidase	adaptation to atypical	other function
0.73	1.07	SA0484		radA	radA	DNA repair or modify	Information pathway
0.79	1.18	SA0485			conserved hypothetical protein		
0.92	1.00	SA0486		gltX	glutamyl-tRNA synthetase	protein synthesis	Information pathway
1.02	1.39	SA0487	cre	cysE	Serine acetyltransferase homologue	aminoacid metabolism	Intermediary metabolism
0.87	1.29	SA0488		cysS	cysteinyl-tRNA synthetase	protein synthesis	Information pathway
0.96	1.29	SA0489			conserved hypothetical protein		
0.75	1.21	SA0490			hypothetical protein, similar to tRNA/rRNA methyltransferase	RNA modification	Information pathway
0.91	1.21	SA0491			conserved hypothetical protein		
0.77	1.40	SA0492		sigH	hypothetical protein	RNA synthesis	Information pathway
0.78	0.90	SA0493		secE	preprotein translocase subunit	protein secretion	cell envelop and process
0.69	1.03	SA0494		nusG	transcription antitermination protein	RNA synthesis	Information pathway
0.59	0.79	SA0495		rplK	50S ribosomal protein L11	protein synthesis	Information pathway
0.59	0.95	SA0496		rplA	50S ribosomal protein L1	protein synthesis	Information pathway
0.68	0.90	SA0497		rplJ	50S ribosomal protein L10	protein synthesis	Information pathway
0.81	0.93	SA0498		rplL	50S ribosomal protein L7/L12	protein synthesis	Information pathway
0.82	1.06	SA0499			conserved hypothetical protein		
0.65	0.93	SA0500		rpoB	RNA polymerase beta chain	RNA synthesis	Information pathway
0.63	0.85	SA0501		rpoC	RNA polymerase beta-prime chain	RNA synthesis	Information pathway
0.64	0.82	SA0503		rpsL	30S ribosomal protein S12	protein synthesis	Information pathway
0.61	0.90	SA0504		rpsG	30S ribosomal protein S7	protein synthesis	Information pathway
0.54	0.81	SA0505		fus	translational elongation factor G	protein synthesis	Information pathway
0.58	0.82	SA0506		tufA	translational elongation factor TU	protein synthesis	Information pathway
0.74	0.76	SA0507			hypothetical protein, similar to N-acyl-L-amino acid amidohydrolase	aminoacid metabolism	Intermediary metabolism
1.67	1.73	SA0508			hypothetical protein, similar to glycine C-acetyltransferase	aminoacid metabolism	Intermediary metabolism
0.37	0.54	SA0509			conserved hypothetical protein		
1.49	1.08	SA0510		araB	probable L-ribulokinase	carbohydrate metabolism	Intermediary metabolism
2.40	2.63	SA0511			hypothetical protein, similar to UDP-glucose 4-epimerase related protein	nucleic acid metabolism	Intermediary metabolism
0.79	0.48	SA0512		ilvE	branched-chain amino acid aminotroansferase homologue	aminoacid metabolism	Intermediary metabolism
0.87	0.65	SA0513	cre		conserved hypothetical protein		
0.81	0.80	SA0514			hypothetical protein, similar to deoxypurine kinase	nucleic acid metabolism	Intermediary metabolism
0.81	0.77	SA0515			hypothetical protein, similar to deoxypurine kinase	nucleic acid metabolism	Intermediary metabolism
0.99	0.82	SA0516			hypothetical protein, similar to Cu binding protein (Mn oxidation	miscellaneous	other function
1.03	0.73	SA0517			conserved hypothetical protein		
0.86	0.79	SA0518			conserved hypothetical protein		
65.01	36.98	SA0519		sdrC	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	pathogenic factor	other function
1.07	0.94	SA0520		sdrD	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	pathogenic factor	other function
0.96	0.88	SA0522			hypothetical protein, similar to poly (glycerol-phosphate) alpha-glucosyltransferas	cell wall	cell envelop and process
0.57	0.55	SA0523			hypothetical protein, similar to poly (glycerol-phosphate) alpha-glucosyltransferas	cell wall	cell envelop and process
0.97	0.76	SA0524			conserved hypothetical protein		
0.88	0.83	SA0525			conserved hypothetical protein		
1.00	0.81	SA0526			conserved hypothetical protein		
0.98	0.98	SA0527		nagB	probable glucosamine-6-phosphate isomerase	carbohydrate metabolism	Intermediary metabolism
0.99	1.12	SA0528			hypothetical protein, similar to hexulose-6-phosphate synthase	carbohydrate metabolism	Intermediary metabolism
0.84	1.09	SA0529			conserved hypothetical protein		
1.26	0.84	SA0530			hypothetical protein, similar to indigoidine systhesis protein	miscellaneous	other function
0.88	0.81	SA0533		vraA	hypothetical protein, similar to long chain fatty acid CoA ligase	lipid metabolism	Intermediary metabolism
0.93	0.93	SA0534		vraB	acetyl-CoA c-acetyltransferase	lipid metabolism	Intermediary metabolism
1.10	0.92	SA0535		vraC	hypothetical protein		
1.21	0.94	SA0536			hypothetical protein		
0.86	0.72	SA0537			hypothetical protein, similar to phosphomethylpyrimidine kinase, thiD homologu	coenzyme metabolism	Intermediary metabolism
1.17	0.91	SA0538		ung	uracil-DNA glycosylase	DNA repair or modify	Information pathway
1.06	0.90	SA0539			hypothetical protein		
1.05	0.88	SA0540			conserved hypothetical protein		
0.96	0.80	SA0541			hypothetical protein, similar to cationic amino acid transporter	transport/binding	cell envelop and process
1.03	1.00	SA0542			conserved hypothetical protein		
1.18	0.94	SA0543			conserved hypothetical protein		
1.14	1.00	SA0544			conserved hypothetical protein		
0.59	0.62	SA0545		pta	phosphotransacetylase	nucleic acid metabolism	Intermediary metabolism
0.58	0.75	SA0546			conserved hypothetical protein		
0.96	0.88	SA0547		mvaK1	mevalonate kinase	lipid metabolism	Intermediary metabolism
0.85	0.97	SA0548		mvaD	mevalonate diphosphate decarboxylase	lipid metabolism	Intermediary metabolism
0.35	0.64	SA0549		mvaK2	phosphomevalonate kinase	lipid metabolism	Intermediary metabolism
0.84	0.96	SA0550			conserved hypothetical protein		
1.24	0.95	SA0551			mercuric reductase homologue	detoxification	other function
1.01	1.01	SA0552			hypothetical protein		
1.11	0.99	SA0553			conserved hypothetical protein		
1.03	0.88	SA0554			conserved hypothetical protein		
1.50	1.06	SA0555			conserved hypothetical protein		
1.22	1.25	SA0557			hypothetical protein, similar to oxidoreductase, ion channel	transport/binding	cell envelop and process
3.56	2.55	SA0558			conserved hypothetical protein		
0.94	1.11	SA0559			conserved hypothetical protein		
0.33	0.30	SA0560			conserved hypothetical protein		
0.97	1.01	SA0561			conserved hypothetical protein		
2.34	1.07	SA0562		adh1	alcohol dehydrogenase I	carbohydrate metabolism	Intermediary metabolism
0.93	1.11	SA0563			conserved hypothetical protein		
0.96	0.99	SA0564		argS	arginyl-tRNA synthetase	protein synthesis	Information pathway
0.89	1.01	SA0565			hypothetical protein, similar to endonuclease III	DNA repair or modify	Information pathway
0.85	0.80	SA0566			hypothetical protein, similar to iron-binding protein	transport/binding	cell envelop and process
3.79	1.52	SA0567			hypothetical protein, similar to iron(III) ABC transporter permease protein	transport/binding	cell envelop and process
1.09	1.19	SA0568			hypothetical protein, similar to L-2-haloalkanoic acid dehalogenase	carbohydrate metabolism	Intermediary metabolism
0.93	1.36	SA0569			hypothetical protein similar to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid hydr	miscellaneous	other function
0.71	0.91	SA0570			hypothetical protein		
0.79	0.91	SA0571			hypothetical protein		
0.97	0.88	SA0572			hypothetical protein, similar to esterase/lipase	lipid metabolism	Intermediary metabolism
1.26	1.06	SA0573		sarA	staphylococcal accessory regulator A	RNA synthesis	Information pathway
0.96	0.97	SA0574			conserved hypothetical protein		
1.06	1.18	SA0575			hypothetical protein		
1.06	1.45	SA0576			hypothetical protein		
1.28	1.11	SA0577			hypothetical protein, similar to FimE recombinase	[illegible]	Information pathway
0.98	0.93	SA0578			hypothetical protein, similar to NADH dehydrogenase	membrane bioenergetics	cell envelop and process

0.75	0.86	SA0579			hypothetical protein, similar to Na+/H+ antiporter	membrane bioenergetics	cell envelop and process
0.75	0.84	SA0580			hypothetical protein, similar to Na+/H+ antiporter	membrane bioenergetics	cell envelop and process
1.51	1.07	SA0581_b			MnhD homologue, similar to Na+/H+ antiporter subunit	membrane bioenergetics	cell envelop and process
1.02	0.98	SA0581a			MnhD homologue, similar to Na+/H+ antiporter subunit	membrane bioenergetics	cell envelop and process
1.11	1.10	SA0582			hypothetical protein, similar to Na+/H+ antiporter	membrane bioenergetics	cell envelop and process
1.16	1.06	SA0583			hypothetical protein, similar to Na+/H+ antiporter	membrane bioenergetics	cell envelop and process
1.16	1.12	SA0584			conserved hypothetical protein		
0.91	0.91	SA0585	cre		conserved hypothetical protein		
0.60	1.02	SA0587			lipoprotein, Streptococcal adhesin PsaA homologue	pathogenic factor	other function
0.63	1.17	SA0588			conserved hypothetical protein		
1.26	0.72	SA0590			hypothetical protein, similar to iron dependent repressor	RNA synthesis	Information pathway
1.04	1.01	SA0591			hypothetical protein		
1.02	0.95	SA0592		tagA	teichoic acid biosynthesis protein	cell wall	cell envelop and process
0.75	0.96	SA0593		tagH	teichoic acid translocation ATP-binding protein	cell wall	cell envelop and process
0.33	0.52	SA0594		tagG	teichoic acid translocation permease protein	cell wall	cell envelop and process
0.86	1.25	SA0595		tagB	teichoic acid biosynthesis protein B	cell wall	cell envelop and process
0.91	0.99	SA0596		tagX	teichoic acid biosynthesis protein X	cell wall	cell envelop and process
0.84	0.92	SA0597		tagD	teichoic acid biosynthesis protein D	cell wall	cell envelop and process
0.85	0.81	SA0598		pbp4	penicillin binding protein 4	cell wall	cell envelop and process
1.12	0.84	SA0599			ATP-binding cassette transporter A	transport/binding	cell envelop and process
1.04	0.76	SA0600			hypothetical protein, similar to pyrimidine nucleoside transporter	transport/binding	cell envelop and process
2.08	1.30	SA0601			conserved hypothetical protein		
0.43	0.53	SA0602		fhuA	ferrichrome transport ATP-binding protein	transport/binding	cell envelop and process
0.42	0.47	SA0603		fhuB	ferrichrome transport permease	transport/binding	cell envelop and process
0.48	0.56	SA0604		fhuG	ferrichrome transport permease	transport/binding	cell envelop and process
3.52	2.37	SA0605			hypothetical protein, similar to dihydroxyacetone kinase	carbohydrate metabolism	Intermediary metabolism
3.29	2.33	SA0606			conserved hypothetical protein		
3.35	2.17	SA0607			conserved hypothetical protein		
1.06	0.84	SA0608			hypothetical protein		
1.03	0.94	SA0609			conserved hypothetical protein		
1.08	1.10	SA0610			hypothetical protein, similar to lipase LipA	pathogenic factor	other function
1.40	1.14	SA0611			hypothetical protein		
0.80	0.80	SA0612			conserved hypothetical protein		
1.18	0.94	SA0613			hypothetical protein		
1.17	1.10	SA0614			hypothetical protein, similar to two-component response regulator	RNA synthesis	Information pathway
0.57	0.80	SA0615			hypothetical protein, similar to two-component sensor histidine kinas	sensor	cell envelop and process
1.05	1.19	SA0616		vraF	ABC transporter ATP-binding protein	transport/binding	cell envelop and process
0.77	0.82	SA0617		vraG	ABC transporter permease	transport/binding	cell envelop and process
1.13	1.15	SA0618			conserved hypothetical protein		
1.07	1.13	SA0619			hypothetical protein, similar to low-affinity inorganic phosphate transporter	transport/binding	cell envelop and process
1.12	0.98	SA0620		ssaA	secretory antigen SsaA homologue	pathogenic factor	other function
0.95	0.94	SA0621			conserved hypothetical protein		
1.00	1.00	SA0622			hypothetical protein, similar to AraC/XylS family transcriptional regulator	RNA synthesis	Information pathway
0.89	0.53	SA0622a			hypothetical protein, similar to AraC/XylS family transcriptional regulator	RNA synthesis	Information pathway
0.45	0.63	SA0623			hypothetical protein		
0.66	0.73	SA0624			conserved hypothetical protein		
1.20	1.64	SA0625			conserved hypothetical protein		
1.19	1.28	SA0626			conserved hypothetical protein		
1.17	1.16	SA0627			hypothetical protein, similar to LysR family transcriptional regulator	RNA synthesis	Information pathway
1.02	1.07	SA0628			hypothetical protein, similar to sugar efflux transpoter	transport/binding	cell envelop and process
1.02	1.32	SA0629			conserved hypothetical protein		
0.93	1.02	SA0630			conserved hypothetical protein		
0.91	0.88	SA0631			hypothetical protein		
0.76	0.98	SA0632			conserved hypothetical protein		
0.89	1.12	SA0633			hypothetical protein		
0.41	0.75	SA0634			conserved hypothetical protein		
0.33	0.63	SA0635			conserved hypothetical protein		
0.35	0.61	SA0636			conserved hypothetical protein		
0.70	1.08	SA0637	cre		conserved hypothetical protein		
0.55	0.84	SA0638		bacA	bacitracin resistance protein (putative undecaprenol kinase) homologue	cell wall	cell envelop and process
0.81	1.17	SA0639			hypothetical protein, similar to ABC transporter required for expression of cytochron	transport/binding	cell envelop and process
0.86	1.26	SA0640			hypothetical protein, similar to ABC transporter required for expression of cytochron	transport/binding	cell envelop and process
0.79	0.79	SA0641		mgrA	conserved hypothetical protein, similar to transcriptional regulator	RNA synthesis	Information pathway
1.96	1.08	SA0642			hypothetical protein, similar to cobalamin synthesis related protein	coenzyme metabolism	Intermediary metabolism
0.78	0.64	SA0643			hypothetical protein, similar to aryl-alcohol dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.49	1.21	SA0644			hypothetical protein		
2.88	1.74	SA0645			conserved hypothetical protein		
1.07	1.41	SA0646			hypothetical protein, similar to deoxyribodipyrimidine photolyase	nucleic acid metabolism	Intermediary metabolism
0.96	1.29	SA0647			hypothetical protein		
1.15	1.23	SA0648			conserved hypothetical protein		
1.22	1.22	SA0649			conserved hypothetical protein		
1.32	1.03	SA0650		norA	quinolone resistance protein	detoxification	other function
0.52	0.61	SA0651			hypothetical protein		
0.66	0.74	SA0652			hypothetical protein, similar to transcription regulation protein	RNA synthesis	Information pathway
0.64	2.38	SA0653			hypothetical protein, similar to transcription repressor of fructose operon	RNA synthesis	Information pathway
0.64	2.08	SA0654		fruB	fructose 1-phosphate kinase	carbohydrate metabolism	Intermediary metabolism
0.27	0.98	SA0655		fruA	fructose specific permease	transport/binding	cell envelop and process
0.40	0.68	SA0656		nagA	probable N-acetylglucosamine-6-phosphate deacetylase	carbohydrate metabolism	Intermediary metabolism
0.38	0.32	SA0657			hypothetical protein, similar to hemolysin homologue	pathogenic factor	other function
0.82	0.68	SA0658			hypothetical protein, similar to plant-metabolite dehydrogenases	carbohydrate metabolism	Intermediary metabolism
0.75	1.04	SA0659			hypothetical protein, similar to CsbB stress response protein	adaptation to atypical	other function
0.70	0.62	SA0660		saeS	histidine protein kinase	sensor	cell envelop and process
0.72	0.65	SA0661		saeR	response regulator	RNA synthesis	Information pathway
0.78	0.60	SA0662			hypothetical protein		
0.79	1.11	SA0664			hypothetical protein		
1.02	1.28	SA0665			coenzyme PQQ synthesis homologue	coenzyme metabolism	Intermediary metabolism
1.00	1.37	SA0666			6-pyruvoyl tetrahydrobiopterin synthase homologue	coenzyme metabolism	Intermediary metabolism
0.94	1.14	SA0667			conserved hypothetical protein		
0.89	0.90	SA0668			hypothetical protein, similar to anthranilate synthase component II	aminoacid metabolism	Intermediary metabolism
0.91	0.88	SA0669			hypothetical protein, similar to para-aminobenzoate synthase component I	carbohydrate metabolism	Intermediary metabolism
0.81	0.89	SA0670			hypothetical protein, similar to para-aminobenzoate synthase component I	carbohydrate metabolism	Intermediary metabolism
1.13	0.91	SA0672			hypothetical protein, similar to urea amidolyase	aminoacid metabolism	Intermediary metabolism
0.95	0.91	SA0673			conserved hypothetical protein		
0.76	1.09	SA0674			hypothetical protein, similar to anion-binding protein	transport/binding	cell envelop and process
1.25	0.74	SA0675			hypothetical protein, similar to ABC transporter ATP-binding protein	transport/binding	cell envelop and process
1.04	0.97	SA0676		recQ	probable DNA helicase	DNA [illegible]	Information pathway
0.64	0.87	SA0677			hypothetical protein, similar to choline transport ATP-binding protein	transport/binding	cell envelop and process

0.49	0.69	SA0678			hypothetical protein, similar to choline transporter	transport/binding	cell envelop and process
1.24	0.94	SA0679			hypothetical protein, similar to histidinol-phosphate aminotransferase	aminoacid metabolism	Intermediary metabolism
1.14	0.88	SA0680			conserved hypothetical protein		
1.33	1.00	SA0681			hypothetical protein, similar to multidrug resistance protein	detoxification	other function
1.15	0.74	SA0682			hypothetical protein, similar to di-tripepride ABC transporter	transport/binding	cell envelop and process
1.16	1.20	SA0683			conserved hypothetical protein		
1.17	1.04	SA0684			conserved hypothetical protein		
1.45	0.51	SA0685		nrdI	NrdI protein involved in ribonucleotide reductase function	[illegible]	Intermediary metabolism
1.23	0.63	SA0686	cre	nrdE	hypothetical protein, similar to comF operon protein 3	[illegible]	Intermediary metabolism
1.15	0.73	SA0687		nrdF	ribonucleoside-diphosphate reductase minor subunit	[illegible]	Intermediary metabolism
2.44	0.97	SA0688			hypothetical protein, similar to ferrichrome ABC transporter permease	transport/binding	cell envelop and process
1.83	0.89	SA0689			hypothetical protein, similar to ferrichrome ABC transporter permease	transport/binding	cell envelop and process
1.57	0.97	SA0690			hypothetical protein, similar to ferrichrome ABC transporter ATP-binding protein	transport/binding	cell envelop and process
1.44	0.93	SA0691			lipoprotein, similar to ferrichrome ABC transporter	transport/binding	cell envelop and process
0.92	0.98	SA0692			conserved hypothetical protein		
0.81	0.95	SA0693			hypothetical protein, similar to UDP-N-acetylenolpyruvoylglucosamine reductase	cell wall	cell envelop and process
0.80	0.86	SA0694			conserved hypothetical protein		
0.87	0.93	SA0695			hypothetical protein		
0.81	1.19	SA0696			conserved hypothetical protein		
0.74	1.40	SA0697			hypothetical protein, similar to glycerate kinase	carbohydrate metabolism	Intermediary metabolism
1.03	1.10	SA0698		pepT	aminotripeptidase	protein modification	Information pathway
0.95	1.16	SA0699			conserved hypothetical protein		
1.00	1.18	SA0700			conserved hypothetical protein		
2.00	1.20	SA0701			conserved hypothetical protein		
0.74	0.83	SA0702		llm	lipophilic protein affecting bacterial lysis rate and methicillin resistance level	cell wall	cell envelop and process
0.73	0.96	SA0703			conserved hypothetical protein		
1.01	0.87	SA0704			conserved hypothetical protein		
1.80	0.91	SA0705		comFA	hypothetical protein, similar to comF operon protein 1	transformation/competence	cell envelop and process
0.97	0.93	SA0706		comFC	hypothetical protein, similar to comF operon protein 3 .	transformation/competence	cell envelop and process
0.84	0.85	SA0707			conserved hypothetical protein		
0.58	0.94	SA0708		secA	preprotein translocase subunit	protein secretion	cell envelop and process
0.91	0.85	SA0709		prfB	peptide chain release factor 2	protein synthesis	Information pathway
1.04	1.01	SA0710	cre		conserved hypothetical protein		
0.96	0.95	SA0711			conserved hypothetical protein		
1.14	0.93	SA0712			hypothetical protein		
1.12	1.11	SA0713		uvrB	exinuclease ABC subunit B	DNA repair or modify	Information pathway
0.93	1.34	SA0714		uvrA	exinuclease ABC subunit A	DNA repair or modify	Information pathway
0.85	0.82	SA0715		hprK	HPr kinase/phosphatase	RNA synthesis	Information pathway
0.45	0.53	SA0716		lgt	prolipoprotein diacylglyceryl transferase	protein modification	Information pathway
0.91	1.06	SA0717			hypothetical protein, similar to O-acetyltransferase	carbohydrate metabolism	Intermediary metabolism
0.81	0.86	SA0718			conserved hypothetical protein		
0.78	0.90	SA0719		trxB	thioredoxine reductase	membrane bioenergetics	cell envelop and process
0.90	0.91	SA0720			conserved hypothetical protein		
0.95	0.86	SA0721			conserved hypothetical protein		
1.08	0.85	SA0722			conserved hypothetical protein		
0.74	0.92	SA0723		clpP	clpP	adaptation to atypical	other function
1.05	0.72	SA0724	cre		hypothetical protein, similar to cell-division inhibitor	cell division	cell envelop and process
0.87	0.89	SA0725			conserved hypothetical protein		
0.67	0.62	SA0726		gapR	glycolytic operon regulator	RNA synthesis	Information pathway
0.54	0.45	SA0727		gap	glyceraldehyde-3-phosphate dehydrogenase	carbohydrate metabolism	Intermediary metabolism
0.52	0.46	SA0728		pgk	phosphoglycerate kinase	carbohydrate metabolism	Intermediary metabolism
0.63	0.58	SA0729		tpi	triosephosphate isomerase	carbohydrate metabolism	Intermediary metabolism
0.50	0.46	SA0730		pgm	2, 3-diphosphoglycerate-independentphosphoglycer ate mutase	carbohydrate metabolism	Intermediary metabolism
0.44	0.52	SA0731		eno	enolase	carbohydrate metabolism	Intermediary metabolism
1.32	0.96	SA0732			hypothetical protein		
0.94	0.92	SA0733		secG	probable protein-export membrane protein	protein secretion	cell envelop and process
0.92	1.09	SA0734			carboxyesterase precursor homologue	lipid metabolism	Intermediary metabolism
0.96	0.94	SA0736		ssrP	ssrA-binding protein	protein synthesis	Information pathway
0.55	0.56	SA0738			hypothetical protein		
0.43	0.49	SA0739			conserved hypothetical protein		
0.87	0.99	SA0740			hypothetical protein		
1.41	0.98	SA0741			conserved hypothetical protein		
1.17	0.87	SA0742		clfA	fibrinogen-binding protein A, clumping factor	pathogenic factor	other function
0.99	0.78	SA0743			hypothetical protein, similar to staphylocoagulase precursor	pathogenic factor	other function
0.71	0.74	SA0744		ssp	extracellular ECM and plasma binding protein	pathogenic factor	other function
0.78	0.85	SA0745			hypothetical protein, similar to extracellular matrix and plasma binding	pathogenic factor	other function
0.77	0.44	SA0746			staphylococcal nuclease	pathogenic factor	other function
0.98	0.47	SA0747		cspC	cold-shock protein C	adaptation to atypical	other function
0.97	0.81	SA0748			hypothetical protein		
0.84	1.04	SA0749			hypothetical protein		
1.32	1.17	SA0750	cre		conserved hypothetical protein		
1.14	0.80	SA0751			hypothetical protein		
1.63	0.86	SA0752			hypothetical protein		
1.29	0.89	SA0753			conserved hypothetical protein		
1.64	0.55	SA0754			hypothetical protein, similar to lactococcal prophage ps3 protein 05	phage-related	other function
1.20	1.29	SA0754a			hypothetical protein, similar to lactococcal prophage ps3 protein 05	phage-related	other function
1.08	0.82	SA0755			hypothetical protein, similar to general stress protein 170	adaptation to atypical	other function
0.92	0.82	SA0756			hypothetical protein, similar to 3-dehydroquinate dehydratase	aminoacid metabolism	Intermediary metabolism
1.05	0.83	SA0757			conserved hypothetical protein		
0.38	0.93	SA0758			hypothetical protein, similar to thioredoxin	membrane bioenergetics	cell envelop and process
0.92	1.32	SA0759			hypothetical protein, similar to arsenate reductase	detoxification	other function
1.30	1.47	SA0760	cre		glycine cleavage system protein H homologue	aminoacid metabolism	Intermediary metabolism
1.00	0.94	SA0761		truncated-SA	conserved hypothetical protein		
0.90	1.14	SA0768			conserved hypothetical protein		
1.76	1.14	SA0769			ABC transporter ATP-binding protein homologue category	transport/binding	cell envelop and process
1.90	1.04	SA0770			conserved hypothetical protein		
1.73	1.04	SA0771			conserved hypothetical protein		
1.61	1.01	SA0772			conserved hypothetical protein		
0.82	0.84	SA0773			conserved hypothetical protein		
1.12	1.22	SA0774			ABC transporter ATP-binding protein homologue	transport/binding	cell envelop and process
0.88	1.16	SA0775			conserved hypothetical protein		
0.93	1.06	SA0776		nifS	aminotransferase NifS homologue	coenzyme metabolism	Intermediary metabolism
0.92	1.12	SA0777			hypothetical protein, similar to nitrogen fixation protein NifU	miscellaneous	other function
0.65	0.90	SA0778			conserved hypothetical protein		
1.02	1.20	SA0779			hypothetical protein		
0.64	1.01	SA0780			hypothetical protein, similar to hemolysin	pathogenic factor	other function
0.75	0.81	SA0781			hypothetical protein, similar to 2-nitropropane dioxygenase	detoxification	other function

0.67	0.88	SA0782			conserved hypothetical protein		
0.72	1.17	SA0783			conserved hypothetical protein		
0.79	1.03	SA0784			conserved hypothetical protein		
0.97	0.70	SA0785		lipA	lipoic acid synthetase	lipid metabolism	Intermediary metabolism
0.77	0.89	SA0786			conserved hypothetical protein		
0.91	1.05	SA0788			conserved hypothetical protein		
0.67	0.85	SA0789			conserved hypothetical protein		
0.68	0.83	SA0790			hypothetical protein, similar to N-acetyl-glucosamine catabolism homologue	carbohydrate metabolism	Intermediary metabolism
0.81	0.76	SA0791			hypothetical protein, similar to glycerate dehydrogenase	carbohydrate metabolism	Intermediary metabolism
0.57	0.68	SA0793		dltA	D-alanine-D-alanyl carrier protein ligase	cell wall	cell envelop and process
0.53	0.64	SA0794		dltB	DltB membrane protein	transport/binding	cell envelop and process
0.49	0.64	SA0795		dltC	D-alanyl carrier protein	cell wall	cell envelop and process
0.48	0.69	SA0796		dltD	poly D-alanine transfer protein	transport/binding	cell envelop and process
0.66	0.89	SA0797		nifU	hypothetical protein, similar to nitrogen fixation protein NifU	miscellaneous	other function
1.02	1.11	SA0798			conserved hypothetical protein		
1.05	0.81	SA0799			hypothetical protein, similar to NADH dehydrogenase	membrane bioenergetics	cell envelop and process
0.76	0.93	SA0800			conserved hypothetical protein		
0.92	0.94	SA0801			conserved hypothetical protein		
0.50	0.75	SA0802			hypothetical protein, similar to NADH dehydrogenase	membrane bioenergetics	cell envelop and process
0.56	0.83	SA0803		ampA	probable cytosol aminopeptidase	protein modification	Information pathway
3.73	1.12	SA0804			conserved hypothetical protein		
2.08	1.23	SA0805			conserved hypothetical protein		
1.28	0.78	SA0806			hypothetical protein		
0.98	0.98	SA0807		mnhG	Na+/H+ antiporter subunit	membrane bioenergetics	cell envelop and process
0.89	0.88	SA0808		mnhF	Na+/H+ antiporter subunit	membrane bioenergetics	cell envelop and process
0.92	0.71	SA0809		mnhE	Na+/H+ antiporter subunit	membrane bioenergetics	cell envelop and process
0.95	0.83	SA0810		mnhD	Na+/H+-antiporter subunit	membrane bioenergetics	cell envelop and process
1.01	0.83	SA0811		mnhC	Na+/H+ antiporter subunit	membrane bioenergetics	cell envelop and process
0.91	0.79	SA0812		mnhB	Na+/H+ antiporter subunit	membrane bioenergetics	cell envelop and process
1.04	0.86	SA0813		mnhA	Na+/H+ antiporter subunit	membrane bioenergetics	cell envelop and process
1.25	1.09	SA0814			conserved hypothetical protein	RNA synthesis	Information pathway
0.44	0.77	SA0815			peptidyl-prolyl cis-trans isomerase homologue	protein folding	Information pathway
0.73	1.06	SA0816			hypothetical protein, similar to polyribonucleotide nucleotidyltransferase	nucleic acid metabolism	Intermediary metabolism
0.51	0.96	SA0817			hypothetical protein, similar to NADH-dependent flavin oxidoreductase	membrane bioenergetics	cell envelop and process
3.53	4.74	SA0818		rocD	ornithine aminotransferase	aminoacid metabolism	Intermediary metabolism
4.19	4.80	SA0819	cre	gudB	NAD-specific glutamate dehydrogenase	aminoacid metabolism	Intermediary metabolism
19.14	5.62	SA0820		glpQ	glycerophosphoryl diester phosphodiesterase	lipid metabolism	Intermediary metabolism
0.77	1.50	SA0821		argH	argininosuccinate lyase	aminoacid metabolism	Intermediary metabolism
0.90	1.41	SA0822		argG	argininosuccinate synthase	aminoacid metabolism	Intermediary metabolism
0.45	0.82	SA0823	cre	pgi	glucose-6-phosphate isomerase A	carbohydrate metabolism	Intermediary metabolism
1.06	0.93	SA0824			conserved hypothetical protein		
0.97	0.98	SA0825		spsA	type-I signal peptidase	protein secretion	cell envelop and process
1.23	1.10	SA0826		spsB	type-1 signal peptidase 1B	protein secretion	cell envelop and process
1.07	0.98	SA0827			hypothetical protein, similar to ATP-dependent nuclease subunit B	DNA repair or modify	Information pathway
0.92	0.79	SA0828			hypothetical protein, similar to ATP-dependent nuclease subunit A	DNA repair or modify	Information pathway
0.73	0.96	SA0829			hypothetical protein, similar to 5-oxo-1,2,5-tricarboxilic-3-penten acid decarboxyl	aminoacid metabolism	Intermediary metabolism
0.98	0.86	SA0830			conserved hypothetical protein		
0.53	0.69	SA0831		cdr	coenzyme A disulfide reductase	coenzyme metabolism	Intermediary metabolism
0.65	0.64	SA0832			conserved hypothetical protein		
0.85	0.89	SA0833			conserved hypothetical protein		
0.71	0.91	SA0834			hypothetical protein, similar to lipopolysaccharide modification acyltransferase	cell wall	cell envelop and process
1.62	1.81	SA0835		clpB	clpB	adaptation to atypical	other function
0.86	1.08	SA0836			hypothetical protein, similar to transcription regulator LysR family	RNA synthesis	Information pathway
1.32	1.05	SA0837			hypothetical protein, similar to 2-isopropylmalate synthase	aminoacid metabolism	Intermediary metabolism
1.18	0.87	SA0838			conserved hypothetical protein		
0.94	0.76	SA0839			hypothetical protein		
0.94	0.93	SA0840			conserved hypothetical protein		
0.94	1.19	SA0841			hypothetical protein, similar to cell surface protein Map-w	pathogenic factor	other function
0.48	0.67	SA0842		FabH	FabH	lipid metabolism	Intermediary metabolism
0.52	0.63	SA0843		fab	3-oxoacyl- synthase	lipid metabolism	Intermediary metabolism
1.02	1.00	SA0844			hypothetical protein		
1.80	0.69	SA0845		oppB	oligopeptide transport system permease protein	transport/binding	cell envelop and process
1.85	0.70	SA0846			hypothetical protein, similar to oligopeptide transport system permease protein Op	transport/binding	cell envelop and process
1.61	0.87	SA0847		oppD	oligopeptide transport system ATP-binding protein OppD homologue	transport/binding	cell envelop and process
1.40	0.99	SA0848		oppF	oligopeptide transport system ATP-binding protein OppF homologue	transport/binding	cell envelop and process
1.48	0.87	SA0849			hypothetical protein, similar to peptide binding protein OppA	transport/binding	cell envelop and process
1.19	0.91	SA0850			hypothetical protein, similar to oligopeptide ABC transporter oligopeptide-binding pr	transport/binding	cell envelop and process
1.22	0.83	SA0851			oligopeptide ABC transporter ATP-binding protein homologue	transport/binding	cell envelop and process
1.07	0.90	SA0852		appF	oligopeptide transport system ATP-binding protein AppF homologue	transport/binding	cell envelop and process
1.22	0.86	SA0853		oppB	probable oligopeptide transport system permease protein OppB	transport/binding	cell envelop and process
1.06	0.77	SA0854			Hypothetical protein, similar to oligopeptide transport system permease protein Op	transport/binding	cell envelop and process
0.58	0.64	SA0855		trpS	tryptophanyl-tRNA synthetase	protein synthesis	Information pathway
1.13	0.83	SA0856			conserved hypothetical protein		
0.83	0.90	SA0857			hypothetical protein, similar to negative regulator of genetic competence MecA		
0.47	0.56	SA0858			hypothetical protein, similar to transcription factor	RNA synthesis	Information pathway
0.15	0.41	SA0859			thimet oligopeptidase homologue	aminoacid metabolism	Intermediary metabolism
0.26	0.55	SA0860			conserved hypothetical protein		
0.23	0.41	SA0861			conserved hypothetical protein		
0.42	0.86	SA0862			conserved hypothetical protein		
0.32	0.71	SA0863			conserved hypothetical protein		
0.35	0.63	SA0864		relA	GTP pyrophosphokinase	nucleic acid metabolism	Intermediary metabolism
0.86	1.07	SA0865			conserved hypothetical protein		
1.11	0.94	SA0866			conserved hypothetical protein		
0.43	0.53	SA0867			hypothetical protein, similar to Mg2+ transporter	transport/binding	cell envelop and process
0.60	1.09	SA0868			Na+/H+ antiporter homologue	membrane bioenergetics	cell envelop and process
0.46	0.87	SA0869		fabI	trans-2-enoyl-ACP reductase	lipid metabolism	Intermediary metabolism
0.92	0.74	SA0870			conserved hypothetical protein		
1.42	1.01	SA0871			hypothetical protein, similar to Na+/H+-dependent alanine carrier protein	transport/binding	cell envelop and process
1.38	1.17	SA0872			conserved hypothetical protein		
5.33	3.73	SA0873			conserved hypothetical protein		
0.62	0.85	SA0874			hypothetical protein, similar to multidrug resistance protein-related protein	detoxification	
0.58	0.87	SA0875	cre		hypothetical protein, similar to cell wall synthesis protein	cell wall	cell envelop and process
0.61	0.82	SA0876		murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	cell wall	cell envelop and process
0.60	0.77	SA0877		prfC	peptide chain release factor 3	protein synthesis	Information pathway
0.54	0.81	SA0878			toxic anion resistance protein homologue	detoxification	
0.86	0.81	SA0880			hypothetical protein, similar to Na+-transporting ATP synthase	membrane bioenergetics	cell envelop and process
1.07	0.97	SA0881			hypothetical protein, similar to nucleotidase	phosphate metabolism	Intermediary metabolism

1.10	0.60	SA0882			hypothetical protein, similar to competence transcription factor	transformation/competence	cell envelop and process
2.90	1.20	SA0883			hypothetical protein		
0.14	0.48	SA0884			lipoate-protein ligase homolog	protein modification	Information pathway
0.55	0.76	SA0885			hypothetical protein		
1.00	0.23	SA0886			hypothetical protein, similar to lactococcin 972 immunity factor	transport/binding	cell envelop and process
1.28	1.11	SA0887			conserved hypothetical protein		
1.07	0.92	SA0888			conserved hypothetical protein		
1.04	1.12	SA0889			hypothetical protein		
0.36	0.26	SA0890			conserved hypothetical protein		
1.26	0.92	SA0891	cre		hypothetical protein, similar to ferrichrome ABC transporter	transport/binding	cell envelop and process
0.84	1.08	SA0892			hypothetical protein		
0.17	0.33	SA0893			conserved hypothetical protein		
0.95	0.84	SA0894			hypothetical protein, similar to 1,4-dihydroxy-2-naphthodate octaprenyltransfera	coenzyme metabolism	Intermediary metabolism
0.66	1.11	SA0895			hypothetical protein, similar to menaquinone-specific isochorismate synthase	coenzyme metabolism	Intermediary metabolism
0.65	0.97	SA0896		menD	menaquinone biosynthesis protein	coenzyme metabolism	Intermediary metabolism
0.66	1.00	SA0897			hypothetical protein, similar to prolyl aminopeptidase	protein modification	Information pathway
1.73	2.96	SA0898		menB	naphthoate synthase	coenzyme metabolism	Intermediary metabolism
0.96	1.04	SA0899		sspC	cysteine protease	pathogenic factor	other function
1.21	1.53	SA0900		sspB	cysteine protease precursor	pathogenic factor	other function
1.06	1.01	SA0900a		sspB	cysteine protease precursor	pathogenic factor	other function
0.91	1.02	SA0901		sspA	serine protease; V8 protease; glutamyl endopeptidase	pathogenic factor	other function
0.29	0.20	SA0902		hisC	HisC homolog	aminoacid metabolism	Intermediary metabolism
0.85	0.88	SA0903			conserved hypothetical protein		
1.75	1.05	SA0904		atlR	hypothetical protein, probable ATL autolysin transcription regulator	RNA synthesis	Information pathway
0.23	0.25	SA0905		atl	autolysin	cell division	cell envelop and process
0.93	0.93	SA0906			conserved hypothetical protein		
0.62	0.94	SA0907			conserved hypothetical protein		
0.71	0.96	SA0908			conserved hypothetical protein		
0.69	0.92	SA0909		fmtA	FmtA, autolysis and methicillin resistant-related protein	pathogenic factor	other function
0.95	0.77	SA0910			hypothetical protein, similar to quinol oxidase polypeptide IV QoxD	membrane bioenergetics	cell envelop and process
1.54	1.12	SA0911		qoxC	Quinol oxidase polypeptide III QoxC	membrane bioenergetics	cell envelop and process
1.36	1.04	SA0912		qoxB	Quinol oxidase polypeptide I QoxB	membrane bioenergetics	cell envelop and process
1.40	1.18	SA0913			hypothetical protein, similar to quinol oxidase polypeptide II QoxA	membrane bioenergetics	cell envelop and process
1.53	1.19	SA0914			hypothetical protein, similar to chitinase B	miscellaneous	other function
1.60	1.96	SA0915		folD	FolD bifunctional protein	coenzyme metabolism	Intermediary metabolism
1.24	1.19	SA0916			hypothetical protein, similar to phosphoribosylaminoimidazole carboxylase PurE	nucleic acid metabolism	Intermediary metabolism
0.79	1.18	SA0917		purK	sphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain PurK hom	nucleic acid metabolism	Intermediary metabolism
0.83	0.97	SA0918		purC	phosphoribosylaminoimidazolesuccinocarboxamide synthetase homolog	nucleic acid metabolism	Intermediary metabolism
0.79	1.15	SA0919			conserved hypothetical protein		
0.69	1.05	SA0920		purQ	phosphoribosylformylglycinamidine synthase I PurQ	nucleic acid metabolism	Intermediary metabolism
0.19	0.66	SA0921		purL	phosphoribosylformylglycinamidine synthetase PurL	nucleic acid metabolism	Intermediary metabolism
0.38	0.94	SA0922		purF	phosphoribosylpyrophosphate amidotransferase PurF	nucleic acid metabolism	Intermediary metabolism
0.12	0.38	SA0923		purM	phosphoribosylformylglycinamidine cyclo-ligase PurM	nucleic acid metabolism	Intermediary metabolism
0.37	0.95	SA0924		purN	phosphoribosylglycinamide formyltransferase	nucleic acid metabolism	Intermediary metabolism
0.33	0.73	SA0925		purH	bifunctional purine biosynthesis protein PurH	nucleic acid metabolism	Intermediary metabolism
0.36	0.76	SA0926		purD	phosphoribosylamine--glycine ligase PurD	nucleic acid metabolism	Intermediary metabolism
0.59	0.85	SA0927			conserved hypothetical protein	nucleic acid metabolism	Intermediary metabolism
0.45	0.52	SA0928			hypothetical protein, similar to cation ABC transporter	transport/binding	cell envelop and process
1.09	1.09	SA0929			conserved hypothetical protein		
2.64	1.76	SA0931			hypothetical protein		
3.99	1.24	SA0932			conserved hypothetical protein		
1.27	1.27	SA0933			hypothetical protein		
1.00	0.73	SA0934		ptsH	phophocarrier protein HPR	protein modification	Information pathway
0.91	0.75	SA0935		ptsI	phosphoenolpyruvate-protein phosphatase	protein modification	Information pathway
0.98	1.29	SA0936			conserved hypothetical protein		
0.81	1.36	SA0937		cydA	cytochrome D ubiquinol oxidase subunit 1 homolog	membrane bioenergetics	cell envelop and process
1.02	1.19	SA0939			conserved hypothetical protein		
0.78	1.21	SA0940			conserved hypothetical protein		
0.90	1.07	SA0941			conserved hypothetical protein		
0.60	1.34	SA0942		pdf1	formylmethionine deformylase homolog	aminoacid metabolism	Intermediary metabolism
0.50	0.84	SA0943			conserved hypothetical protein		
0.46	1.76	SA0943-1		pdhA	pyruvate dehydrogenase E1 component alpha subunit	carbohydrate metabolism	Intermediary metabolism
0.50	1.70	SA0944		pdhB	pyruvate dehydrogenase E1 component beta subunit	carbohydrate metabolism	Intermediary metabolism
0.42	1.59	SA0945		pdhC	drolipoamide S-acetyltransferase component of pyruvate dehydrogenase compl	carbohydrate metabolism	Intermediary metabolism
0.39	1.29	SA0946		pdhD	dihydrolipoamide dehydrogenase component of pyruvate dehydrogenase E3	carbohydrate metabolism	Intermediary metabolism
1.01	1.15	SA0947			conserved hypothetical protein		
1.05	1.43	SA0949			conserved hypothetical protein		
1.05	1.28	SA0950		potA	spermidine/putrescine ABC transporter, ATP-binding protein homolog	transport/binding	cell envelop and process
0.90	1.29	SA0951		potB	potB	transport/binding	cell envelop and process
0.85	1.20	SA0952		potC	spermidine/putrescine ABC transporter homolog	transport/binding	cell envelop and process
0.89	1.36	SA0953		potD	spermidine/putrescine-binding protein precursor homolog	transport/binding	cell envelop and process
1.00	0.72	SA0954			conserved hypothetical protein		
0.81	0.98	SA0955			hypothetical protein		
0.83	0.82	SA0956			hypothetical protein, similar to Mn2+-transport protein	transport/binding	cell envelop and process
0.73	0.76	SA0957			conserved hypothetical protein		
1.09	0.80	SA0958			myo-inositol-1(or 4)-monophosphatase homolog	carbohydrate metabolism	Intermediary metabolism
0.83	0.57	SA0959			GTP-binding elongation factor homolog	protein synthesis	Information pathway
1.12	0.99	SA0960			conserved hypothetical protein		
1.23	1.00	SA0961			conserved hypothetical protein		
0.84	0.79	SA0962			conserved hypothetical protein		
1.18	0.80	SA0963		pycA	pyruvate carboxylase	carbohydrate metabolism	Intermediary metabolism
1.07	0.87	SA0964			hypothetical protein, similar to heme synthase	membrane bioenergetics	cell envelop and process
1.00	1.44	SA0965		ctaB	cytochrome caa3 oxidase (assembly factor) homolog	membrane bioenergetics	cell envelop and process
1.05	0.88	SA0966			conserved hypothetical protein		
0.24	0.29	SA0967			conserved hypothetical protein		
1.16	1.05	SA0968			conserved hypothetical protein		
0.76	0.99	SA0969			hypothetical protein, similar to glycerophosphoryl diester phosphodiesterase	lipid metabolism	Intermediary metabolism
0.86	1.24	SA0970			conserved hypothetical protein		
0.85	1.12	SA0971			conserved hypothetical protein		
0.81	1.06	SA0972			conserved hypothetical protein		
0.85	1.04	SA0973			phosphopantetheine adenyltransferase homolog	coenzyme metabolism	Intermediary metabolism
0.90	1.08	SA0974			conserved hypothetical protein		
0.81	1.13	SA0975			conserved hypothetical protein		
0.98	0.93	SA0976		isdB	conserved hypothetical protein		
0.88	0.94	SA0977		isdA	cell surface protein	pathogenic factor	other function
1.14	0.89	SA0978		isdC	conserved hypothetical protein		
0.92	0.89	SA0979		isdD	conserved hypothetical protein		

0.59	0.34	SA0980		isdE	hypothetical protein, similar to ferrichrome ABC transporter	transport/binding	cell envelop and process
1.09	0.81	SA0981	cre	isdF	hypothetical protein, similar to ferrichrome ABC transporter	transport/binding	cell envelop and process
0.77	0.85	SA0982		srtB	NPQTN specific sortase B		
0.89	0.95	SA0983		isdG	conserved hypothetical protein		
1.75	1.28	SA0984			hypothetical protein, similar to rRNA methylase	RNA modification	Information pathway
0.59	0.83	SA0985		pheS	Phe-tRNA synthetase alpha chain	protein synthesis	Information pathway
0.59	0.70	SA0986	cre	pheT	Phe-tRNA synthetase beta chain	protein synthesis	Information pathway
0.70	1.12	SA0987			hypothetical protein, similar to ribonuclease HIII	RNA modification	Information pathway
0.91	1.49	SA0988			conserved hypothetical protein		
0.81	1.36	SA0989			conserved hypothetical protein		
0.54	0.88	SA0990			DNA-dependent DNA polymerase beta chain	DNA replication	Information pathway
0.55	1.98	SA0991		mutS2	MutS-like protein	DNA repair/recovery	Information pathway
0.62	0.89	SA0992		trxA	thioredoxin	membrane bioenergetics	cell envelop and process
0.86	1.41	SA0993		uvrC	excinuclease ABC subunit C	DNA repair/recovery	Information pathway
3.01	2.34	SA0994	cre	sdhC	succinate dehydrogenase cytochrome b-558	carbohydrate metabolism	Intermediary metabolism
3.57	3.53	SA0995		sdhA	succinate dehydrogenase flavoprotein subunit	carbohydrate metabolism	Intermediary metabolism
2.58	2.75	SA0996		sdhB	succinate dehydrogenase iron-sulfur protein subunit	carbohydrate metabolism	Intermediary metabolism
1.11	0.99	SA0997		murI	glutamate racemase	cell wall	cell envelop and process
1.29	0.91	SA0998			conserved hypothetical protein		
1.55	0.76	SA0999			conserved hypothetical protein		
0.67	0.49	SA1000			hypothetical protein, similar to fibrinogen-binding protein	pathogenic factor	other function
1.32	0.54	SA1001			hypothetical protein		
0.98	0.72	SA1003			hypothetical protein, similar to fibrinogen-binding protein	pathogenic factor	other function
1.26	0.90	SA1004			hypothetical protein, similar to fibrinogen-binding protein	pathogenic factor	other function
1.06	0.82	SA1005			hypothetical protein		
3.58	3.52	SA1007	cre	hla	Alpha-Hemolysin precursor	pathogenic factor	other function
1.42	1.27	SA1008	cre		hypothetical protein		
1.04	1.04	SA1009			hypothetical protein, similar to exotoxin 1	pathogenic factor	other function
0.98	1.02	SA1010			hypothetical protein, similar to exotoxin 4	pathogenic factor	other function
1.32	1.41	SA1011	cre		hypothetical protein, similar to exotoxin 3	pathogenic factor	other function
20.14	2.42	SA1012		argF	ornithine carbamoyltransferase	aminoacid metabolism	Intermediary metabolism
24.60	2.50	SA1013			hypothetical protein, similar to carbamate kinase	nucleic acid metabolism	Intermediary metabolism
12.11	1.98	SA1014			conserved hypothetical protein		
1.34	0.89	SA1015			hypothetical protein		
1.66	1.21	SA1016			conserved hypothetical protein		
0.98	1.05	SA1018			conserved hypothetical protein		
1.01	1.46	SA1019			conserved hypothetical protein		
0.82	1.18	SA1020	cre		conserved hypothetical protein		
0.91	0.94	SA1021			conserved hypothetical protein		
0.94	1.00	SA1022			conserved hypothetical protein		
0.95	1.12	SA1023		ftsL	cell division protein	cell division	cell envelop and process
0.57	1.09	SA1024		pbpA	penicillin-binding protein 1	cell wall	cell envelop and process
0.56	1.13	SA1025		mraY	phospho-N-muramic acid-pentapeptide translocase	cell wall	cell envelop and process
0.69	0.84	SA1026		murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	cell wall	cell envelop and process
0.88	1.10	SA1027		div1b	cell division protein, FtsQ homolog	cell division	cell envelop and process
0.81	0.84	SA1028		ftsA	cell division protein	cell division	cell envelop and process
0.68	0.80	SA1029		ftsZ	cell division protein	cell division	cell envelop and process
0.82	1.06	SA1030			conserved hypothetical protein		
1.00	0.87	SA1031			conserved hypothetical protein		
0.92	0.88	SA1032			conserved hypothetical protein		
1.02	1.06	SA1033			conserved hypothetical protein		
0.80	0.77	SA1034			hypothetical protein, similar to cell-division protein	cell division	cell envelop and process
0.84	0.87	SA1035			hypothetical protein, similar to cell-divisio initiation protein	cell division	cell envelop and process
0.40	1.01	SA1036		ileS	Ile-tRNA synthetase	protein synthesis	Information pathway
0.82	1.23	SA1037			conserved hypothetical protein		
0.89	1.13	SA1039		lsp	lipoprotein signal peptidase	protein modification	Information pathway
1.08	0.99	SA1040			conserved hypothetical protein		
1.29	0.42	SA1041		pyrR	pyrimidine operon repressor chainA	RNA synthesis	Information pathway
0.88	0.45	SA1042		pyrP	uracil permease	transport/binding	cell envelop and process
1.07	0.71	SA1043		pyrB	aspartate transcarbamoylase chain A	nucleic acid metabolism	Intermediary metabolism
1.03	0.61	SA1044		pyrC	dihydroorotase	nucleic acid metabolism	Intermediary metabolism
1.07	0.69	SA1045		pyrAA	carbamoyl-phosphate synthase small chain	nucleic acid metabolism	Intermediary metabolism
0.97	0.52	SA1046		pyrAB	carbamoyl-phosphate synthase large chain	nucleic acid metabolism	Intermediary metabolism
0.67	0.57	SA1046a		pyrAB	carbamoyl-phosphate synthase large chain	nucleic acid metabolism	Intermediary metabolism
1.10	0.73	SA1047		pyrF	orotidine-5-phosphate decarboxylase	nucleic acid metabolism	Intermediary metabolism
0.94	0.60	SA1048		pyrE	orotate phosphoribosyltransferase	nucleic acid metabolism	Intermediary metabolism
1.07	0.71	SA1049			hypothetical protein		
1.04	0.75	SA1050			conserved hypothetical protein		
0.86	1.09	SA1051			hypothetical protein, similar to fibrinogen binding protein	pathogenic factor	other function
0.73	0.64	SA1052		gmk	guanylate kinase homolog	nucleic acid metabolism	Intermediary metabolism
0.68	0.54	SA1053			conserved hypothetical protein		
0.74	0.93	SA1054			pantothenate metabolism flavoprotein homolog	coenzyme metabolism	Intermediary metabolism
0.71	0.97	SA1055		priA	PriA, primosomal protein	DNA replication	Information pathway
0.87	0.64	SA1056			hypothetical protein		
0.64	1.19	SA1057			conserved hypothetical protein		
0.87	0.96	SA1058			hypothetical protein, similar to polypeptide deformylase	protein modification	Information pathway
1.19	1.19	SA1059			methionyl-tRNA formyltransferase	protein synthesis	Information pathway
1.01	1.20	SA1060			hypothetical protein, similar to RNA-binding Sun protein	RNA modification	Information pathway
0.93	1.14	SA1061			conserved hypothetical protein		
0.84	1.07	SA1062			conserved hypothetical protein		
0.81	1.14	SA1063			protein kinase	protein modification	Information pathway
0.94	1.18	SA1064			conserved hypothetical protein		
0.97	1.10	SA1064a			conserved hypothetical protein		
0.90	1.04	SA1065		cfxE	ribulose-5-phosphate 3-epimerase homolog	carbohydrate metabolism	Intermediary metabolism
0.77	1.00	SA1066			conserved hypothetical protein		
0.87	0.86	SA1067		rpmB	50S ribosomal protein L28	protein synthesis	Information pathway
0.87	1.02	SA1068			conserved hypothetical protein		
0.50	0.77	SA1069			conserved hypotehtical protein		
0.57	0.76	SA1069a			conserved hypotehtical protein		
0.84	0.95	SA1070		recG	ATP-dependent DNA helicase	[illegible]	Information pathway
0.55	1.05	SA1071			conserved hypothetical protein		
0.52	1.01	SA1072		plsX	fatty acid/phospholipid synthesis protein	lipid metabolism	Intermediary metabolism
0.45	0.87	SA1073		fabD	malonyl CoA-acyl carrier protein transacylase	lipid metabolism	Intermediary metabolism
0.52	0.86	SA1074		fabG	3-oxoacyl- reductase	lipid metabolism	Intermediary metabolism
0.42	0.58	SA1075		hmrB	HmrB protein	lipid metabolism	Intermediary metabolism
0.53	0.79	SA1076		rnc	RNase III	RNA modification	Information pathway
0.42	0.83	SA1077		smc	chromosome segregation SMC protein	DNA packaging	Information pathway

0.77	1.14	SA1078		ffh	signal recognition particle	protein secretion	cell envelop and process
0.65	0.96	SA1079			conserved hypothetical protein		
0.79	1.22	SA1080		ffh	signal recognition particle homolog	protein secretion	cell envelop and process
0.70	1.10	SA1081		rpsP	30S ribosomal protein S16	protein synthesis	Information pathway
0.79	1.22	SA1082		rimM	probable 16S rRNA processing protein	RNA modification	Information pathway
0.78	1.17	SA1083		trmD	tRNA	RNA modification	Information pathway
0.69	0.97	SA1084		rplS	50S ribosomal protein L19	protein synthesis	Information pathway
0.79	0.99	SA1085			conserved hypothetical protein		
1.02	1.33	SA1086			conserved hypothetical protein		
0.94	1.36	SA1087		rnhB	RNase HII	DNA replication	Information pathway
3.10	5.78	SA1088		sucC	succinyl-CoA synthetase	carbohydrate metabolism	Intermediary metabolism
3.50	5.65	SA1089		sucD	succinyl-CoA synthetase	carbohydrate metabolism	Intermediary metabolism
0.92	1.11	SA1090		lytN	LytN protein	cell wall	cell envelop and process
1.01	1.29	SA1091		fmhC#eprh	FmhC protein	cell wall	cell envelop and process
1.03	1.10	SA1092			hypothetical protein, similar to DNA processing Smf protein	DNA packaging	Information pathway
0.61	0.94	SA1093		topA	DNA topoisomerase I topA homolog	DNA replication	Information pathway
0.86	0.78	SA1094		gid	glucose-inhibited division protein gid	cell division	cell envelop and process
0.91	1.12	SA1095		xerC	site-specific recombinase XerC homolog	phage-related	other function
1.05	0.92	SA1096		clpQ	heat shock protein HslV	adaptation to atypical	other function
0.65	1.18	SA1097		clpY	heat shock protein HslU	adaptation to atypical	other function
0.78	1.07	SA1098		codY	transcription pleiotropic repressor codY	RNA synthesis	Information pathway
0.63	1.15	SA1099		rpsB	30S ribosomal protein S2	protein synthesis	Information pathway
0.56	1.08	SA1100			elongation factor TS	protein synthesis	Information pathway
0.53	0.88	SA1101		smbA	uridylate kinase	nucleic acid metabolism	Intermediary metabolism
0.49	0.79	SA1102		frr	ribosome recycling factor	protein synthesis	Information pathway
0.99	0.99	SA1103		uppS	undecaprenyl pyrophosphate synthetase	cell wall	cell envelop and process
0.91	0.91	SA1104		cdsA	phosphatidate cytidylyltransferase	lipid metabolism	Intermediary metabolism
0.53	0.83	SA1105			conserved hypotehtical protein		
0.59	0.85	SA1106		proS	proline-tRNA ligase	protein synthesis	Information pathway
0.76	1.12	SA1107		polC	DNA polymerase III, alpha chain PolC-type	DNA replication	Information pathway
0.74	1.09	SA1108			conserved hypotehtical protein		
0.87	0.97	SA1109		nusA	transcription termination-antitermination factor	RNA synthesis	Information pathway
0.00	2.31	SA1110			conserved hypotehtical protein		
0.83	1.18	SA1111			hypothetical protein, similar to ribosomal protein L7AE family	protein synthesis	Information pathway
0.81	0.87	SA1112		infB	translation initiation factor IF-2	protein synthesis	Information pathway
0.83	1.11	SA1113		rbfA	ribosome-binding factor A (rbfA)	protein synthesis	Information pathway
0.69	0.96	SA1114		truB	tRNA pseudouridine 5S synthase	RNA modification	Information pathway
0.86	1.12	SA1115		ribC	riboflavin kinase / FAD synthase ribC	coenzyme metabolism	Intermediary metabolism
0.74	1.03	SA1116		rpsO	30Sribosomal protein S15	protein synthesis	Information pathway
0.63	0.68	SA1117		pnpA	polyribonucleotide nucleotidyltransferase	nucleic acid metabolism	Intermediary metabolism
0.84	0.98	SA1118			conserved hypotehtical protein		
0.57	0.93	SA1119		spoIIIE	sporulation-related protein SpoIIIE homolog	sporulation	cell envelop and process
0.54	0.68	SA1120			hypothetical protein, similar to transcription regulator GntR family	RNA synthesis	Information pathway
0.59	0.91	SA1121			hypothetical protein, similar to processing proteinase homolog	aminoacid metabolism	Intermediary metabolism
0.58	0.79	SA1122			hypothetical protein, similar to precessing proteinase	aminoacid metabolism	Intermediary metabolism
0.45	0.77	SA1123			hypothetical protein, similar to 3-oxoacyl- acyl-carrier protein reductase homolog y	lipid metabolism	Intermediary metabolism
0.43	0.58	SA1124			conserved hypothetical protein		
0.91	0.95	SA1125			conserved hypotehtical protein		
0.47	0.56	SA1126		pgsA	phosphatidylglycerophosphate synthase	lipid metabolism	Intermediary metabolism
0.86	1.18	SA1127		cinA	competence-damage inducible protein cinA		
0.99	0.77	SA1128		recA	RecA protein	[illegible]	Information pathway
0.90	0.88	SA1129			conserved hypothetical protein		
0.72	0.85	SA1130			conserved hypothetical protein		
0.33	0.56	SA1131			hypothetical protein, similar to 2-oxoacid ferredoxin oxidoreductase, alpha subun	membrane bioenergetics	cell envelop and process
0.82	1.00	SA1132			hypothetical protein, similar to 2-oxoacid ferredoxin oxidoreductase, beta subun	membrane bioenergetics	cell envelop and process
1.11	1.28	SA1133			conserved hypothetical protein		
0.83	0.77	SA1134			conserved hypotehtical protein		
0.72	0.91	SA1135			conserved hypothetical protein		
0.87	0.88	SA1136			conserved hypothetical protein		
0.68	0.99	SA1137		mutS	DNA mismatch repair protein	DNA repair or modify	Information pathway
0.74	1.24	SA1138		mutL	DNA mismatch repair protein	DNA repair or modify	Information pathway
0.69	1.11	SA1139		glpP	glycerol uptake operon antiterminator regulatory protein	RNA synthesis	Information pathway
8.85	1.98	SA1140		glpF	glycerol uptake facilitator	transport/binding	cell envelop and process
4.39	1.66	SA1141		glpK	glycerol kinase	carbohydrate metabolism	Intermediary metabolism
3.87	1.18	SA1142		glpD	aerobic glycerol-3-phosphate dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.20	0.87	SA1143			hypothetical protein, similar to lysophospholipase	lipid metabolism	Intermediary metabolism
0.95	1.00	SA1144		miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	RNA modification	Information pathway
0.72	1.06	SA1145			hypothetical protein, similar to host factor-1	phage-related	other function
0.90	1.08	SA1146		bsaA	glutathione peroxidase	adaptation to atypical	other function
0.32	0.55	SA1147			hypothetical protein, similar to GTP-binding protein proteinase modulator homolog y	adaptation to atypical	other function
0.89	1.00	SA1148			hypothetical protein, similar to aluminum resistance protein	transport/binding	cell envelop and process
1.04	1.14	SA1149		glnR	glutamine synthetase repressor	RNA synthesis	Information pathway
0.95	0.95	SA1150		glnA	glutamine-ammonia ligase	aminoacid metabolism	Intermediary metabolism
1.46	0.95	SA1151			hypothetical protein		
1.00	1.01	SA1152			hypothetical protein		
1.26	1.12	SA1153			hypothetical protein		
1.07	0.86	SA1154			conserved hypothetical protein		
1.88	1.52	SA1155			cardiolipin synthetase homolog	lipid metabolism	Intermediary metabolism
1.29	1.01	SA1156			ABC transporter (ATP-binding protein) homolog category	transport/binding	cell envelop and process
1.11	1.15	SA1157			hypothetical protein, similar to ABC transporter integral membrane protein	transport/binding	cell envelop and process
0.92	1.04	SA1158			hypothetical protein, similar to two-component sensor histidine kinase	sensor	cell envelop and process
1.22	1.24	SA1159			hypothetical protein, similar to two-component response regulator	RNA synthesis	Information pathway
1.43	1.21	SA1160		nuc	thermonuclease	nucleic acid metabolism	Intermediary metabolism
1.90	1.43	SA1161			hypothetical protein		
4.14	2.97	SA1162	cre		hypothetical protein		
2.73	1.03	SA1163			aspartate kinase homolog	aminoacid metabolism	Intermediary metabolism
2.13	0.84	SA1164		dhoM	homoserine dehydrogenase	aminoacid metabolism	Intermediary metabolism
1.51	0.85	SA1165		thrC	threonine synthase	aminoacid metabolism	Intermediary metabolism
1.52	0.91	SA1166		thrB	homoserine kinase homolog	aminoacid metabolism	Intermediary metabolism
1.11	0.76	SA1167			conserved hypothetical protein		
1.02	0.99	SA1168			hypothetical protein		
0.71	0.43	SA1169		gabP	gamma-aminobutyrate permease	transport/binding	cell envelop and process
1.46	1.99	SA1170		katA	catalase	detoxification	other function
1.07	1.16	SA1171		rpsN	rpsN	protein synthesis	Information pathway
1.48	1.48	SA1172			hypothetical protein, similar to GMP reductase	nucleic acid metabolism	Intermediary metabolism
1.03	1.27	SA1173			conserved hypothetical protein		
1.19	0.71	SA1174	cre	lexA	SOS regulatory LexA protein	RNA synthesis	Information pathway

0.56	1.05	SA1176			conserved hypothetical protein		
0.39	0.66	SA1177		tkt	transketolase	carbohydrate metabolism	Intermediary metabolism
0.68	1.04	SA1178			conserved hypothetical protein		
0.75	1.17	SA1179			conserved hypothetical protein		
0.89	1.09	SA1180			hypothetical protein, similar to exonuclease SbcD	[illegible]	Information pathway
1.56	1.29	SA1181			hypothetical protein, similar to exonuclease SbcC	[illegible]	Information pathway
0.54	0.44	SA1182		mscL	large-conductance mechanosensitive channel	transport/binding	cell envelop and process
0.63	0.91	SA1183		opuD	glycine betaine transporter	transport/binding	cell envelop and process
1.04	1.61	SA1184		citB	aconitate hydratase	carbohydrate metabolism	Intermediary metabolism
0.99	1.00	SA1185			conserved hypothetical protein		
1.25	1.15	SA1186			conserved hypothetical protein		
0.80	0.60	SA1187			conserved hypothetical protein		
0.72	0.81	SA1188		parE	topoisomerase IV subunit B	DNA packaging	Information pathway
0.72	1.25	SA1189		parC	topoisomerase IV subunit A		
0.67	1.10	SA1189a		parC	topoisomerase IV subunit A	DNA packaging	Information pathway
1.07	0.95	SA1190		alsT	amino acid carrier protein	transport/binding	cell envelop and process
0.92	1.04	SA1191		glcT	transcription antiterminator	RNA synthesis	Information pathway
0.88	1.00	SA1192			conserved hypothetical protein		
0.95	0.79	SA1193		fmtC	oxacillin resistance-related FmtC protein	miscellaneous	other function
1.14	1.09	SA1194		msrA	peptide methionine sulfoxide reductase homolog	protein modification	Information pathway
0.67	0.89	SA1195		msrR	peptide methionine sulfoxide reductase regulator MsrR	RNA synthesis	Information pathway
1.94	1.53	SA1196			hypothetical protein, similar to DNA-damage repair protein	DNA repair or modify	Information pathway
1.15	1.22	SA1197		tyrA	prephenate dehydrogenase	aminoacid metabolism	Intermediary metabolism
1.30	1.36	SA1198			hypothetical protein, similar to glucanase	carbohydrate metabolism	Intermediary metabolism
1.18	1.12	SA1199	cre		hypothetical protein, similar to anthranilate synthase component I	aminoacid metabolism	Intermediary metabolism
1.16	1.06	SA1200		trpG	anthranilate synthase component II	aminoacid metabolism	Intermediary metabolism
0.96	0.95	SA1201		trpD	anthranilate phosphoribosyltransferase	aminoacid metabolism	Intermediary metabolism
1.00	0.91	SA1202		trpC	indole-3-glycerol phosphate synthase	aminoacid metabolism	Intermediary metabolism
1.26	1.11	SA1203		trpF	phosphoriborylanthranilate isomerase	aminoacid metabolism	Intermediary metabolism
1.15	0.95	SA1204		trpB	tryptophan synthase beta chain	aminoacid metabolism	Intermediary metabolism
0.90	1.03	SA1205		trpA	tryptophan synthase alpha chain	aminoacid metabolism	Intermediary metabolism
0.65	0.85	SA1206		femA	factor essential for expression of methicillin resistance	cell wall	cell envelop and process
0.64	0.88	SA1207		femB	FemB protein	cell wall	cell envelop and process
1.06	0.75	SA1209			conserved hypothetical protein		
1.10	0.97	SA1210			hypothetical protein		
1.19	0.99	SA1211		opp-2F	oligopeptide transporter putative ATPase domain	transport/binding	cell envelop and process
1.08	1.01	SA1212		opp-2D	oligopeptide transport ATPase	transport/binding	cell envelop and process
0.79	0.82	SA1214		opp-2B	oligopeptide transporter membrane permease domain	transport/binding	cell envelop and process
0.77	1.09	SA1215			hypothetical protein		
0.57	0.70	SA1216			hypothetical protein, similar to oligoendopeptidase	aminoacid metabolism	Intermediary metabolism
0.91	0.92	SA1217			hypothetical protein, similar to negative regulator PhoU	RNA synthesis	Information pathway
1.00	1.04	SA1218		pstB	phosphate ABC transporter, ATP-binding protein	transport/binding	cell envelop and process
1.14	1.18	SA1219			hypothetical protein, similar to phosphate ABC transporter	transport/binding	cell envelop and process
1.00	1.10	SA1220			hypothetical protein, similar to phosphate ABC transporter	transport/binding	cell envelop and process
1.30	1.12	SA1221			thioredoxine reductase	membrane bioenergetics	cell envelop and process
1.26	1.05	SA1222		truncated-SA	truncated transposase	transposon and IS	other function
0.96	0.89	SA1223			conserved hypothetical protein		
0.43	0.79	SA1224			ABC transporter (ATP-binding protein) homolog	transport/binding	cell envelop and process
1.45	0.71	SA1225		lysC	aspartokinase II	aminoacid metabolism	Intermediary metabolism
1.28	0.70	SA1226		asd	aspartate semialdehyde dehydrogenase	aminoacid metabolism	Intermediary metabolism
1.70	0.87	SA1227		dapA	dihydrodipicolinate synthase	aminoacid metabolism	Intermediary metabolism
0.31	0.32	SA1228		dapB	dihydrodipicolinate reductase	aminoacid metabolism	Intermediary metabolism
1.55	0.78	SA1229		dapD	tetrahydrodipicolinate acetyltransferase	aminoacid metabolism	Intermediary metabolism
0.49	0.49	SA1230			hippurate hydrolase	nucleic acid metabolism	Intermediary metabolism
2.07	0.99	SA1231			hypothetical protein, similar to alanine racemase	aminoacid metabolism	Intermediary metabolism
1.00	0.87	SA1232		lysA	diaminopimelate decarboxylase	aminoacid metabolism	Intermediary metabolism
1.31	0.90	SA1233			hypothetical protein		
0.76	0.88	SA1234		cspA	major cold shock protein CspA	adaptation to atypical	other function
0.73	0.94	SA1235			conserved hypothetical protein		
1.11	1.44	SA1236			conserved hypothetical protein		
1.06	1.39	SA1237			hypothetical protein, similar to 5-bromo-4-chloroindolyl phosphate hydrolysis protein	phosphate metabolism	Intermediary metabolism
0.87	1.14	SA1238			hypothetical protein, similar to tellurite resistance protein	detoxification	other function
0.80	1.01	SA1239		braB	branched-chain amino acid carrier protein	transport/binding	cell envelop and process
0.81	1.03	SA1241			hypothetical protein, similar to nitric-oxide reductase	membrane bioenergetics	cell envelop and process
0.91	1.22	SA1242			conserved hypothetical protein		
1.03	1.22	SA1243			ABC transporter homolog	transport/binding	cell envelop and process
3.28	2.85	SA1244		odhB	dihydrolipoamide succinyltransferase	carbohydrate metabolism	Intermediary metabolism
4.69	3.86	SA1245	cre	odhA	2-oxoglutarate dehydrogenase E1	carbohydrate metabolism	Intermediary metabolism
6.67	5.09	SA1245a		odhA	2-oxoglutarate dehydrogenase E1	carbohydrate metabolism	Intermediary metabolism
1.53	1.29	SA1246		arlS	putative protein histidine kinase ArlS	sensor	cell envelop and process
0.97	1.51	SA1248a		truncated-arl	truncated (putative response regulator ArlR [S	RNA synthesis	Information pathway
0.98	1.28	SA1250			conserved hypothetcial protein		
1.13	1.45	SA1251		murG	undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase	cell wall	cell envelop and process
1.10	0.86	SA1252			conserved hypothetical protein		
0.82	0.87	SA1253		ctpA	probable carboxy-terminal processing proteinase ctpA	aminoacid metabolism	Intermediary metabolism
1.22	1.42	SA1254			conserved hypothetical protein		
1.45	1.60	SA1255			PTS system, glucose-specific enzyme II, A component	transport/binding	cell envelop and process
0.83	1.35	SA1256			conserved hypothetical protein		
0.80	1.21	SA1257			peptide methionine sulfoxide reductase	protein modification	Information pathway
0.92	0.94	SA1258			conserved hypothetical protein		
0.95	1.27	SA1259		dfrA	dihydrofolate reductase	coenzyme metabolism	Intermediary metabolism
0.63	0.75	SA1260		thyA	thymidylate synthase	nucleic acid metabolism	Intermediary metabolism
0.69	0.82	SA1261			conserved hypothetical protein		
0.76	0.80	SA1262			conserved hypothetical protein		
1.15	1.21	SA1263			conserved hypothetical protein		
1.25	1.31	SA1264			conserved hypothetical protein		
0.73	1.05	SA1265			conserved hypothetical protein		
#NUM!	5.53	SA1267		ebhA	hypothetical protein, similar to streptococcal adhesin emb	pathogenic factor	other function
0.87	1.21	SA1267a		ebhA	hypothetical protein, similar to streptococcal adhesin emb	pathogenic factor	other function
2.08	0.83	SA1269			Blt-like protein	transport/binding	cell envelop and process
2.15	1.05	SA1270			hypothetical protein, similar to amino acid pearmease	transport/binding	cell envelop and process
0.87	0.63	SA1271			threonine deaminase IlvA homolog	aminoacid metabolism	Intermediary metabolism
1.52	1.25	SA1272		ald	alanine dehydrogenase	aminoacid metabolism	Intermediary metabolism
1.09	1.45	SA1273			hypothetical protein, similar to 5'-3' exonuclease	DNA replication	Information pathway
1.14	1.61	SA1275			conserved hypothetical protein		
1.44	1.33	SA1276			hypothetical protein		
0.97	0.99	SA1277			conserved hypothetical protein		

0.85	0.93	SA1279			conserved hypothetical protein		
0.80	1.01	SA1280			conserved hyothetical protein		
0.84	1.34	SA1281			conserved hypothetical protein		
1.01	1.10	SA1282		recU	recombination protein U homolog	[illegible]	Information pathway
0.95	1.16	SA1283		pbp2	PBP2	cell wall	cell envelop and process
0.86	1.19	SA1284			hypothetical protein		
1.12	1.34	SA1285		nth	endonuclease-like protein	DNA repair or modify	Information pathway
1.09	1.26	SA1286			hypothetical protein, similar to chromosome replication initiation protein dnaD	DNA replication	Information pathway
0.66	1.21	SA1287		asnS	asparaginyl-tRNA synthetase	protein synthesis	Information pathway
0.78	1.34	SA1288		dinG	probable ATP-dependent DNA helicase dinG	DNA repair or modify	Information pathway
1.00	1.28	SA1289			hypothetical protein, similar to bifunctional biotin ligase/biotin operon repressor	RNA synthesis	Information pathway
0.69	1.45	SA1290			hypothetical protein, similar to poly(A) polymerase	RNA synthesis	Information pathway
0.97	1.08	SA1291			hypothetical protein, similar to lipopolysaccharide biosynthesis-related pr homolc	cell wall	cell envelop and process
0.86	1.16	SA1292			conserved hypothetical protein		
0.79	0.99	SA1293			conserved hypothetical protein		
0.91	0.91	SA1294			conserved hypothetical protein		
1.11	1.02	SA1295			conserved hypothetical protein		
1.07	1.21	SA1296			conserved hypothetical protein		
1.10	1.09	SA1297		aroA	3-phosphoshikimate 1-carboxyvinyltransferase	aminoacid metabolism	Intermediary metabolism
1.03	0.97	SA1298		aroB	3-dehydroquinate synthase	aminoacid metabolism	Intermediary metabolism
1.09	1.02	SA1299		aroC	chorismate synthase	aminoacid metabolism	Intermediary metabolism
1.30	1.22	SA1300			hypothetical protein		
1.81	1.92	SA1301		ndk	nucleoside diphosphate kinase	nucleic acid metabolism	Intermediary metabolism
0.53	0.85	SA1302		gerCC	heptaprenyl diphosphate syntase component II	germination	cell envelop and process
0.62	0.90	SA1303		gerCB	menaquinone biosynthesis methyltransferase	germination	cell envelop and process
0.60	0.93	SA1304			hypothetical protein, similar to component A of hexaprenyl diphosphate synthase		
0.47	0.48	SA1305		hu	DNA-binding protein II	DNA packaging	Information pathway
0.44	0.72	SA1306		gpsA	glycerol-3-phosphate dehydrogenase	carbohydrate metabolism	Intermediary metabolism
0.33	0.56	SA1307			hypothetical protein, similar to GTP binding protein		
0.39	0.59	SA1308		rpsA	30S ribosomal protein S1	nucleic acid metabolism	Intermediary metabolism
0.13	0.33	SA1309		cmk	cytidylate kinase	nucleic acid metabolism	Intermediary metabolism
0.82	1.17	SA1310		ansA	probable L-asparaginase	aminoacid metabolism	Intermediary metabolism
1.21	1.74	SA1311			hypothetical protein, similar to thioredoxin reductase homolog	membrane bioenergetics	cell envelop and process
0.81	1.48	SA1312		ebpS	elastin binding protein	pathogenic factor	other function
1.06	1.28	SA1313		recQ	probable ATP-dependent DNA helicase RecQ	DNA recombination	Information pathway
1.19	1.32	SA1314			conserved hypothetical protein		
1.17	1.59	SA1315		fer	ferredoxin	membrane bioenergetics	cell envelop and process
1.13	1.65	SA1316			conserved hypothetical protein		
0.95	0.94	SA1317			hypothetical protein		
0.82	1.09	SA1318			hypothetical protein		
0.82	1.37	SA1320			hypothetical protein		
1.00	1.34	SA1321			hypothetical protein		
1.47	1.32	SA1322		srrB	staphylococcal respiratory response protein SrrB	sensor	cell envelop and process
1.37	1.79	SA1323		srrA	staphylococcal respiratory response protein SrrA	RNA synthesis	Information pathway
1.00	1.16	SA1324		rluB	ribosomal large subunit pseudouridine synthase B	nucleic acid metabolism	Intermediary metabolism
1.21	1.21	SA1325			conserved hypothetical protein		
1.35	1.17	SA1326			conserved hypothetical protein		
1.05	1.21	SA1327			conserved hypothetical protein		
0.19	0.33	SA1328		xerD	site-specific recombinase	phage-related	other function
1.13	1.03	SA1329		fur	ferric uptake regulator homolog	RNA synthesis	Information pathway
0.99	1.03	SA1330			conserved hypothetical protein		
0.61	0.96	SA1331	cre		conserved hypothetical protein		
1.03	1.14	SA1333			hypothetical protein, similar to oxidoreductase	lipid metabolism	Intermediary metabolism
0.95	0.86	SA1334			hypothetical protein, similar to pyrroline-5-carboxylate reductase	aminoacid metabolism	Intermediary metabolism
1.35	1.06	SA1335			conserved hypothetical protein		
0.76	0.86	SA1336		zwf	glucose-6-phosphate 1-dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.26	1.45	SA1337			transcription regulator AraC/XylS family homolog	RNA synthesis	Information pathway
3.66	1.79	SA1338		malA	alpha-D-1,4-glucosidase	carbohydrate metabolism	Intermediary metabolism
0.37	0.58	SA1339	cre	malR	maltose operon transcriptional repressor	RNA synthesis	Information pathway
0.79	0.97	SA1340			conserved hypothetical protein		
1.01	0.83	SA1341			hypothetical protein, similar to export protein SpcT protein	transport/binding	cell envelop and process
0.55	0.86	SA1342		gnd	phosphogluconate dehydrogenase	carbohydrate metabolism	Intermediary metabolism
0.89	1.41	SA1343			hypothetical protein, similar to tripeptidase	aminoacid metabolism	Intermediary metabolism
0.77	1.02	SA1344			conserved hypothetical protein		
0.95	1.20	SA1345			conserved hypothetical protein		
0.91	0.98	SA1346		bmfBB	branched-chain alpha-keto acid dehydrogenase E2	aminoacid metabolism	Intermediary metabolism
0.66	1.20	SA1347		bfmBAB	branched-chain alpha-keto acid dehydrogenase E1	aminoacid metabolism	Intermediary metabolism
0.82	1.24	SA1348		bfmBAA	branched-chain alpha-keto acid dehydrogenase E1	aminoacid metabolism	Intermediary metabolism
0.71	1.21	SA1349			dihydrolipoamide dehydrogenase	carbohydrate metabolism	Intermediary metabolism
0.78	1.36	SA1350		recN	DNA repair protein	[illegible]	Information pathway
0.73	1.23	SA1351		ahrC	arginine repressor	RNA synthesis	Information pathway
0.67	0.96	SA1352		ispA	geranyltranstransferase homolog	lipid metabolism	Intermediary metabolism
0.85	1.24	SA1353			hypothetical protein, similar to exodeoxyribonuclease, small subunit	nucleic acid metabolism	Intermediary metabolism
0.86	1.17	SA1354			hypothetical protein, similar to exodeoxyribonuclease large subunit	nucleic acid metabolism	Intermediary metabolism
0.80	0.97	SA1355			hypothetical protein, similar to transcription termination factor	RNA synthesis	Information pathway
0.67	0.81	SA1356			conserved hypothetical protein		
0.57	0.77	SA1357		accC	acetyl-CoA carboxylase accC	lipid metabolism	Intermediary metabolism
0.57	0.95	SA1358		accB	acetyl-CoA carboxylase biotin carboxyl carrier subunit	lipid metabolism	Intermediary metabolism
0.58	0.87	SA1359			translation elongation factor EF-P	protein synthesis	Information pathway
0.86	1.16	SA1360			Xaa-Pro dipeptidase	protein modification	Information pathway
0.69	1.49	SA1362			hypothetical protein		
1.04	1.06	SA1363			conserved hypothetical protein		
0.50	0.93	SA1364			conserved hypothetical protein		
2.38	3.48	SA1365			glycine dehydrogenase (decarboxylating) subunit 2 homolog	aminoacid metabolism	Intermediary metabolism
2.81	4.36	SA1366			glycine dehydrogenase subunit 1		
2.00	3.58	SA1367		gcvT	aminomethyltransferase	aminoacid metabolism	Intermediary metabolism
1.40	1.56	SA1368			hypothetical protein, similar to shikimate kinase (SK)	aminoacid metabolism	Intermediary metabolism
0.96	1.43	SA1369		comYC	hypothetical protein, similar to ComYC protein	transformation/competence	cell envelop and process
1.20	1.28	SA1370			hypothetical protein		
1.21	1.38	SA1371			hypothetical protein, similar to competence protein	transformation/competence	cell envelop and process
0.96	1.21	SA1372		comGC	exogenous DNA-binding protein comGC	transformation/competence	cell envelop and process
1.28	1.22	SA1373			hypothetical protein, similar to DNA transport machinery protein comGB	transformation/competence	cell envelop and process
1.11	1.27	SA1374			hypothetical protein, similar to late competence protein comGA	transformation/competence	cell envelop and process
0.83	1.46	SA1375			conserved hypothetical protein		
0.82	1.73	SA1376			conserved hypothetical protein		
0.90	1.28	SA1377		glcK	glucokinase	carbohydrate metabolism	Intermediary metabolism
0.96	1.27	SA1379			conserved hypothetical protein		

1.15	1.18	SA1380			conserved hypothetical protein		
0.97	1.15	SA1381		pbp3	penicillin-binding protein 3	cell wall	cell envelop and process
1.03	0.96	SA1382		sodA	superoxide dismutase SodA	detoxification	other function
0.89	1.46	SA1383			ferric uptake regulator homolog	RNA synthesis	Information pathway
1.16	1.29	SA1384			hypothetical protein, similar to ABC transporter	transport/binding	cell envelop and process
0.96	1.30	SA1385			hypothetical protein, similar to ABC transporter ATP-binding protein	transport/binding	cell envelop and process
1.06	1.18	SA1386			hypothetical protein, similar to endonuclease IV	DNA repair or modify	Information pathway
0.83	1.06	SA1387			hypothetical protein, similar to ATP-dependent RNA helicase	RNA modification	Information pathway
0.86	1.32	SA1388			conserved hypothetical protein		
0.80	1.22	SA1389			conserved hypothetical protein		
0.75	1.22	SA1390		sigA	RNA polymerase sigma factor	RNA synthesis	Information pathway
0.76	0.95	SA1391		dnaG	DNA primase	DNA replication	Information pathway
1.07	1.24	SA1392			conserved hypothetical protein		
0.17	0.37	SA1393	cre		conserved hypothetical protein		
0.60	0.91	SA1394		glyS	glycyl-tRNA synthetase	protein synthesis	Information pathway
0.87	1.19	SA1395			hypothetical protein, similar to DNA repair protein RecO	[illegible]	Information pathway
0.85	1.21	SA1396		bex	bex(GTP-binding protein)	miscellaneous	other function
0.84	1.33	SA1397		cdd	cytidine deaminase	nucleic acid metabolism	Intermediary metabolism
0.79	1.26	SA1398			hypothetical protein, similar to diacylglycerol kinase	lipid metabolism	Intermediary metabolism
0.65	1.03	SA1399			conserved hypothetical protein		
0.83	1.11	SA1400		phoH	phosphate starvation-induced protein phoH homolog	phosphate metabolism	Intermediary metabolism
0.67	0.98	SA1401			conserved hypothetical protein		
0.63	0.94	SA1402			conserved hypothetical protein		
0.68	0.77	SA1403			conserved hypothetical protein		
0.97	1.00	SA1404		rpsU	30S ribosomal protein S21	protein synthesis	Information pathway
0.73	0.88	SA1405			conserved hypothetical protein		
0.87	1.04	SA1406			conserved hypothetical protein		
0.92	1.36	SA1407			conserved hypothetical protein		
0.79	1.22	SA1408		dnaJ	DnaJ protein (Hsp40)	adaptation to atypical	other function
1.32	2.42	SA1409		dnaK	DnaK protein	protein folding	Information pathway
1.48	1.91	SA1410		grpE	GrpE protein (Hsp70 Cofactor Hsp20)	adaptation to atypical	other function
1.41	2.13	SA1411		hrcA	Heat-inducible transcriptional repressor	RNA synthesis	Information pathway
1.05	1.20	SA1412		hemN	oxygen-independent coproporphyrinogen oxidase III	coenzyme metabolism	Intermediary metabolism
0.85	0.95	SA1413		lepA	GTP-binding protein	protein synthesis	Information pathway
0.63	1.15	SA1414		rpsT	30S ribosomal protein S20	protein synthesis	Information pathway
1.39	1.19	SA1415			conserved hypothetical protein		
1.02	1.07	SA1416			hypothetical protein, similar to ComEC late competence protein 3 (comE operon	transformation/competence	cell envelop and process
0.77	1.01	SA1417		comEB	late competence operon required for DNA binding and uptake comEB	transformation/competence	cell envelop and process
0.83	0.97	SA1418			hypothetical protein, similar to late competence operon required for DNA binding and upta	transformation/competence	cell envelop and process
0.78	1.12	SA1419			conserved hypothetical protein		
0.77	1.05	SA1420			conserved hypothetical protein		
0.75	1.10	SA1421			conserved hypothetical protein		
0.86	1.16	SA1422			conserved hypothetical protein		
0.86	1.45	SA1423			conserved hypothetical protein	aminoacid metabolism	Intermediary metabolism
0.82	1.07	SA1424		aroE	shikimate dehydrogenease	aminoacid metabolism	Intermediary metabolism
0.83	1.27	SA1425			conserved hypothetical protein		
0.92	1.28	SA1426			conserved hypothetical protein		
0.90	1.36	SA1427		pfs	5'-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase	nucleic acid metabolism	Intermediary metabolism
1.83	1.50	SA1428			hypothetical protein		
0.20	0.30	SA1430		sea	hypothetical protein, similar to enterotoxin A precursor	pathogenic factor	other function
1.20	1.19	SA1431			conserved hypothetical protein		
1.38	1.34	SA1432			conserved hypothetical protein		
1.37	1.52	SA1433			conserved hypothetical protein		
1.07	0.93	SA1434			acetyl-CoA carboxylase (biotin carboxylase subunit), accC homolog	lipid metabolism	Intermediary metabolism
1.19	1.44	SA1435			hypothetical protein, similar to acetyl-CoA carboxylase (biotin carboxyl carrier subunit), ac	lipid metabolism	Intermediary metabolism
1.29	1.38	SA1436			conserved hypothetical protein		
1.11	1.26	SA1437			conserved hypothetical protein		
0.84	1.26	SA1438		greA	transcription elongation factor	RNA synthesis	Information pathway
0.79	1.24	SA1439		udk	uridine kinase	nucleic acid metabolism	Intermediary metabolism
0.82	1.27	SA1440			hypothetical protein, similar to protease	aminoacid metabolism	Intermediary metabolism
0.85	1.21	SA1441			hypothetical protein, similar to protease	aminoacid metabolism	Intermediary metabolism
0.83	1.18	SA1442			hypothetical protein, similar to caffeoyl-CoA O-methyltransferase	coenzyme metabolism	Intermediary metabolism
0.69	0.94	SA1443			conserved hypothetical protein		
0.62	0.74	SA1444			conserved hypothetical protein		
1.15	0.94	SA1445			conserved hypothetical protein		
0.11	0.35	SA1446		alaS	alanyl-tRNA synthetase	protein synthesis	Information pathway
0.77	1.06	SA1447			hypothetical protein, similar to deoxyribonuclease	[illegible]	Information pathway
0.52	0.90	SA1448			conserved hypothetical protein		
0.48	0.81	SA1449		trmU	(5-methylaminomethyl-2-thiouridylate)-methyltran sferase		
0.58	0.78	SA1450			iron-sulfur cofactor synthesis protein homolog	miscellaneous	other function
1.05	1.31	SA1451	cre		conserved hypothetical protein		
1.84	1.22	SA1453			conserved hypothetical protein		
0.92	1.03	SA1454			conserved hypothetical protein		
1.08	1.46	SA1455			conserved hypothetical protein		
0.50	1.04	SA1456		aspS	aspartyl-tRNA synthetase	protein synthesis	Information pathway
0.56	1.17	SA1457		hisS	histidyl-tRNA synthetase	protein synthesis	Information pathway
1.07	0.77	SA1458		lytH	N-acetylmuramoyl-L-alanine amidase	cell wall	cell envelop and process
1.21	0.81	SA1459			conserved hypothetical protein		
1.12	0.84	SA1460		relA	GTP pyrophosphokinase	nucleic acid metabolism	Intermediary metabolism
1.23	1.20	SA1461		apt	adenine phosphoribosyl transferase	nucleic acid metabolism	Intermediary metabolism
1.28	1.08	SA1462			hypothetical protein, similar to single-strand DNA-specific exonuclease	[illegible]	Information pathway
0.98	0.89	SA1463		secF	protein-export membrane protein SecDF	protein secretion	cell envelop and process
0.68	1.05	SA1464			conserved hypothetical protein		
0.62	1.06	SA1465		tgt	tRNA-guanine transglycosylase	RNA modification	Information pathway
1.04	1.15	SA1466		queA	S-adenosylmethionine tRNA ribosyltransferase	RNA modification	Information pathway
1.08	1.03	SA1467		ruvB	holliday junction DNA helicase	[illegible]	Information pathway
1.17	1.14	SA1468		ruvA	holliday junction DNA helicase	[illegible]	Information pathway
1.26	1.44	SA1469			hypothetical protein, similar to chorismate mutase	aminoacid metabolism	Intermediary metabolism
1.19	1.09	SA1470		obg	SpoOB-associated GTP-binding protein	sporulation	cell envelop and process
0.85	0.92	SA1471		rpmA	50S ribosomal protei L27	protein synthesis	Information pathway
0.83	1.02	SA1472			conserved hypothetical protein		
0.76	0.95	SA1473		rplU	50S ribosomal protein L21	protein synthesis	Information pathway
0.79	1.46	SA1474			hypothetical protein, similar to cell shape determinant mreD	cell wall	cell envelop and process
0.80	1.47	SA1475			hypothetical protein, similar to cell shape determinant mreC	cell wall	cell envelop and process
1.45	1.80	SA1476			hypothetical protein		
0.96	1.17	SA1478			hypothetical protein, similar to transporter PAB2175 from Pyrococcus abyssi	transport/binding	cell envelop and process
1.35	0.94	SA1485		truncated#rad	truncated hypothetical protein, similar to DNA repair protein	DNA repair or modify	Information pathway

1.15	0.93	SA1486			hypothetical protein, similar to type IV prepilin peptidase	protein modification	Information pathway
0.61	1.18	SA1487		folC	folylpolyglutamate synthase	coenzyme metabolism	Intermediary metabolism
1.00	1.21	SA1489		tag	DNA-3-methyladenine glycosidase	DNA repair or modify	Information pathway
1.01	1.09	SA1490			conserved hypothetical protein		
0.73	1.00	SA1491		hemL	glutamate-1-semialdehyde 2,1-aminomutase	coenzyme metabolism	Intermediary metabolism
0.69	1.25	SA1492		hemB	delta-aminolevulinic acid dehydratase	coenzyme metabolism	Intermediary metabolism
0.86	1.56	SA1493		hemD	uroporphyrinogen III synthase	coenzyme metabolism	Intermediary metabolism
0.57	1.01	SA1494		hemC	porphobilinogen deaminase	coenzyme metabolism	Intermediary metabolism
0.73	1.09	SA1495		hemX	hemA concentration negative effector hemX	coenzyme metabolism	Intermediary metabolism
0.72	0.74	SA1496		hemA	glutamyl-tRNA reductase	coenzyme metabolism	Intermediary metabolism
0.46	0.83	SA1497			conserved hypothetical protein		
0.26	0.87	SA1498		clpX	protease ClpX	adaptation to atypical	other function
0.64	1.48	SA1499		tig	trigger factor	protein folding	Information pathway
0.38	0.92	SA1500			hypothetical protein		
0.64	0.73	SA1501			conserved hypothetical protein		
0.65	0.95	SA1502		rplT	50S ribosomal protein L20	protein synthesis	Information pathway
0.85	1.01	SA1503		rpmI	50S ribosomal protein L35	protein synthesis	Information pathway
0.91	1.10	SA1504		infC	translation initiation factor IF-3 infC	protein synthesis	Information pathway
4.84	1.05	SA1505		lysP	lysine-specific permease	transport/binding	cell envelop and process
11.86	1.68	SA1506		thrS	threonyl-tRNA synthetase 1	protein synthesis	Information pathway
1.08	1.11	SA1507		dnaI	primosomal protein	DNA replication	Information pathway
1.34	1.10	SA1508		dnaB	chromosome replication initiation/membrane attachment protein	DNA replication	Information pathway
1.34	1.22	SA1509			conserved hypothetical protein		
2.22	2.09	SA1510		gapB	glyceraldehyde 3-phosphate dehydrogenase 2	carbohydrate metabolism	Intermediary metabolism
0.96	1.42	SA1511			conserved hypothetical protein		
1.35	0.97	SA1512			hypothetical protein, similar to formamidopyrimidine-DNA glycosylase	DNA repair or modify	Information pathway
0.81	1.16	SA1513		polA	DNA polymerase I	DNA replication	Information pathway
1.33	1.55	SA1514			hypothetical protein		
1.18	1.72	SA1515		phoR	alkaline phosphatase synthesis sensor protein	sensor	cell envelop and process
1.38	1.86	SA1516		phoP	alkaline phosphatase synthesis transcriptional regulatory protein	RNA synthesis	Information pathway
2.21	2.84	SA1517		citC	isocitrate dehyrogenase	carbohydrate metabolism	Intermediary metabolism
1.40	1.99	SA1518		citZ	citrate synthase II	carbohydrate metabolism	Intermediary metabolism
0.77	0.77	SA1519		aapA	D-serine/D-alanine/glycine TRANSPORTER	transport/binding	cell envelop and process
0.14	0.27	SA1520		pykA	pyruvate kinase	carbohydrate metabolism	Intermediary metabolism
0.16	0.31	SA1521		pfk	6-phosphofructokinase	carbohydrate metabolism	Intermediary metabolism
1.02	1.09	SA1522		accA	acetyl-CoA carboxylase carboxyl transferase subunit alpha	lipid metabolism	Intermediary metabolism
1.16	1.10	SA1523			acetyl-CoA carboxylase transferase beta subunit	carbohydrate metabolism	Intermediary metabolism
0.94	1.03	SA1524		mdh	malate dehydrogenase homolog	carbohydrate metabolism	Intermediary metabolism
1.04	1.24	SA1525		dnaE	DNA polymerase III, alpha chain	DNA replication	Information pathway
0.80	1.28	SA1525a		dnaE	DNA polymerase III, alpha chain	DNA replication	Information pathway
1.38	1.24	SA1526			conserved hypothetical protein		
1.34	1.08	SA1527			conserved hypothetical protein		
1.01	1.08	SA1528			conserved hypothetical protein		
1.60	1.22	SA1529			conserved hypothetical protein		
1.29	1.17	SA1530			Xaa-Pro dipeptidase homolog	protein modification	Information pathway
2.52	2.80	SA1531		ald	alanine dehydrogenase	aminoacid metabolism	Intermediary metabolism
7.08	3.17	SA1532	cre		conserved hypothetical protein		
0.92	1.27	SA1533		ackA	acetate kinase homolog	carbohydrate metabolism	Intermediary metabolism
0.83	1.09	SA1534			conserved hypothetical protein		
0.10	0.33	SA1535			hypothetical protein, similar to thioredoxin peroxidase	detoxification	other function
1.03	1.21	SA1536			conserved hypothetical protein		
0.88	1.08	SA1537			hypothetical protein, similar to thiamine biosynthesis protein ThiI	coenzyme metabolism	Intermediary metabolism
0.80	1.00	SA1538			hypothetical protein, similar to iron-sulfur cofactor synthesis protein nifZ	coenzyme metabolism	Intermediary metabolism
0.90	1.10	SA1539			hypothetical protein, similar to septation ring formation regulator	RNA synthesis	Information pathway
0.83	1.06	SA1540			conserved hypothetical protein		
1.00	0.94	SA1542			hypothetical protein, similar to glycerophosphoryl diester phosphodiesterase	lipid metabolism	Intermediary metabolism
0.89	1.04	SA1543			conserved hypothetical protein		
1.04	0.70	SA1544			hypothetical protein, similar to soluble hydrogenase 42 kD subunit		
0.84	0.62	SA1545		serA	D-3-phosphoglycerate dehydrogenase	aminoacid metabolism	Intermediary metabolism
1.13	0.61	SA1546			hypothetical protein		
0.71	0.78	SA1547		ptaA	PTS system, N-acetylglucosamine-specific IIABC component	transport/binding	cell envelop and process
0.68	0.89	SA1548			hypothetical protein, similar to acylglycerol-3-phosphate O-acyltransfera homolo	lipid metabolism	Intermediary metabolism
0.35	0.90	SA1549			hypothetical protein, similar to serine proteinase Do, heat-shock protein htrA	adaptation to atypical	other function
0.65	1.36	SA1550	cre	tyrS	tyrosyl-tRNA synthetase	protein synthesis	Information pathway
0.94	1.21	SA1551		sgtA	probable transglycosylase	cell wall	cell envelop and process
1.14	1.48	SA1552			hypothetical protein		
1.02	2.32	SA1553		fhs	formyltetrahydrofolate synthetase	carbohydrate metabolism	Intermediary metabolism
3.52	4.44	SA1554		acsA	acetyl-CoA synthetase	carbohydrate metabolism	Intermediary metabolism
4.62	3.37	SA1555	cre	acuA	acetoin dehydrogenase homolog	carbohydrate metabolism	Intermediary metabolism
6.32	3.25	SA1556		acuC	acetoin utilization protein	carbohydrate metabolism	Intermediary metabolism
25.64	33.73	SA1557		ccpA	catabolite control protein A	RNA synthesis	Information pathway
1.23	0.81	SA1558			chorismate mutase homolog	aminoacid metabolism	Intermediary metabolism
0.83	1.40	SA1559			hypothetical protein, similar to smooth muscle caldesmon	miscellaneous	other function
0.96	1.30	SA1560			hypothetical protein, similar to general stress protein homolog	adaptation to atypical	other function
0.91	1.19	SA1561		murC	UDP-N-Aacerylmuramate-alanine ligase	cell wall	cell envelop and process
0.94	1.31	SA1562		ftsK/spoIIIE	DNA translocase stage III sporulation prot homolog	sporulation	cell envelop and process
0.77	1.66	SA1563			phenylalanyl-tRNA synthetase (beta subunit) homolog	protein synthesis	Information pathway
0.90	1.37	SA1564			conserved hypothetical protein		
0.89	1.43	SA1565			thioredoxin homolog	membrane bioenergetics	cell envelop and process
0.97	1.26	SA1566			endo-1,4-beta-glucanase homolog	carbohydrate metabolism	Intermediary metabolism
0.83	1.15	SA1567			hypothetical protein		
1.06	1.18	SA1568			conserved hypothetical protein		
1.10	0.95	SA1569			conserved hypothetical protein		
1.26	1.03	SA1570			conserved hypothetical protein		
0.97	0.87	SA1571		dat	D-alanine aminotransferase	aminoacid metabolism	Intermediary metabolism
0.88	0.75	SA1572			Xaa-His dipeptidase homolog	protein modification	Information pathway
1.13	1.16	SA1573			hypothetical protein		
1.18	1.10	SA1575			spore cortex protein homolog	sporulation	cell envelop and process
1.28	1.01	SA1576			conserved hypothetical protein		
0.92	0.99	SA1577			hypothetical protein, similar to FmtB protein	pathogenic factor	other function
0.88	1.04	SA1578			conserved hypothetical protein		
0.52	0.97	SA1579		leuS	leucyl-tRNA synthetase	protein synthesis	Information pathway
1.00	1.13	SA1580			multidrug resistance protein homolog	transport/binding	cell envelop and process
0.96	0.86	SA1581			conserved hypothetical protein		
1.02	1.14	SA1582			conserved hypothetical protein		
#NUM!	#NUM!	SA1583		rot	repressor of toxins Rot	RNA synthesis	Information pathway
1.03	1.64	SA1583a		rot	repressor of toxins Rot	RNA synthesis	Information pathway

1.04	1.50	SA1584			lysophospholipase homolog	lipid metabolism	Intermediary metabolism
5.04	3.54	SA1585	cre		proline dehydrohenase homolog	aminoacid metabolism	Intermediary metabolism
1.28	1.47	SA1586		ribH	6,7-dimethyl-8-ribityllumazine synthase	coenzyme metabolism	Intermediary metabolism
1.00	1.25	SA1587		ribA	riboflavin biosynthesis protein	coenzyme metabolism	Intermediary metabolism
0.70	1.03	SA1588		ribB	riboflavin synthase alpha chain	coenzyme metabolism	Intermediary metabolism
0.66	1.02	SA1589		ribD	riboflavin specific deaminase	coenzyme metabolism	Intermediary metabolism
1.00	0.86	SA1590			hypothetical protein		
1.05	1.03	SA1592			aesenical pump membrane protein homolog	transport/binding	cell envelop and process
0.76	0.69	SA1593			conserved hypothetical protein		
0.96	0.86	SA1594			hypothetical protein		
0.94	0.96	SA1595			hypothetical protein		
0.91	0.87	SA1596			hypothetical protein		
0.79	0.83	SA1597			hypothetical protein		
1.26	1.28	SA1598			hypothetical protein		
0.52	0.99	SA1599			hypothetical protein, similar to transaldolase	carbohydrate metabolism	Intermediary metabolism
0.76	1.08	SA1600			hypothetical protein		
0.99	0.98	SA1601			conserved hypothetical protein		
0.91	1.10	SA1602			hypothetical protein		
1.02	1.02	SA1605a		truncated-SA	truncated transposase	transposon and IS	other function
1.04	0.93	SA1605b		truncated-SA	truncated transposase	transposon and IS	other function
1.00	1.17	SA1606	cre		plant metabolite dehydrogenase homolog	miscellaneous	other function
0.96	1.03	SA1607			hypothetical protein		
1.12	1.11	SA1608		metK	S-adenosylmethionine synthetase	aminoacid metebolism	Intermediary metabolism
7.21	4.56	SA1609		pckA	phosphoenolpyruvate carboxykinase	carbohydrate metabolism	Intermediary metabolism
1.15	0.92	SA1611			conserved hypothetical protein		
0.89	1.06	SA1612			conserved hypothetical protein		
0.96	1.03	SA1613			conserved hypothetical protein		
0.94	1.16	SA1614		menC	o-succinylbenzoic acid synthetase	coenzyme metabolism	Intermediary metabolism
0.77	0.98	SA1615		menE	O-succinylbenzoic acid-CoA ligase	coenzyme metabolism	Intermediary metabolism
1.16	1.12	SA1616			hypothetical protein		
6.38	5.08	SA1617			hypothetical protein, similar to latent nuclear antigen [Kaposi's sarcoma-associated her	miscellaneous	other function
3.74	2.77	SA1618			conserved hypothetical protein		
1.58	1.44	SA1619			hypothetical protein		
1.44	1.18	SA1620			hypothetical protein		
1.18	1.20	SA1621			hypothetical protein		
1.00	0.93	SA1625			probable specificity determinant HsdS	DNA repair or modify	Information pathway
1.08	0.88	SA1626			type I restriction enzyme EcoR124II M PROTEIN homolog [Pathogenicity island SaPI	DNA repair or modify	Information pathway
1.09	0.81	SA1627		splF	serine protease SplF	pathogenic factor	other function
1.09	0.87	SA1628		splD	serine protease SplD	pathogenic factor	other function
1.27	1.04	SA1629		splC	serine protease SplC	pathogenic factor	other function
1.23	1.06	SA1630		splB	serine protease SplB	pathogenic factor	other function
1.10	0.93	SA1631		splA	serine protease SplA	pathogenic factor	other function
0.92	1.04	SA1633	cre		probable beta-lactamase	detoxification	
1.32	1.24	SA1634		truncated-SA	truncated hypothetical protein	transport/binding	cell envelop and process
0.93	0.98	SA1637		lukD	leukotoxin, LukD	pathogenic factor	other function
0.75	0.90	SA1638		lukE	leukotoxin LukE	pathogenic factor	other function
0.64	0.90	SA1639			hypothetical protein		
0.72	1.01	SA1649			conserved hypothetical protein		
1.15	1.47	SA1650		hemY	protoporphyrinogen oxidase	coenzyme metabolism	Intermediary metabolism
1.04	1.55	SA1651		hemH	ferrochelatase homolog	coenzyme metabolism	Intermediary metabolism
1.15	1.38	SA1652		hemE	uroporphyrinogen decarboxylase	coenzyme metabolism	Intermediary metabolism
1.45	1.66	SA1653		TRAP	signal transduction protein TRAP	sensor	cell envelop and process
1.36	1.08	SA1654			hypothetical protein, similar to ABC transporter ecsB	transport/binding	cell envelop and process
1.87	1.31	SA1655			ABC transporter ecsA homolog	transport/binding	cell envelop and process
2.02	1.18	SA1656		hit	Hit-like protein involved in cell-cycle regulation	miscellaneous	other function
1.24	0.93	SA1657			conserved hypothetical protein		
1.08	1.19	SA1658			conserved hypothetical protein		
0.64	1.19	SA1659		prsA	peptidyl-prolyl cis/trans isomerase homolog	protein folding	Information pathway
0.87	0.92	SA1660		cbf1	cmp-binding-factor 1	pathogenic factor	other function
1.03	1.21	SA1661			conserved hypothetical protein		
1.05	1.02	SA1662			conserved hypothetical protein		
0.85	1.06	SA1663			conserved hypothetical protein		
0.74	0.88	SA1664			conserved hypothetical protein		
1.16	1.01	SA1666			two-component response regulator homolog	RNA synthesis	Information pathway
0.98	0.84	SA1667			two-component sensor histidine kinase homolog	sensor	cell envelop and process
0.71	0.71	SA1668			conserved hypothetical protein		
2.54	2.47	SA1669		citG	fumarate hydratase, class-II	carbohydrate metabolism	Intermediary metabolism
1.01	1.22	SA1670			hypothetical protein		
0.77	0.99	SA1671			hypothetical protein		
0.91	1.09	SA1672_b			conserved hypothetical protein		
1.07	1.17	SA1672a			conserved hypothetical protein		
0.79	1.24	SA1673			conserved hypothetical protein		
0.92	1.09	SA1674			glutamate ABC transporter ATP-binding protein	transport/binding	cell envelop and process
0.85	1.06	SA1675			hypothetical protein, similar to glutamine-binding periplasmic protein	transport/binding	cell envelop and process
0.86	0.86	SA1676			hypothetical protein, similar to regulatory protein (pfoS/R)	RNA synthesis	Information pathway
1.86	1.36	SA1678			transcription regulator Fur family homolog	RNA synthesis	Information pathway
0.91	1.21	SA1679			hypothetical protein, similar to D-3-phosphoglycerate dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.06	1.34	SA1680			conserved hypothetical protein		
0.85	0.87	SA1681		gsaB	glutamate-1-semialdehyde aminotransferase	aminoacid metabolism	Intermediary metabolism
1.19	1.19	SA1682			conserved hypothetical protein		
0.87	1.06	SA1683			ABC transporter (ATP-binding protein) homolog	transport/binding	cell envelop and process
1.05	1.34	SA1684			conserved hypothetical protein		
0.77	0.99	SA1685			hypothetical protein, similar to A/G-specific adenine glycosylase	[illegible]	Intermediary metabolism
0.46	0.82	SA1686			conserved hypothetical protein		
0.83	1.04	SA1687			hypothetical protein, similar to teichoic acid transport protein tagG	transport/binding	cell envelop and process
0.42	0.72	SA1688			hypothetical protein, similar to teichoic acid translocation ATP-binding protein tag	transport/binding	cell envelop and process
1.14	1.41	SA1689			conserved hypothetical protein		
0.47	0.91	SA1690			conserved hypothetical protein		
0.50	0.91	SA1691		sgtB	hypothetical protein, similar to penicillin-binding protein 1A/1B	cell wall	cell envelop and process
0.80	1.16	SA1692			conserved hypothetical protein		
1.02	1.02	SA1693			conserved hypothetical protein		
0.81	1.12	SA1694			conserved hypothetical protein	lipid metabolism	Intermediary metabolism
0.61	1.12	SA1695		ampS	aminopeptidase ampS	protein modification	Information pathway
0.73	1.45	SA1696			conserved hypothetical protein		
1.44	1.13	SA1697			hypothetical protein, similar to protein-tyrosine phosphatase	protein modification	Information pathway
1.09	1.08	SA1698			hypothetical protein		
0.78	1.06	SA1699			hypothetical protein, similar to transporter	transport/binding	cell envelop and process

0.79	1.12	SA1700		vraR	two-component response regulator	RNA synthesis	Information pathway
0.76	1.00	SA1701		vraS	two-component sensor histidine kinase	sensor	cell envelop and process
0.83	1.14	SA1702			conserved hypothetical protein		
1.00	1.03	SA1703			hypothetical protein		
0.95	0.89	SA1704		map	methionyl aminopeptidase map	protein modification	Information pathway
1.29	1.18	SA1705			conserved hypothetical protein		
0.94	0.97	SA1706			hypothetical protein		
0.89	1.05	SA1707			hypothetical protein, similar to cobyric acid synthase CobQ		
0.85	1.24	SA1708			hypothetical protein, similar to UDP-N-acetylmuramyl tripeptide synthetase homol	cell wall	cell envelop and process
0.93	1.05	SA1709			hypothetical protein, similar to ferritin	miscellaneous	other function
0.66	1.69	SA1710			hypothetical protein, similar to DNA polymerase III, alpha chain PolC type	DNA replication	Information pathway
0.97	1.26	SA1711			hypothetical protein, similar to DNA-damage inducible protein P	DNA repair or modify	Information pathway
0.99	1.01	SA1713			RNA methyltransferase homolog	RNA modification	Information pathway
0.89	1.11	SA1714			conserved hypothetical protein		
0.58	0.83	SA1715			glutamyl-tRNAGln amidotransferase subunit B	protein synthesis	Information pathway
1.11	0.98	SA1716_b			glutamyl-tRNAGln amidotransferase subunit A	protein synthesis	Information pathway
0.66	1.00	SA1716a			glutamyl-tRNAGln amidotransferase subunit A	protein synthesis	Information pathway
0.70	0.89	SA1717			glutamyl-tRNAGln amidotransferase subunit C	protein synthesis	Information pathway
2.70	1.45	SA1718		putP	high affinity proline permease	transport/binding	cell envelop and process
0.86	1.16	SA1719			conserved hypothetical protein		
0.78	1.25	SA1720		lig	DNA ligase	DNA replication	Information pathway
0.70	1.11	SA1721		pcrA	ATP-dependend DNA helicase	DNA replication	Information pathway
0.93	1.14	SA1722		pcrB	conserved hypothetical protein		
0.80	1.37	SA1723			conserved hypothetical protein		
0.67	0.91	SA1724		purB	adenylosuccinate lyase	carbohydrate metabolism	Intermediary metabolism
0.15	0.31	SA1725		scpA	Staphopain, Cysteine Proteinase	protein modification	Information pathway
0.74	1.05	SA1727			conserved hypothetical protein		
1.05	1.16	SA1728		nadE	NAD synthetase, prefers NH3 over glutamine	miscellaneous	other function
1.09	1.11	SA1729			nicotinate phosphoribosyltransferase homolog	coenzyme metabolism	Intermediary metabolism
1.69	1.07	SA1730			nitric-oxide synthase homolog	detoxification	other function
1.53	1.04	SA1731			hypothetical protein, similar to chorismate mutase/prephenate dehydratase (phe	aminoacid metabolism	Intermediary metabolism
5.00	4.00	SA1732	cre		hypothetical protein, similar to sodium-dependent transporter	transport/binding	cell envelop and process
0.98	1.32	SA1733			conserved hypothetical protein		
0.95	0.70	SA1734			pyrazinamidase/nicotinamidase homolog	coenzyme metabolism	Intermediary metabolism
0.88	0.99	SA1735			manganese-dependent inorganic pyrophosphatase	phosphate metabolism	Intermediary metabolism
0.96	1.09	SA1736		aldH	aldehyde dehydrogenase	carbohydrate metabolism	Intermediary metabolism
0.97	1.34	SA1737			conserved hypothetical protein		
2.47	1.39	SA1738			hypothetical protein		
1.27	0.94	SA1739			hypothetical protein		
1.00	0.91	SA1740			hypothetical protein		
0.97	0.85	SA1741			conserved hypothetical protein		
1.03	0.98	SA1742			hypothetical protein		
1.19	1.11	SA1744			conserved hypothetical protein		
0.93	0.85	SA1745			hypothetical protein, similar to ABC transporter, ATP-binding protein	transport/binding	cell envelop and process
1.36	1.26	SA1746			hypothetical protein		
1.32	1.26	SA1747			hypothetical protein, similar to ABC transporter, ATP-binding protein	transport/binding	cell envelop and process
1.16	1.24	SA1748			hypothetical protein, similar to transcription regulator, GntR family	RNA synthesis	Information pathway
0.75	0.90	SA1749			hypothetical protein, similar to aspartate transaminase protein	aminoacid metabolism	Intermediary metabolism
0.83	0.97	SA1751a		truncated#map	truncated map-w protein	pathogenic factor	other function
0.71	0.88	SA1751b		truncated#map	truncated map-w protein	pathogenic factor	other function
0.41	0.58	SA1752		truncated#hl	truncated beta-hemolysin	pathogenic factor	other function
1.00	1.21	SA1754			hypothetical protein		
0.86	0.97	SA1755			hypothetical protein		
1.10	1.22	SA1757a		truncated#lyt	truncated amidase	phage-related	other function
0.50	0.61	SA1758		sak	STAPHYLOKINASE PRECURSOR	pathogenic factor	other function
0.81	0.62	SA1759			lytic enzyme	phage-related	other function
0.45	0.91	SA1760			holin homolog	phage-related	other function
1.18	1.24	SA1763			hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related	other function
1.32	1.18	SA1764			hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related	other function
1.19	1.00	SA1765			hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related	other function
1.07	1.13	SA1766			hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related	other function
1.31	1.11	SA1770			hypothetical protein		
0.47	0.85	SA1775			hypothetical protein, similar to scaffolding protein	phage-related	other function
1.26	1.22	SA1777			hypothetical protein(phiN315)	phage-related	other function
1.03	1.13	SA1781			hypothetical protein(phiN315)	phage-related	other function
1.10	1.17	SA1782			hypothetical protein(phiN315)	phage-related	other function
1.20	0.94	SA1784			hypothetical protein(phiN315)	phage-related	other function
1.26	1.24	SA1785			hypothetical protein(phiN315)	phage-related	other function
0.95	0.95	SA1786			hypothetical protein(phiN315)	phage-related	other function
1.05	1.22	SA1787			hypothetical protein		
1.37	1.12	SA1788			hypothetical protein(phiN315)	phage-related	other function
1.13	1.29	SA1797			hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related	other function
1.03	1.03	SA1799			hypothetical protein(phiN315)	phage-related	other function
1.14	1.31	SA1801			anti repressor	phage-related	other function
1.07	0.93	SA1804			hypothetical transcriptional regulator	RNA synthesis	Information pathway
1.64	1.13	SA1805			repressor homolog (Bacteriophage phi Sa 3mw)	RNA synthesis	Information pathway
1.12	0.94	SA1806			probable ATP-dependent helicase	DNA replication	Information pathway
1.15	1.10	SA1807			hypothetical protein		
1.21	1.01	SA1810		int	integrase (Bacteriophage phi Sa 3mw)	phage-related	other function
0.42	0.48	SA1811		truncated#hl	truncated beta-hemolysin	pathogenic factor	other function
0.49	0.46	SA1812		luk	cal protein, similar to synergohymenotropic toxin precursor - Staphylococcus in	pathogenic factor	other function
0.52	0.52	SA1813		lukM	hypothetical protein, similar to leukocidin chain lukM precursor	pathogenic factor	other function
0.98	0.89	SA1814			hypothetical protein, similar to succinyl-diaminopimelate desuccinylase	aminoacid metabolism	Intermediary metabolism
1.03	0.91	SA1815			hypothetical protein, similar to Na+-transporting ATP synthase	transport/binding	cell envelop and process
0.97	0.84	SA1820			hypothetical protein, similar to bacteriophage terminase small subunit	phage-related	other function
0.84	1.34	SA1836		groEL	GroEL protein	protein folding	Information pathway
0.89	1.31	SA1837		groES	GroES protein	protein folding	Information pathway
0.75	0.96	SA1838			conserved hypothetical protein		
1.39	1.12	SA1839			hypothetical protein, similar to SdrH		
1.50	1.20	SA1840			conserved hypothetical protein		
3.48	1.01	SA1841			hypothetical protein		
1.03	0.96	SA1842		agrB	accessory gene regulator B	protein modification	Information pathway
1.95	1.20	SA1843		agrC	accessory gene regulator C	sensor	cell envelop and process
2.06	1.32	SA1844		agrA	accessory gene regulator A	RNA synthesis	Information pathway
1.72	0.96	SA1845			hypothetical protein, similar to fructokinase	carbohydrate metabolism	Intermediary metabolism
1.54	0.82	SA1846	cre	scrB	sucrose-6-phosphate hydrolase	carbohydrate metabolism	Intermediary metabolism
2.58	1.51	SA1847		scrR	sucrose operon repressor	RNA synthesis	Information pathway

1.14	0.94	SA1848		nrgA	probabale ammonium transporter	transport/binding	cell envelop and process
0.92	1.14	SA1849			conserved hypothetical protein		
0.80	1.04	SA1850			conserved hypothetical protein		
1.09	0.86	SA1851			conserved hypothetical protein		
0.93	0.88	SA1852		vga	hypothetical ABC transporter ATP-binding protein	transport/binding	cell envelop and process
1.01	1.01	SA1853			hypothetical protein, similar to DNA mismatch repair protein MutS	DNA repair or modify	Information pathway
0.87	0.95	SA1854			hypothetical protein, similar to O-sialoglycoprotein endopeptidase	protein modification	Information pathway
0.94	0.96	SA1855			hypothetical protein, similar to ribosomal-protein-alanine N-acetyltransfer	protein modification	Information pathway
0.78	0.91	SA1856			hypothetical protein, similar to glycoprotein endopeptidase	protein modification	Information pathway
0.88	1.05	SA1857			conserved hypothetical protein		
1.12	0.71	SA1858	cre	ilvD	dihydroxy-acid dehydratase	aminoacid metabolism	Intermediary metabolism
1.44	0.87	SA1859		ilvB	acetolactate synthase large subunit	aminoacid metabolism	Intermediary metabolism
1.04	0.91	SA1860			hypothetical protein, similar to acetolactate synthase small subunit	aminoacid metabolism	Intermediary metabolism
1.19	0.89	SA1861		ilvC	alpha-keto-beta-hydroxylacil reductoisomerase	aminoacid metabolism	Intermediary metabolism
1.09	0.79	SA1862		leuA	2-isopropylmalate synthase	aminoacid metabolism	Intermediary metabolism
1.06	0.86	SA1863		leuB	3-isopropylmalate dehydrogenase	aminoacid metabolism	Intermediary metabolism
1.08	0.77	SA1864		leuC	3-isopropylmalate dehydratase large subunit	aminoacid metabolism	Intermediary metabolism
1.09	0.90	SA1865		leuD	3-isopropylmalate dehydratase small subunit	aminoacid metabolism	Intermediary metabolism
1.03	0.89	SA1866		ilvA	thereonine dehydratase	aminoacid metabolism	Intermediary metabolism
0.69	0.92	SA1867			conserved hypothetical protein		
0.56	0.81	SA1868			conserved hypothetical protein		
1.47	1.14	SA1869		sigB	sigma factor B	RNA synthesis	Information pathway
1.48	1.25	SA1870		rsbW	anti-sigmaB factor	RNA synthesis	Information pathway
1.40	1.21	SA1871		rsbV	anti-sigmaB factor antagonist	RNA synthesis	Information pathway
1.14	0.83	SA1872		rsbU	sigmaB regulation protein RsbU	RNA synthesis	Information pathway
1.56	1.13	SA1873			conserved hypothetical protein		
0.92	0.92	SA1874		alr	alanine racemase	aminoacid metabolism	Intermediary metabolism
0.84	1.18	SA1875		dpj	holo-ACP synthase	protein modification	Information pathway
0.98	0.88	SA1876			conserved hypothetical protein		
0.91	0.85	SA1877			conserved hypothetical protein		
0.99	0.73	SA1878			hypothetical protein		
1.15	1.02	SA1879		kdpC	probable potassium-transporting ATPase C chain	transport/binding	cell envelop and process
1.34	1.06	SA1880		kdpB	probable potassium-transporting ATPase B chain	transport/binding	cell envelop and process
1.02	0.91	SA1882		kdpD	sensor protein KdpD	sensor	cell envelop and process
0.92	0.82	SA1883		kdpE	KDP operon transcriptional regulatory protein KdpE	RNA synthesis	Information pathway
0.27	0.56	SA1885			hypothetical protein, similar to ATP-dependent RNA helicase	RNA modification	Information pathway
0.79	0.80	SA1886		murF	P-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl lig	cell wall	cell envelop and process
0.67	0.73	SA1887		ddlA	D-alanine-D-alanine ligase	cell wall	cell envelop and process
0.74	0.81	SA1888			hypothetical protein, similar to rod shape determining protein RodA	cell division	cell envelop and process
1.21	1.11	SA1889			hypothetical protein		
1.32	1.04	SA1890			conserved hypothetical protein		
1.12	0.97	SA1891			hypothetical protein, similar to cardiolipin synthetase	lipid metabolism	Intermediary metabolism
1.17	1.00	SA1892			conserved hypothetical protein		
0.94	0.99	SA1893			lipoprotein precursor	transport/binding	cell envelop and process
0.90	1.08	SA1894		thiE	Chain B, thiamin phosphate synthase	coenzyme metabolism	Intermediary metabolism
1.49	1.05	SA1895		thiM	hydroxyethyl thiazole kinase	coenzyme metabolism	Intermediary metabolism
1.29	1.17	SA1896		thiD	phosphomethylpyrimidine kinase	coenzyme metabolism	Intermediary metabolism
1.64	1.04	SA1897	cre		hypothetical protein, similar to trasncriptional activator TenA	RNA synthesis	Information pathway
1.09	1.00	SA1898			hypothetical protein, similar to SceD precursor	pathogenic factor	other function
0.86	0.84	SA1899			hypothetical protein, similar to single strand DNA binding protein	DNA replication	Information pathway
1.17	1.07	SA1900			conserved hypothetical protein		
0.83	1.00	SA1901		fabZ	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	lipid metabolism	Intermediary metabolism
0.81	0.82	SA1902		murA	UDP-N-acetylglucosamine 1-carboxyvinyl transferase 1	cell wall	cell envelop and process
0.99	0.98	SA1903			conserved hypothetical protein		
1.54	1.66	SA1904		atpC	FoF1-ATP synthase epsilon subunit	membrane bioenergetics	cell envelop and process
1.48	1.49	SA1905		atpD	ATP synthase beta chain	membrane bioenergetics	cell envelop and process
1.48	1.40	SA1906		atpG	ATP synthase gamma chain	membrane bioenergetics	cell envelop and process
1.51	1.56	SA1907		atpA	ATP synthase alpha chain	membrane bioenergetics	cell envelop and process
1.58	1.63	SA1908		atpH	ATP synthase delta chain	membrane bioenergetics	cell envelop and process
1.80	1.55	SA1909		atpF	ATP synthase B chain	membrane bioenergetics	cell envelop and process
1.77	1.55	SA1910		atpE	ATP synthase C chain	membrane bioenergetics	cell envelop and process
1.56	1.48	SA1911		atpB	ATP synthase A chain	membrane bioenergetics	cell envelop and process
0.92	1.24	SA1912			hypothetical protein		
0.41	0.80	SA1913		mnaA	UDP-GlcNAc 2-epimerase	carbohydrate metabolism	Intermediary metabolism
0.96	1.03	SA1914		upp	uracil phosphoribosyl transferase	nucleic acid metabolism	Intermediary metabolism
0.46	0.65	SA1915		glyA	serine hydroxymethyl transferase	aminoacid metabolism	Intermediary metabolism
0.48	0.91	SA1916			conserved hypothetical protein		
0.48	0.79	SA1917			hypothetical protein, similar to phosphatase	protein modification	Information pathway
0.46	0.60	SA1918			conserved hypothetical protein		
0.60	0.60	SA1919			hypothetical protein, similar to protoporphyrinogen oxidase (hemK)	coenzyme metabolism	Intermediary metabolism
0.98	1.01	SA1920		prfA	peptide chain release factor 1	protein synthesis	Information pathway
0.86	1.00	SA1921		tdk	thymidine kinase	nucleic acid metabolism	Intermediary metabolism
0.80	1.10	SA1922		rpmE	ribosomal protein L31	protein synthesis	Information pathway
0.52	0.94	SA1923		rho	transcription termination factor Rho	RNA synthesis	Information pathway
0.97	1.11	SA1924			hypothetical protein, similar to aldehyde dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.50	1.02	SA1925			conserved hypothetical protein		
1.29	1.29	SA1926		murZ	UDP-N-acetylglucosamine 1-carboxylvinyl transferase 2	cell wall	cell envelop and process
0.36	0.44	SA1927		fbaA	fructose-bisphosphate aldolase	carbohydrate metabolism	Intermediary metabolism
0.78	0.90	SA1928	cre		hypothetical protein		
0.74	1.31	SA1929		ctrA	CTP synthase	nucleic acid metabolism	Intermediary metabolism
0.55	0.80	SA1930		rpoE	probable DNA-directed RNA polymerase delta subunit	RNA synthesis	Information pathway
0.91	1.12	SA1931			hypothetical protein, similar to spermine/spermidine acetyltransferase blt	aminoacid metabolism	Intermediary metabolism
1.11	1.19	SA1932			hypothetical protein, similar to hypothetical protein T13D8.31 - Arabidopsis thaliana		
1.47	0.95	SA1933			hypothetical protein		
0.99	0.84	SA1934			hypothetical protein		
1.04	0.86	SA1935		hmrA	similar to amidase (HmrA)	cell wall	cell envelop and process
0.89	0.92	SA1936		luxS	autoinducer-2 production protein LuxS	RNA synthesis	Information pathway
5.62	3.69	SA1937			conserved hypothetical protein		
5.96	4.06	SA1938	cre	pdp	pyrimidine nucleoside phosphorylase	nucleic acid metabolism	Intermediary metabolism
2.25	2.30	SA1939			deoxyribose-phosphate aldolase	nucleic acid metabolism	Intermediary metabolism
0.62	1.28	SA1940	cre	deoD	purine nucleoside phosphorylase	nucleic acid metabolism	Intermediary metabolism
0.69	1.42	SA1941		dps	general stress protein 20U	adaptation to atypical	other function
0.59	1.07	SA1942			conserved hypothetical protein		
0.86	0.99	SA1943			hypothetical protein		
1.66	1.34	SA1944			hypothetical protein		
1.56	1.21	SA1945			hypothetical protein, similar to mannnose-6 phospate isomelase pmi	carbohydrate metabolism	Intermediary metabolism
1.21	1.07	SA1946			conserved hypothetical protein		

1.63	1.24	SA1947		czrA	repressor protein	RNA synthesis	Information pathway
1.66	1.11	SA1948		czrB	cation-efflux system membrane protein homolog	transport/binding	cell envelop and process
0.44	0.67	SA1956		truncated-SA	lytic regulatory protein truncated with Tn554	RNA synthesis	Information pathway
0.74	1.06	SA1957			conserved hypothetical protein		
1.12	1.03	SA1958			hypothetical protein, similar to transposase for IS232	transport/binding	cell envelop and process
0.81	0.48	SA1959		glmS	glucosamine-fructose-6-phosphate aminotransferase	amino acid metabolism	Intermediary metabolism
0.54	0.68	SA1960		mtlF	PTS system, mannitol specific IIBC component	transport/binding	cell envelop and process
0.41	0.54	SA1961			hypothetical protein, similar to transcription antiterminator BglG family	RNA synthesis	Information pathway
0.55	0.60	SA1962		mtlA	PTS system, mannitol specific IIA component	transport/binding	cell envelop and process
0.48	0.47	SA1963		mtlD	mannitol-1-phosphate 5-dehydrogenase	carbohydrate metabolism	Intermediary metabolism
0.59	0.48	SA1964		fmtB#mrp	FmtB protein	pathogenic factor	other function
0.91	1.07	SA1965		glmM#femD	phosphoglucosamine-mutase	carbohydrate metabolism	Intermediary metabolism
0.52	0.79	SA1966			conserved hypothetical protein		
0.58	0.64	SA1967			conserved hypothetoical protein		
0.94	1.13	SA1968		arg	arginase	amino acid metabolism	Intermediary metabolism
0.92	0.97	SA1969			hypothetical protein, similar to ATP-binding Mrp-like protein	pathogenic factor	other function
0.82	0.87	SA1970			hypothetical protein, similar to multidrug resistance protein	transport/binding	cell envelop and process
1.05	0.86	SA1970a			hypothetical protein, similar to multidrug resistance protein	transport/binding	cell envelop and process
0.92	0.87	SA1971			hypothetical protein		
0.96	1.05	SA1972			hypothetical protein, similar to multidrug transporter	transport/binding	cell envelop and process
1.13	1.29	SA1973			hypothetical protein, similar to hemolysin III	pathogenic factor	other function
1.29	1.20	SA1974			hypothetical protein, similar to UDP-N-acetylglucosamine pyrophosphorylase	cell wall	cell envelop and process
1.20	0.87	SA1975	cre		conserved hypotehtical protein		
0.73	1.09	SA1976			conserved hypotehtical protein		
1.36	1.07	SA1977			hypothetical protein, similar to ferrichrome ABC transporter (permease)	transport/binding	cell envelop and process
1.35	1.06	SA1978			hypothetical protein, similar to ferrichrome ABC transporter (permease)	transport/binding	cell envelop and process
1.41	0.98	SA1979			hypothetical protein, similar toferrichrome ABC transporter (binding prote)	transport/binding	cell envelop and process
0.83	0.85	SA1980			conserved hypothetical protein		
0.94	0.96	SA1981			conserved hypothetical protein		
1.59	0.97	SA1982			hypothetical protein, similar to transporter	transport/binding	cell envelop and process
1.03	0.88	SA1983			hypothetical protein		
1.23	1.00	SA1984		asp23	alkaline shock protein 23, ASP23	adaptation to atypical	other function
1.13	0.95	SA1985			hypothetical protein		
1.37	0.95	SA1986			hypothetical protein		
1.03	0.82	SA1987			glycine betaine transporter opuD homolog	transport/binding	cell envelop and process
1.10	1.10	SA1988			hypothetical protein, similar to alginate lyase	carbohydrate metabolism	Intermediary metabolism
0.89	0.97	SA1989			hypothetical protein, similar to quinone oxidoreductase	membrane bioenergetics	cell envelop and process
0.67	1.00	SA1990			conserved hypothetical protein		
1.01	0.94	SA1991		lacG	6-phospho-beta-galactosidase	carbohydrate metabolism	Intermediary metabolism
1.13	0.91	SA1992		lacE	PTS system, lactose-specific IIBC component	transport/binding	cell envelop and process
1.25	0.98	SA1993		lacF	PTS system, lactose-specific IIA component	transport/binding	cell envelop and process
1.01	0.88	SA1994		lacD	tagatose 1,6-diphosphate aldolase	carbohydrate metabolism	Intermediary metabolism
1.15	0.92	SA1995		lacC	tagatose-6-phosphate kinase	carbohydrate metabolism	Intermediary metabolism
1.37	1.23	SA1996		lacB	galactose-6-phosphate isomerase LacB subunit	carbohydrate metabolism	Intermediary metabolism
1.36	0.95	SA1997	cre	lacA	galactose-6-phosphate isomerase LacA subunit	carbohydrate metabolism	Intermediary metabolism
0.92	0.99	SA1998		lacR	lactose phosphotransferase system repressor	RNA synthesis	Information pathway
1.05	0.98	SA1999			hypothetical protein, similar to regulatory protein, SIR2 family	RNA synthesis	Information pathway
0.80	0.85	SA2001			hypothetical protein, similar to oxidoreductase, aldo/keto reductase family	carbohydrate metabolism	Intermediary metabolism
1.04	1.01	SA2002			hypothetical protein, similar to transcription regulator MerR family	RNA synthesis	Information pathway
0.84	0.83	SA2003		hysA	hyaluronate lyase precursor	pathogenic factor	other function
1.10	1.24	SA2004			conserved hypothetical protein		
1.13	1.32	SA2005			conserved hypothetical protein		
1.04	0.89	SA2006			hypothetical protein, similar to MHC class II analog	pathogenic factor	other function
0.85	0.88	SA2007			hypothetical protein, similar to alpha-acetolactate decarboxylase	carbohydrate metabolism	Intermediary metabolism
0.61	0.67	SA2008		alsS	alpha-acetolactate synthase	carbohydrate metabolism	Intermediary metabolism
0.77	1.09	SA2016		rpsI	30S ribosomal protein S9	protein synthesis	Information pathway
0.75	1.10	SA2017		rplM	50S ribosomal protein L13	protein synthesis	Information pathway
0.79	1.14	SA2018		truA	tRNA pseudouridine synthase A	RNA modification	Information pathway
0.86	1.05	SA2019			conserved hypothetical protein		
0.86	0.95	SA2020			hypothetical protein, similar to ABC transporter (ATP-binding protein)	transport/binding	cell envelop and process
0.92	0.92	SA2021			hypothetical protein, similar to ABC transporter (ATP-binding protein)	transport/binding	cell envelop and process
0.74	0.81	SA2022		rplQ	50S ribosomal protein L17	protein synthesis	Information pathway
0.61	0.87	SA2023		rpoA	DNA-directed RNA polymerase alpha chain	RNA synthesis	Information pathway
0.59	0.79	SA2024		rpsK	30S ribosomal protein S11	protein synthesis	Information pathway
0.65	0.98	SA2025		rpsM	30S ribosomal protein S13	protein synthesis	Information pathway
0.63	0.87	SA2026		infA	translation initiation factor IF-1	protein synthesis	Information pathway
0.63	0.74	SA2027		adk	adenylate kinase	nucleic acid metabolism	Intermediary metabolism
0.62	0.77	SA2028		secY	preprotein translocase SecY subunit	protein secretion	cell envelop and process
0.54	0.64	SA2029		rplO	50S ribosomal protein L15	protein synthesis	Information pathway
0.74	0.72	SA2030		rpmD	50S ribosomal protein L30	protein synthesis	Information pathway
0.48	0.64	SA2031		rpsE	30S ribosomal protein S5	protein synthesis	Information pathway
0.73	0.92	SA2032		rplR	50S ribosomal protein L18	protein synthesis	Information pathway
0.64	0.73	SA2033		rplF	50S ribosomal protein L6	protein synthesis	Information pathway
0.66	0.84	SA2034		rpsH	30S ribosomal protein S8	protein synthesis	Information pathway
0.63	0.97	SA2035		rplE	50S ribosomal protein L5	protein synthesis	Information pathway
0.70	0.87	SA2036		rplX	50S ribosomal protein L24	protein synthesis	Information pathway
0.68	0.85	SA2037		rplN	50S ribosomal protein L14	protein synthesis	Information pathway
0.65	0.91	SA2038		rpsQ	30S ribosomal protein S17	protein synthesis	Information pathway
0.91	0.99	SA2039		rpmC	50S ribosomal protein L29	protein synthesis	Information pathway
0.76	0.89	SA2040		rplP	50S ribosomal protein L16	protein synthesis	Information pathway
0.69	0.84	SA2041		rpsC	30S ribosomal protein S3	protein synthesis	Information pathway
0.65	0.86	SA2042		rplV	50S ribosomal protein L22	protein synthesis	Information pathway
0.75	1.02	SA2043		rpsS	30S ribosomal protein S19	protein synthesis	Information pathway
0.72	0.99	SA2044		rplB	50S ribosomal protein L2	protein synthesis	Information pathway
0.74	0.98	SA2045		rplW	50S ribosomal protein L23	protein synthesis	Information pathway
0.79	0.91	SA2046		rplD	50S ribosomal protein L4	protein synthesis	Information pathway
0.82	1.18	SA2047		rplC	50S ribosomal protein L3	protein synthesis	Information pathway
0.75	1.10	SA2048		rpsJ	30S ribosomal protein S10	protein synthesis	Information pathway
0.96	0.84	SA2049			hypothetical protein		
0.66	1.05	SA2050			conserved hypothetical protein		
0.92	0.71	SA2051		topB	DNA topoisomerase III topB	DNA packaging	Information pathway
1.66	1.12	SA2052			conserved hypothetical protein		
0.38	0.40	SA2053		glcU	glucose uptake protein homolog	transport/binding	cell envelop and process
1.01	0.72	SA2054			conserved hypothetical protein		
0.86	0.79	SA2055			hypothetical protein		
0.52	0.90	SA2057	cre	fmhB	FmhB protein	cell wall	cell envelop and process
1.09	1.25	SA2059			hypothetical protein		

0.91	1.14	SA2060			hypothetical protein, similar to transcription regulator MarR family	RNA synthesis	Information pathway
1.22	1.24	SA2061			hypothetical protein	transport/binding	cell envelop and process
0.86	1.18	SA2062		sarV	staphylococcal accessory regulator A homolog	RNA synthesis	Information pathway
0.96	1.18	SA2063		moaA	molybdenum cofactor biosynthesis protein A	coenzyme metabolism	Intermediary metabolism
1.02	1.24	SA2064		mobA	molybdopterin-guanine dinucleotide biosynthesis mobA	coenzyme metabolism	Intermediary metabolism
1.01	1.26	SA2065		moaD	probable molybdopterin synthase small subunit	coenzyme metabolism	Intermediary metabolism
1.11	1.16	SA2066		moaE	molybdopterin converting factor moa	coenzyme metabolism	Intermediary metabolism
1.03	1.19	SA2067		mobB	probable molybdopterin-guanine dinucleotide biosynthesis mobB	coenzyme metabolism	Intermediary metabolism
1.07	0.97	SA2068		moeA	molybdopterin biosynthesis protein moeA	coenzyme metabolism	Intermediary metabolism
1.24	1.31	SA2069		moaC	molybdenum cofactor biosynthesis protein C	coenzyme metabolism	Intermediary metabolism
1.26	1.19	SA2070		moaB	molybdopterin precursor biosynthesis moaB	coenzyme metabolism	Intermediary metabolism
1.17	1.04	SA2071		moeB	molybdopterin biosynthesis protein moeB	coenzyme metabolism	Intermediary metabolism
1.36	1.02	SA2072		modC	molybdenum transport ATP-binding protein ModC	transport/binding	cell envelop and process
0.27	0.35	SA2073		modB	probable molybdenum transport permease	transport/binding	cell envelop and process
1.25	1.16	SA2074		modA	probable molybdate-binding protein	transport/binding	cell envelop and process
1.16	0.99	SA2075		narQ	FdhD protein homolog	carbohydrate metabolism	Intermediary metabolism
1.14	0.97	SA2076			hypothetical protein		
1.04	1.14	SA2077			hypothetical protein, similar to biotin biosynthesis protein	coenzyme metabolism	Intermediary metabolism
1.32	0.98	SA2078			hypothetical protein, similar to inosine-adenosine-guanosine-nucleoside hydrolas	nucleic acid metabolism	Intermediary metabolism
0.89	1.02	SA2079			hypothetical protein, similar to ferrichrome ABC transporter fhuD precursor	transport/binding	cell envelop and process
2.20	1.20	SA2080			hypothetical protein, similar to butyryl-CoA dehydrogenase	lipid metabolism	Intermediary metabolism
1.01	0.81	SA2081			hypothetical protein, similar to urea transporter	transport/binding	cell envelop and process
0.91	0.84	SA2082		ureA	urease gamma subunit	aminoacid metabolism	Intermediary metabolism
1.24	0.94	SA2083		ureB	urease beta subunit	aminoacid metabolism	Intermediary metabolism
1.12	1.08	SA2084		ureC	urease alpha subunit	aminoacid metabolism	Intermediary metabolism
1.07	0.89	SA2085		ureE	urease accessory protein UreE	aminoacid metabolism	Intermediary metabolism
1.06	0.78	SA2086		ureF	urease accessory protein UreF	aminoacid metabolism	Intermediary metabolism
0.87	1.15	SA2087		ureG	urease accessory protein UreG	aminoacid metabolism	Intermediary metabolism
0.84	1.00	SA2088		ureD	urease accessory protein UreD	aminoacid metabolism	Intermediary metabolism
0.98	0.59	SA2089		sarR	staphylococcal accessory regulator A homolog	RNA synthesis	Information pathway
1.08	1.12	SA2090			conserved hypothetical protein		
1.31	0.98	SA2091			hypothetical protein		
0.95	0.92	SA2092			hypothetical protein, similar to transcription regulator	RNA synthesis	Information pathway
0.87	1.22	SA2093		ssaA	secretory antigen precursor SsaA homolog	pathogenic factor	other function
0.56	0.72	SA2094			hypothetical protein, similar to Na+/H+ antiporter	transport/binding	cell envelop and process
0.56	0.88	SA2095			hypothetical protein, similar to D-octopine dehydrogenase	aminoacid metabolism	Intermediary metabolism
0.43	0.66	SA2096			conserved hypothetical protein		
0.65	0.51	SA2097		ssaA	hypothetical protein, similar to secretory antigen precursor SsaA	pathogenic factor	other function
1.48	1.15	SA2098	cre		hypothetical protein, similar to glycerate dehydrogenase	aminoacid metabolism	Intermediary metabolism
0.52	0.59	SA2099			hypothetical protein, similar to monooxygenase	aminoacid metabolism	Intermediary metabolism
0.31	0.53	SA2100			hypothetical protein, similar to autolysin E	cell wall	cell envelop and process
0.50	0.54	SA2101			conserved hypothetical protein		
0.41	0.40	SA2102			formate dehydrogenase homolog	carbohydrate metabolism	Intermediary metabolism
1.03	1.03	SA2103			hypothetical protein, similar to lyt divergon expression attenuator LytR	RNA synthesis	Information pathway
1.21	1.46	SA2104			hypothetical protein, similar to suppressor protein suhB	carbohydrate metabolism	Intermediary metabolism
2.59	1.21	SA2105			conserved hypothetical protein	RNA synthesis	Information pathway
0.55	0.85	SA2106			hypothetical protein, similar to protein of pXO2-46		
0.91	1.10	SA2107			hypothetical protein		
0.83	1.03	SA2108			hypothetical protein, similar to transcription regulator, RpiR family	RNA synthesis	Information pathway
1.66	1.17	SA2109	cre		hypothetical protein, similar to transport protein	transport/binding	cell envelop and process
1.01	0.95	SA2110	cre		hypothetical protein		
1.18	1.05	SA2111			hypothetical protein, similar to phosphoglycolate phosphatase	carbohydrate metabolism	Intermediary metabolism
1.16	1.04	SA2112			hypothetical protein, similar to sodium-dependent transporter	transport/binding	cell envelop and process
1.23	1.35	SA2113			hypothetical protein		
3.00	1.59	SA2114	cre	glvC	PTS system, arbutin-like IIBC component	transport/binding	cell envelop and process
0.98	0.88	SA2115			hypothetical protein, similar to transcriptional regulator	RNA synthesis	Information pathway
1.09	1.29	SA2116			hypothetical protein		
1.04	1.03	SA2117			hypothetical protein, similar to Na+/H+ antiporter, putative	transport/binding	cell envelop and process
1.16	1.10	SA2118			hypothetical protein		
1.34	0.85	SA2119			hypothetical protein, similar to dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.23	0.83	SA2120			hypothetical protein, similar to amino acid amidohydrolase	aminoacid metabolism	Intermediary metabolism
1.61	1.07	SA2121		hutI	imidazolonepropionase	aminoacid metabolism	Intermediary metabolism
1.91	1.04	SA2122		hutU	urocanate hydratase	aminoacid metabolism	Intermediary metabolism
1.61	1.29	SA2123			hypothetical protein, similar to transcription regulator LysR family	RNA synthesis	Information pathway
1.12	1.02	SA2124		fosB	fosfomycin resistance protein fofB	detoxification	other function
1.07	1.15	SA2125			hypothetical protein, similar to formiminoglutamase	aminoacid metabolism	Intermediary metabolism
1.56	0.81	SA2126			hypothetical protein		
1.30	1.14	SA2127			hypothetical protein, similar to ribose 5-phosphate isomerase (rpi)	nucleic acid metabolism	Intermediary metabolism
0.99	0.85	SA2128			conserved hypothetical protein		
0.80	0.88	SA2129			hypothetical protein, similar to aldose 1-epimerase	carbohydrate metabolism	Intermediary metabolism
0.59	0.78	SA2130			conserved hypothetical protein		
0.95	0.88	SA2131			conserved hypothetical protein		
0.94	0.90	SA2132			hypothetical protein, similar to ABC transporter (ATP-binding protein)	transport/binding	cell envelop and process
0.85	0.90	SA2133			conserved hypothetical protein		
0.99	1.01	SA2134			hypothetical protein, similar to DNA-3-methyladenine glycosidase	DNA repair or modify	Information pathway
1.06	0.92	SA2136		fni	isopentenyl diphosphate isomerase	lipid metabolism	Intermediary metabolism
1.06	1.08	SA2137			hypothetical protein, similar to divalent cation transport	transport/binding	cell envelop and process
1.05	1.17	SA2138			conserved hypothetical protein		
0.81	1.09	SA2139			hypothetical protein		
0.36	0.65	SA2140	cre		hypothetical protein, similar to esterase	carbohydrate metabolism	Intermediary metabolism
0.50	0.49	SA2141			hypothetical protein		
0.27	0.44	SA2142			hypothetical protein, similar to multidrug resistance protein	transport/binding	cell envelop and process
0.72	0.61	SA2143			conserved hypothetical protein		
0.37	0.57	SA2145		tcaB	TcaB protein	transport/binding	cell envelop and process
1.07	1.01	SA2146		tcaA	TcaA protein		
0.30	0.52	SA2147		tcaR	TcaR transcription regulator	RNA synthesis	Information pathway
0.75	0.81	SA2148			hypothetical protein, similar to membrane protein	transport/binding	cell envelop and process
4.49	1.00	SA2149			hypothetical protein, similar to ABC transporter, ATP-binding protein	transport/binding	cell envelop and process
9.84	1.16	SA2150			conserved hypothetical protein		
0.98	0.99	SA2151			hypothetical protein, similar to two component response regulator	RNA synthesis	Information pathway
1.08	0.99	SA2152			hypothetical protein, similar to two component histidine kinase sensor	sensor	cell envelop and process
1.03	1.37	SA2153			conserved hypothetical protein		
1.19	1.17	SA2154			hypothetical protein		
1.38	1.15	SA2155			hypothetical protein, simialr to malate:quinone oxidoreductase	carbohydrate metabolism	Intermediary metabolism
1.13	0.76	SA2156			L-lactate permease lctP homolog	transport/binding	cell envelop and process
0.96	0.80	SA2157			hypothetical protein		
1.86	1.08	SA2158			hypothetical protein, similar to TpgX protein		

0.93	1.06	SA2159			hypothetical protein, similar to transcription repressor of sporulation, septation and degra	RNA synthesis	Information pathway
0.66	0.97	SA2160			conserved hypothetical protein		
0.94	1.03	SA2161			hypothetical protein, similar to attachment to host cells and virulence		
1.04	0.79	SA2162			hypothetical protein, similar to thioredoxin reductase	membrane bioenergetics	cell envelop and process
1.50	1.37	SA2163			hypothetical protein		
1.25	0.94	SA2164			hypothetical protein, similar to phage infection protein precursor	phage-related	other function
1.18	1.09	SA2165			hypothetical protein, similar to transcriptional regulator tetR-family	RNA synthesis	Information pathway
1.19	1.09	SA2166			hypothetical protein, similar to cationic transporter	transport/binding	cell envelop and process
9.62	0.76	SA2167	cre	scrA	PTS system, sucrose-specific IIBC component	transport/binding	cell envelop and process
2.91	1.76	SA2168	cre		hypothetical protein		
1.17	1.10	SA2169			hypothetical protein, similar to transcription regulatory protein	RNA synthesis	Information pathway
1.12	1.11	SA2170			hypothetical protein, similar to general stress protein 26	adaptation to atypical	other function
0.54	0.54	SA2171			hypothetical protein		
1.22	0.87	SA2172		gltT	proton/sodium-glutamate symport protein	transport/binding	cell envelop and process
1.33	0.97	SA2173			hypothetical protein		
0.72	0.64	SA2174			hypothetical protein, similar to transcriptional regulator	RNA synthesis	Information pathway
1.01	0.93	SA2175			hypothetical protein, similar to small heat shock protein	adaptation to atypical	
2.58	0.86	SA2176		narK	nitrite extrusion protein	transport/binding	cell envelop and process
1.11	0.95	SA2177			conserved hypothetical protein		
1.07	0.97	SA2178			hypothetical protein, similar to transcriptional regulator	RNA synthesis	Information pathway
1.77	1.07	SA2179			hypothetical protein, similar to response regulators of two-component regulator	RNA synthesis	Information pathway
1.65	1.07	SA2180			hypothetical protein, similar to two component sensor histidine kinase	sensor	cell envelop and process
1.65	1.07	SA2181			hypothetical protein		
1.62	1.01	SA2182		narI	nitrate reductase gamma chain	membrane bioenergetics	cell envelop and process
1.44	0.94	SA2183			hypothetical protein, similar to nitrate reductase delta chain	membrane bioenergetics	cell envelop and process
2.07	0.91	SA2184		narH	nitrate reductase beta chain narH	membrane bioenergetics	cell envelop and process
2.10	0.96	SA2185		narG	respiratory nitrate reductase alpha chain	membrane bioenergetics	cell envelop and process
1.54	0.94	SA2186		nasF	uroporphyrin-III C-methyl transferase	coenzyme metabolism	Intermediary metabolism
1.26	1.04	SA2187		nasE	assimilatory nitrite reductase	aminoacid metabolism	Intermediary metabolism
1.56	0.86	SA2188		nasD	nitrite reductase	aminoacid metabolism	Intermediary metabolism
1.37	1.12	SA2189			hypothetical protein, similar to NirR	aminoacid metabolism	Intermediary metabolism
1.25	1.08	SA2190			conserved hypothetcial protein		
1.90	1.08	SA2191			hypothetical protein, similar to NirC	transport/binding	cell envelop and process
1.26	0.96	SA2193			conserved hypothetical protein		
0.89	0.80	SA2194			hypothetical protein, similar to Zn-binding lipoprotein adcA	transport/binding	cell envelop and process
1.25	1.02	SA2195			conserved hypothetical protein		
1.44	1.07	SA2196			conserved hypothetical protein		
1.10	0.78	SA2198			hypothetical protein		
0.83	0.68	SA2199		fmhA	fmhA protein	cell wall	cell envelop and process
0.42	0.73	SA2200			hypothetical protein, similar to ABC transporter, ATP binding subunit	transport/binding	cell envelop and process
0.41	0.65	SA2201			hypothetical protein, similar to ABC transporter, permease protein	transport/binding	cell envelop and process
0.31	0.55	SA2202			hypothetical protein, similar to ABC transporter, periplasmic amino acid-binding pro	transport/binding	cell envelop and process
0.40	0.58	SA2203			hypothetical protein, similar to multidrug resistance protein	transport/binding	cell envelop and process
0.37	0.97	SA2204			phosphoglycerate mutase, pgm homolog	carbohydrate metabolism	Intermediary metabolism
1.11	0.94	SA2205			conserved hypothetical protein		
0.32	0.68	SA2206		sbi	IgG-binding protein SBI	pathogenic factor	other function
1.52	1.31	SA2207		hlgA	gamma-hemolysin chain II precursor	pathogenic factor	other function
2.12	1.36	SA2208		hlgC	gamma-hemolysin component C	pathogenic factor	other function
1.96	1.20	SA2209		hlgB	gamma-hemolysin component B	pathogenic factor	other function
0.98	0.98	SA2210			hypothetical protein, similar to BioX protein		
1.19	1.08	SA2211			hypothetical protein, similar to 6-carboxyhexanoate--CoA ligase	coenzyme metabolism	Intermediary metabolism
1.05	0.80	SA2213		bioB	biotin synthase	coenzyme metabolism	Intermediary metabolism
1.14	0.79	SA2214		bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	coenzyme metabolism	Intermediary metabolism
1.31	0.87	SA2215		bioD	dethiobiotin synthetase	coenzyme metabolism	Intermediary metabolism
1.75	0.96	SA2216			hypothetical protein, similar to ABC transporter, ATP-binding protein	transport/binding	cell envelop and process
1.57	0.85	SA2217			hypothetical protein, similar to lipoprotein inner membrane ABC-transporter	transport/binding	cell envelop and process
1.22	1.01	SA2219			conserved hypothetical protein		
1.26	0.97	SA2220			conserved hypothetical protein		
1.43	1.05	SA2221			hypothetical protein		
0.82	0.82	SA2222			hypothetical protein, similar to bicyclomycin resistance protein TcaB	transport/binding	cell envelop and process
1.22	0.95	SA2223			hypothetical protein, similar to transcriptional activator	RNA synthesis	Information pathway
0.64	1.19	SA2224			hypothetical protein		
1.12	1.05	SA2225	cre		conserved hypothetical protein		
11.67	3.96	SA2227a		truncated-SA	truncated hypothetical protein, similar to D-serine/D-alanine/glycine transporte	transport/binding	cell envelop and process
0.68	0.81	SA2229			conserved hypothetical protein		
0.88	0.93	SA2230			hypothetical protein, similar to beta-lactamase	cell wall	cell envelop and process
0.83	0.78	SA2231			hypothetical protein, similar to glucose epimerase	carbohydrate metabolism	Intermediary metabolism
0.48	0.65	SA2232			hypothetical protein, similar to 2-dehydropantoate 2-reductase	coenzyme metabolism	Intermediary metabolism
3.81	1.25	SA2234		opuCD	probable glycine betaine/carnitine/choline ABC transporter opuCD	transport/binding	cell envelop and process
2.71	1.05	SA2235		opuCC	glycine betaine/carnitine/choline ABC transporter opuCC	transport/binding	cell envelop and process
4.86	1.32	SA2236		opuCB	probable glycine betaine/carnitine/choline ABC transporter opuCB	transport/binding	cell envelop and process
4.36	1.15	SA2237		opuCA	glycine betaine/carnitine/choline ABC transporter opuCA	transport/binding	cell envelop and process
0.41	0.55	SA2238			conserved hypothetical protein		
0.51	0.41	SA2239			hypothetical protein, similar to amino acid transporter	transport/binding	cell envelop and process
0.82	0.63	SA2240			hypothetical protein, similar to para-nitrobenzyl esterase chain A	lipid metabolism	Intermediary metabolism
1.17	0.81	SA2241			hypothetical protein, similar to chloramphenicol resistance protein	transport/binding	cell envelop and process
0.35	0.35	SA2242			conserved hypotehtical protein	transport/binding	cell envelop and process
0.57	0.45	SA2243			hypothetical protein, similar to ABC transporter (ATP-binding protein	transport/binding	cell envelop and process
1.18	1.04	SA2244			hypothetical protein, similar to endo-1,4-beta-glucanase	carbohydrate metabolism	Intermediary metabolism
1.28	1.17	SA2245			conserved hypothetical protein		
1.34	1.00	SA2246			hypothetical protein		
1.50	0.96	SA2247			conserved hypothetical protein		
1.00	1.17	SA2248	cre		hypothetical protein, similar to glutamate synthase (ferredoxin)	aminoacid metabolism	Intermediary metabolism
2.95	1.73	SA2250			hypothetical protein, similar to antibiotic resistance protein	transport/binding	cell envelop and process
3.12	1.35	SA2251		opp-1F	oligopeptide transporter putative ATPase domain	transport/binding	cell envelop and process
2.43	1.33	SA2252		opp-1D	oligopeptide transporter putative ATPase domain	transport/binding	cell envelop and process
3.24	1.37	SA2253		opp-1C	oligopeptide transporter putative membrane permease domain	transport/binding	cell envelop and process
0.93	0.86	SA2254		opp-1B	oligopeptide transporter putative membrane permease domain	transport/binding	cell envelop and process
3.66	1.63	SA2255		opp-1A	oligopeptide transporter putative substrate binding domain	transport/binding	cell envelop and process
1.14	1.03	SA2256			conserved hypothetical protein		
1.21	0.93	SA2257			conserved hypothetical protein		
1.34	0.86	SA2258			hypothetical protein, similar to diaminopimelate epimerase	aminoacid metabolism	Intermediary metabolism
1.41	0.94	SA2260			hypothetical protein, similar to glucose 1-dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.24	0.86	SA2261			hypothetical protein, similar to efflux pump	transport/binding	cell envelop and process
1.02	0.98	SA2262			conserved hypothetical protein		
1.31	1.12	SA2264			hypothetical protein		
1.05	1.02	SA2265			hypothetical protein		

0.92	1.43	SA2266			hypothetical protein, similar to oxidoreductase	carbohydrate metabolism	Intermediary metabolism
1.71	0.97	SA2267			hypothetical protein		
1.78	0.85	SA2268			hypothetical protein		
1.16	1.14	SA2269			hypothetical protein		
1.13	1.04	SA2270			hypothetical protein		
1.26	1.10	SA2271			hypothetical protein		
1.21	1.01	SA2272			hypothetical protein		
1.11	1.15	SA2273			hypothetical protein		
0.97	1.25	SA2275			hypothetical protein		
0.93	1.14	SA2276			conserved hypothetical protein		
0.93	1.00	SA2278			hypothetical protein, similar to mutator protein mutT	DNA repair or modify	Information pathway
1.41	1.14	SA2279			hypothetical protein, similar to phosphomannomutase	carbohydrate metabolism	Intermediary metabolism
1.10	0.87	SA2280			hypothetical protein		
0.83	0.86	SA2281			hypothetical protein		
0.98	0.80	SA2283			conserved hypothetical protein		
0.82	0.92	SA2285			hypothetical protein, similar to accumulation-associated protein		
1.05	0.82	SA2286		sarT	staphylococcal accessory regulator A homolog	RNA synthesis	Information pathway
1.19	0.79	SA2287		sarH2(sarU)	staphylococcal accessory regulator A homolog	RNA synthesis	Information pathway
0.98	0.82	SA2288		gtaB	UTP-glucose-1-phosphate uridyltransferase	cell wall	cell envelop and process
0.76	0.86	SA2290		fnbB	fibronectin-binding protein homolog(fmbB)	pathogenic factor	other function
1.03	0.92	SA2291		fnb	fibronectin-binding protein homolog(fnbA)	pathogenic factor	other function
1.79	1.58	SA2292			hypothetical protein		
0.68	13.40	SA2293		gntP	gluconate permease	transport/binding	cell envelop and process
0.72	11.53	SA2294		gntK	gluconokinase	carbohydrate metabolism	Intermediary metabolism
0.63	7.62	SA2295		gntR	gluconate operon transcriptional repressor	RNA synthesis	Information pathway
0.97	1.97	SA2296			hypothetical protein, similar to transcriptional regulator, MerR family	RNA synthesis	Information pathway
0.69	1.59	SA2297			hypothetical protein, similar to GTP-pyrophosphokinase	nucleic acid metabolism	Intermediary metabolism
1.16	1.44	SA2298			conserved hypothetical protein		
1.51	1.15	SA2299			conserved hypothetical protein		
5.70	3.84	SA2300			hypothetical protein, similar to glucarate transporter	transport/binding	cell envelop and process
1.41	1.19	SA2301			hypothetical protein, similar to alkaline phosphatase	phosphate metabolism	Intermediary metabolism
0.94	0.74	SA2302			hypothetical protein, similar to ABC transporter	transport/binding	cell envelop and process
0.90	0.73	SA2303			hypothetical protein, similar to membrane spanning protein	transport/binding	cell envelop and process
5.77	3.89	SA2304		fbp	fructose-bisphosphatase	carbohydrate metabolism	Intermediary metabolism
1.11	1.13	SA2305			conserved hypothetical protein		
1.07	1.05	SA2306			conserved hypothetical protein		
1.20	0.89	SA2307			hypothetical protein, similar to ABC transporter (binding protein)	transport/binding	cell envelop and process
1.22	0.91	SA2308			hypothetical protein, similar to transcription regulator MarR family	RNA synthesis	Information pathway
1.56	0.86	SA2310			conserved hypothetical protein		
1.15	1.04	SA2311	cre		hypothetical protein, similar to NAD(P)H-flavin oxidoreductase	membrane bioenergetics	cell envelop and process
1.85	0.95	SA2312		ddh	D-specific D-2-hydroxyacid dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.17	1.09	SA2313			conserved hypothetical protein		
1.45	1.03	SA2314			hypothetical protein, similar to ABC transporter (ATP-binding protein)	transport/binding	cell envelop and process
1.20	0.89	SA2315			conserved hypothetical protein		
0.74	0.56	SA2316		srtA	sortase	cell wall	cell envelop and process
1.36	1.10	SA2317			hypothetical protein, similar to N-acetyltransferase	detoxification	other function
1.38	0.97	SA2318			hypothetical protein, similar to L-serine dehydratase	aminoacid metabolism	Intermediary metabolism
1.19	1.04	SA2319			hypothetical protein, similar to beta-subunit of L-serine dehydratas	aminoacid metabolism	Intermediary metabolism
1.01	0.95	SA2320	cre		hypothetical protein, similar to regulatory protein pfoR	RNA synthesis	Information pathway
1.05	1.52	SA2321			hypothetical protein		
1.26	0.92	SA2322			conserved hypothetical protein		
0.81	0.91	SA2323			conserved hypothetical protein	pathogenic factor	other function
0.94	0.91	SA2324			hypothetical protein, similar to thioredoxin	membrane bioenergetics	cell envelop and process
0.87	1.14	SA2325			conserved hypothetical protein		
1.23	2.58	SA2326		ptsG	PTS system, glucose-specific IIABC component	transport/binding	cell envelop and process
0.19	0.58	SA2327			hypothetical protein, similar to pyruvate oxidase	carbohydrate metabolism	Intermediary metabolism
0.31	0.64	SA2328			conserved hypothetical protein		
0.67	0.80	SA2329			conserved hypothetical protein		
0.98	0.81	SA2330			hypothetical protein, similar to transcription regulator	RNA synthesis	Information pathway
0.85	0.80	SA2331			hypothetical protein		
0.74	0.86	SA2332			hypothetical protein, similar to secretory antigen precursor SsaA	pathogenic factor	other function
1.26	1.06	SA2333		mvaA	hydroxymethylglutaryl-CoA reductase	lipid metabolism	Intermediary metabolism
0.14	0.34	SA2334		mvaS	3-hydroxy-3-methylglutaryl CoA synthase	lipid metabolism	Intermediary metabolism
0.93	0.88	SA2335		adaB	probable methylated DNA-protein cysteine methyltransferase	DNA repair or modify	Information pathway
1.41	0.94	SA2336		clpL	ATP-dependent Clp proteinase chain clpL	adaptation to atypical	other function
0.86	0.78	SA2337		feoB	ferrous iron transport protein B homolog	transport/binding	cell envelop and process
1.10	0.54	SA2338			hypothetical protein		
0.66	0.83	SA2339			hypothetical protein, similar to antibiotic transport-associated protein	transport/binding	cell envelop and process
1.07	1.09	SA2340			hypothetical protein, similar to transcriptional regulator tetR-family	RNA synthesis	Information pathway
6.76	7.01	SA2341	cre	rocA	1-pyrroline-5-carboxylate dehydrogenase	aminoacid metabolism	Intermediary metabolism
1.10	1.47	SA2342			hypothetical protein, similar to O-acetyltransferase	carbohydrate metabolism	Intermediary metabolism
1.44	1.71	SA2343			hypothetical protein		
1.21	1.23	SA2344		copA	copper-transporting ATPase copA	transport/binding	cell envelop and process
0.91	1.33	SA2345			hypothetical protein, similar to mercuric ion-binding protein	transport/binding	cell envelop and process
1.15	0.86	SA2346			hypothetical protein, similar to D-specific D-2-hydroxyacid dehydrogenase ddh hom	carbohydrate metabolism	Intermediary metabolism
1.15	0.97	SA2347			hypothetical protein, similar to aspartate aminotransferase	aminoacid metabolism	Intermediary metabolism
0.92	0.87	SA2348		crtN	squalene desaturase	lipid metabolism	Intermediary metabolism
0.99	0.83	SA2349		crtM	squalene synthase	lipid metabolism	Intermediary metabolism
1.08	0.88	SA2350		crtQ	conserved hypothetical protein		
0.93	0.69	SA2351		crtP	hypothetical protein, similar to phytoene dehydrogenase	lipid metabolism	Intermediary metabolism
1.24	1.03	SA2352		crtO	hypothetical protein		
1.04	1.00	SA2353			hypothetical protein, similar to secretory antigen precursor SsaA	pathogenic factor	other function
0.83	0.78	SA2354			hypothetical protein, similar to acyltransferase	cell wall	cell envelop and process
0.91	0.83	SA2355			conserved hypothetical protein		
0.59	0.72	SA2356		isaA	immunodominant antigen A	pathogenic factor	other function
2.67	0.87	SA2357			hypothetical protein, similar to regulatory protein (pfoS/R)	RNA synthesis	Information pathway
0.97	0.87	SA2358			hypothetical protein, similar to transcriptional regulator (TetR/AcrR family)	RNA synthesis	Information pathway
1.49	1.14	SA2359			hypothetical protein		
1.49	1.16	SA2360			conserved hypothetical protein		
1.01	1.13	SA2361			conserved hypothetical protein		
1.22	0.95	SA2362			conserved hypothetical protein		
0.91	1.24	SA2363			hypothetical protein		
1.01	1.23	SA2364			hypothetical protein, similar to transcription regulator acrR	RNA synthesis	Information pathway
1.02	1.05	SA2365			hypothetical protein, similar to short chain oxidoreductase		
0.95	0.94	SA2366			conserved hypothetical protein		
1.17	1.08	SA2367			conserevd hypothetical protein		
1.09	0.91	SA2368			hypothetical protein, similar to cobalamin synthesis related protein CobW	aminoacid metabolism	Intermediary metabolism

1.07	0.70	SA2369			hypothetical protein, similar to ferrous iron transporter protein B	transport/binding	cell envelop and process
0.92	0.62	SA2370			conserved hypothetical protein		
0.99	0.92	SA2371			conserved hypothetical protein		
0.89	0.95	SA2372			hypothetical protein		
1.02	0.81	SA2374			conserved hypothetical protein		
1.19	0.80	SA2375			hypothetical protein, similar to dihydroorotate dehydrogenase	nucleic acid metabolism	Intermediary metabolism
1.27	1.00	SA2376			hypothetical protein		
0.81	0.85	SA2377			conserved hypothetical protein		
0.88	0.75	SA2378			conserved hypothetical protein		
0.35	0.56	SA2379			hypothetical protein, similar to transcriptional regulator tetR-family	RNA synthesis	Information pathway
0.33	0.50	SA2380			conserved hypothetical protein		
0.31	0.71	SA2390		panD	aspartate 1-decarboxylase	coenzyme metabolism	Intermediary metabolism
0.45	0.57	SA2392		panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	coenzyme metabolism	Intermediary metabolism
0.87	0.86	SA2393			hypothetical protein, similar to 2-dehydropantoate 2-reductase	coenzyme metabolism	Intermediary metabolism
1.24	1.19	SA2394			hypothetical protein, similar to alpha-acetolactate decarboxylase	carbohydrate metabolism	Intermediary metabolism
2.49	1.65	SA2395		ldh	L-lactate dehydrogenase	carbohydrate metabolism	Intermediary metabolism
1.47	0.65	SA2396	cre		hypothetical protein, similar to amino acid transporter	transport/binding	cell envelop and process
1.70	0.79	SA2397			hypothetical protein, similar to pyridoxal-phosphate dependent aminotransferas	aminoacid metabolism	Intermediary metabolism
0.87	1.01	SA2398			hypothetical protein		
0.41	0.50	SA2399			fructose-bisphosphate aldolase homolog	carbohydrate metabolism	Intermediary metabolism
0.63	0.91	SA2400		mqo2	malate:quinone oxidoreductase	carbohydrate metabolism	Intermediary metabolism
1.15	1.15	SA2401			hypothetical protein		
0.59	0.65	SA2402			acetate-CoA ligase	carbohydrate metabolism	Intermediary metabolism
0.92	0.93	SA2403			conserved hypothetical protein		
0.89	0.76	SA2404			hypothetical protein		
2.46	0.77	SA2405		betA	choline dehydrogenase	adaptation to atypical	other function
4.41	0.85	SA2406		gbsA	glycine betaine aldehyde dehydrogenase gbsA	adaptation to atypical	other function
1.52	0.95	SA2407			conserved hypothetical protein		
1.54	0.81	SA2408		cudT	choline transporter	transport/binding	cell envelop and process
4.23	0.93	SA2409			hypothetical protein, similar to anaerobic ribonucleotide reductase activator prot	nucleic acid metabolism	Intermediary metabolism
3.20	0.71	SA2410		nrdD	anaerobic ribonucleoside-triphosphate reductase	nucleic acid metabolism	Intermediary metabolism
1.21	0.85	SA2411			hypothetical protein, similar to magnesium citrate secondary transporter	transport/binding	cell envelop and process
1.20	0.97	SA2412			hypothetical protein, similar to uroporphyrin-III C-methyltransferase	coenzyme metabolism	Intermediary metabolism
1.16	0.87	SA2413		cysJ	sulfite reductase flavoprotein	sulfur metabolism	Intermediary metabolism
0.92	0.99	SA2414	cre		hypothetical protein, similar to glutathione peroxidase	adaptation to atypical	other function
1.09	0.87	SA2415			hypothetical protein, similar to ABC transporter (permease)	transport/binding	cell envelop and process
1.09	0.95	SA2416			hypothetical protein, similar to ABC transporter (ATP-binding protein)	transport/binding	cell envelop and process
0.80	1.17	SA2417			hypothetical protein, similar to two-component sensor histidine kinase	sensor	cell envelop and process
0.80	1.15	SA2418			hypothetical protein, similar to two-component response regulator	RNA synthesis	Information pathway
0.86	1.08	SA2419			hypothetical protein		
0.86	0.81	SA2420		phoB	alkaline phosphatase III precursor	phosphate metabolism	Intermediary metabolism
1.09	0.94	SA2421			hypothetical protein, similar to transcriptional regulator	RNA synthesis	Information pathway
1.42	1.10	SA2422			hypothetical protein, similar to tributyrin esterase	lipid metabolism	Intermediary metabolism
1.14	0.62	SA2423		clfB	Clumping factor B	pathogenic factor	other function
1.09	0.52	SA2423a		clfB	Clumping factor B	pathogenic factor	other function
1.12	0.84	SA2424			hypothetical protein, similar to transcription regulator Crp/Fnr family protein	RNA synthesis	Information pathway
1.24	0.96	SA2425		arcC	carbamate kinase	aminoacid metabolism	Intermediary metabolism
1.22	0.85	SA2426		arcD	arginine/oirnithine antiporter	transport/binding	cell envelop and process
5.35	1.17	SA2427		arcB	ornithine transcarbamoylase	aminoacid metabolism	Intermediary metabolism
1.06	0.74	SA2428		arcA	arginine deiminase	aminoacid metabolism	Intermediary metabolism
1.17	0.96	SA2429			hypothetical protein, similar to arginine repressor	RNA synthesis	Information pathway
1.16	0.86	SA2430		aur	zinc metalloproteinase aureolysin	pathogenic factor	other function
0.92	0.81	SA2431		isaB	immunodominant antigen B	pathogenic factor	other function
1.26	0.96	SA2432			conserved hypothetical protein		
3.44	1.59	SA2433			hypothetical protein, similar to transcription antiterminator BglG family	RNA synthesis	Information pathway
0.77	0.75	SA2434			fructose phosphotransferase system enzyme fruA homolog	transport/binding	cell envelop and process
2.74	1.35	SA2435		pmi	mannose-6-phosphate isomerase	carbohydrate metabolism	Intermediary metabolism
0.29	0.43	SA2436			hypothetical protein, similar to phage infection protein	phage-related	other function
0.28	0.64	SA2437			hypothetical protein, similar to autolysin precursor	cell wall	cell envelop and process
0.80	0.87	SA2438			hypothetical protein, similar to N-Carbamoylsarcosine Amidohydrolase	coenzyme metabolism	Intermediary metabolism
0.82	0.84	SA2439			conserved hypothetical protein		
0.82	0.83	SA2440			hypothetical protein		
0.81	0.83	SA2441			hypothetical protein, similar to lipopolysaccharide biosynthesis protein	cell wall	cell envelop and process
0.93	0.88	SA2442			preprotein translocase secA homolog	protein secretion	cell envelop and process
0.98	0.97	SA2443			hypothetical protein		
1.03	0.91	SA2444			hypothetical protein		
0.88	0.94	SA2445			hypothetical protein		
0.99	0.97	SA2446			hypothetical protein, similar to preprotein translocase secY	protein secretion	cell envelop and process
1.47	1.15	SA2447	cre		hypothetical protein, similar to streptococcal hemagglutinin protein	pathogenic factor	other function
0.87	0.97	SA2448			conserved hypothetical protein		
1.13	1.00	SA2449			hypothetical protein		
0.92	1.01	SA2450			hypothetical protein		
1.03	0.93	SA2451			hypothetical protein		
0.96	0.82	SA2452			conserved hypothetical protein		
1.10	0.91	SA2453			hypothetical protein, similar to peptide methionine sulfoxide reductase	protein modification	Information pathway
1.06	0.85	SA2454			conserved hypothetical protein		
0.87	0.85	SA2455		capC	capsular polysaccharide biosynthesis, capC	adaptation to atypical	other function
0.90	0.00	SA2456		capB	capsular polysaccharide biosynthesis, capB	adaptation to atypical	other function
1.24	0.88	SA2457		capA	capsular polysaccharide biosynthesis, capA	adaptation to atypical	other function
0.82	1.04	SA2458		icaR	ica operon transcriptional regulator IcaR	RNA synthesis	Information pathway
1.07	0.80	SA2459		icaA	intercellular adhesion protein A	pathogenic factor	other function
1.00	0.81	SA2461		icaB	intercellular adhesion protein B	pathogenic factor	other function
0.98	0.88	SA2462		icaC	intercellular adhesion protein C	pathogenic factor	other function
1.12	1.08	SA2463	cre	lip	triacylglycerol lipase precursor	pathogenic factor	other function
1.26	0.92	SA2465		hisF	cyclase-like protein hisF	amino acid metabolism	Intermediary metabolism
1.26	0.88	SA2466			hypothetical protein, similar to phosphoribosylformimino-5-aminoimidazole carboxamide ribot	aminoacid metabolism	Intermediary metabolism
1.04	0.80	SA2467		hisH	amidotransferase hisH	aminoacid metabolism	Intermediary metabolism
1.35	0.93	SA2468		hisB	imidazoleglycerol-phosphate dehydratase	aminoacid metabolism	Intermediary metabolism
1.29	0.86	SA2469			hypothetical protein, similar to histidinol-phosphate transaminase	amino acid metabolism	Intermediary metabolism
1.09	0.82	SA2470			hypothetical protein, similar to histidinol dehydrogenase	aminoacid metabolism	Intermediary metabolism
1.04	0.91	SA2471		hisG	ATP phosphoribosyltransferase	aminoacid metabolism	Intermediary metabolism
1.30	0.90	SA2472			hypothetical protein, similar to ATP phosphoribosyltransferase regulatory subuni	nucleic acid metabolism	Intermediary metabolism
1.13	0.75	SA2473			hypothetical protein		
1.06	0.95	SA2474			conserved hypothetical protein		
1.02	0.83	SA2475			conserved hypothetical protein	transport/binding	cell envelop and process
1.29	0.73	SA2476			hypothetical protein, similar to cation ABC transporter (ATP-binding protei)	transport/binding	cell envelop and process
1.32	0.88	SA2477			conserved hypotehtical protein		

1.17	0.86	SA2478			conserved hypothetical protein		
1.34	1.18	SA2479			conserved hypothetical protein		
2.29	1.17	SA2480	cre	drp35	Drp35	cell wall	cell envelop and process
0.94	0.98	SA2481			conserved hypotehtical protein		
1.03	0.87	SA2482		pcp	pyrrolidone-carboxylate peptidase	protein modification	Information pathway
1.06	0.92	SA2483			hypothetical protein		
1.40	1.19	SA2484			conserved hypothetical protein		
1.21	0.95	SA2485			hypothetical protein		
0.55	0.75	SA2486			2-oxoglutarate/malate translocator homolog	transport/binding	cell envelop and process
0.49	0.55	SA2488			hypothetical protein		
0.83	0.86	SA2489			hypothetical protein, similar to high-affinity nickel-transport protein	transport/binding	cell envelop and process
1.14	1.03	SA2490	cre		hypothetical protein, similar to N-hydroxyarylamine O-acetyltransferase	carbohydrate metabolism	Intermediary metabolism
0.41	0.58	SA2491	cre		conserved hypothetical protein		
0.48	0.50	SA2492		vraD	hypothetical protein, similar to ABC transporter	transport/binding	cell envelop and process
0.39	0.25	SA2494		cspB	cold shock protein cspB	adaptation to atypical	other function
0.65	0.40	SA2495			hypothetical protein, similar to hypothetical protein	RNA synthesis	Information pathway
4.15	1.72	SA2496			hypothetical protein		
1.35	1.21	SA2497			hypothetical protein		
0.87	1.16	SA2498			hypothetical protein, similar to DNA-binding protein Spo0J-like homolog	sporulation	cell envelop and process
1.00	1.12	SA2499		gidB	glucose inhibited division protein B	cell division	cell envelop and process
0.68	1.01	SA2500		gidA	glucose inhibited division protein A	cell division	cell envelop and process
0.72	0.72	SA2501		thdF	possible thiophene and furan oxidation protein	detoxification	other function
1.07	1.03	SA2502		rnpA	ribonuclease P protein component	RNA modification	Information pathway
1.24	0.92	SAS001			Conserved hypothetical protein		
1.08	1.13	SAS007			hypothetical protein		
0.98	0.62	SAS008			hypothetical protein		
1.28	1.37	SAS009			hypothetical protein		
0.63	0.75	SAS010			hypothetical protein		
1.21	0.87	SAS012			hypothetical protein		
4.23	4.55	SAS016			hypothetical protein		
1.52	0.83	SAS020			hypothetical protein, similar to phosphoglycerate mutase	carbohydrate metabolism	Intermediary metabolism
1.02	1.15	SAS023			hypothetical protein, similar to thioredoxin	membrane bioenergetics	cell envelop and process
0.86	1.09	SAS025			hypothetical protein		
0.68	0.81	SAS026			hypothetical protein		
0.68	0.94	SAS027			conserved hypothetical protein		
1.09	1.10	SAS030			hypothetical protein		
0.94	0.74	SAS031			hypothetical protein		
1.25	1.20	SAS032			conserved hypothetical protein		
1.10	1.15	SAS035			hypothetical protein		
0.71	0.74	SAS037			hypothetical protein		
0.33	0.42	SAS039			hypothetical protein		
1.11	1.34	SAS040		dmpI	4-oxalocrotonate tautomerase	lipid metabolism	Intermediary metabolism
1.14	1.25	SAS041			hypothetical protein		
0.95	0.88	SAS043			hypothetical protein		
1.00	0.85	SAS044		dmpI	4-oxalocrotonate tautomerase		
0.75	1.30	SAS047		rpmG	50S ribosomal protein L33	protein synthesis	Information pathway
0.22	0.32	SAS049	cre		hypothetical protein		
1.09	1.27	SAS051			hypothetical protein		
0.73	1.10	SAS052		rpsD	30S ribosomal protein S4	protein synthesis	Information pathway
0.73	1.08	SAS053			hypothetical protein		
0.81	1.11	SAS054			conserved hypothetical protein		
1.11	1.24	SAS056			hypothetical protein		
0.82	1.03	SAS057			hypothetical protein		
1.00	1.15	SAS058			hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related	other function
0.94	0.46	SAS061			hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related	other function
1.24	1.15	SAS062			hypothetical protein(phiN315)	phage-related	other function
1.00	1.01	SAS063			hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related	other function
1.21	0.76	SAS065		hld	delta-hemolysin	pathogenic factor	other function
1.46	1.18	SAS067			hypothetical protein		
2.40	1.19	SAS068	cre		hypothetical protein		
2.86	4.36	SAS074	cre		conserved hypothetical protein		
0.59	0.84	SAS078		rpmJ	50S ribosomal protein L36	protein synthesis	Information pathway
0.62	0.78	SAS079		rpsN	30S ribosomal protein S14	protein synthesis	Information pathway
1.05	0.93	SAS081			conserved hypothetical protein		
1.19	0.95	SAS084			hypothetical protein		
1.35	1.22	SAS085			hypothetical protein		
1.20	0.90	SAS091			hypothetical protein		
0.90	1.16	SAS092			hypothetical protein		
0.81	0.90	SAS093		rpmH	50S ribosomal protein L34	protein synthesis	Information pathway

表7　種々の糖源によるメチシリンのMIC

Chemically defined medium	COL	MW2	BB270
glucose (10% wt/vol)	1024	16	256
glucose + GlcNAc (2%)	1024	16	64
fructose (10%)	no growth	8	no growth
fructose + GlcNAc (2%)	no growth	16	no growth
lactose (10%)	1024	16	512
lactose + GlcNAc (2%)	1024	256	32
manitol (10%)	1024	16	256
sucrose (10%)	1024	16	512
sucrose + GlcNAc (2%)	1024	16	128
maltose (10%)	1024	16	512
maltose + GlcNAc (2%)	1024	16	256
galactose (10%)	1024	16	512
galactose + GlcNAc (2%)	1024	32	64
trehalose (10%)	1024	64	1024
trehalose + GlcNAc (2%)	1024	256	128
raffinose (10%)	1024	32	512
raffinose + GlcNAc (2%)	1024	32	512
mannose (10%)	1024	16	512
mannose + GlcNAc (2%)	1024	32	512
all (1% each)	1024	16	256
all + GlcNAc (2%)	1024	16	64
TSB	1024	16	512
TSB + GlcNAc (2%)	1024	16	512

単位:μg/ml

表8.　種々の糖添加時における各遺伝子の発現パターン
（グルコース培養時における発現量に対する割合を示す）

Fructose	Lactose	Galactose	Sucrose	Maltose	Raffinose	Manitol	Mannose	Trehalose	All	TSB	MW.I.D.	name	characteristic	DOGAN
0.86	1.10	1.06	1.38	1.20	1.14	0.84	0.92	1.06	1.07	0.95	MW0001	dnaA	chromosomal replication initiator protein	DNA replication
1.61	0.81	1.07	0.73	1.25	0.94	1.24	1.61	1.22	0.86	1.29	MW0002	dnaN	DNA polymerase III, beta chain	DNA replication
1.00	0.84	0.89	1.31	0.90	1.52	0.86	0.73	0.94	0.91	0.92	MW0003		conserved hypothetical protein	
1.05	1.35	1.10	1.27	1.04	1.59	1.02	1.29	1.02	1.06	0.95	MW0004	recF	DNA repair and genetic recombination protein	DNA repair or modify
0.93	1.44	1.34	1.38	1.10	2.04	0.93	1.16	1.26	1.10	0.79	MW0005	gyrB	DNA gyrase subunit B	DNA replication
0.98	1.04	0.94	1.20	0.86	1.15	1.26	1.44	1.11	1.02	1.13	MW0006	gyrA	DNA gyrase subunit A	DNA replication
0.78	0.70	0.85	0.97	1.00	0.53	0.83	0.40	0.82	1.13	1.19	MW0007		conserved hypothetical protein	
0.81	0.56	0.66	0.53	0.59	0.67	0.77	0.71	0.55	1.06	1.23	MW0008	hutH	histidine ammonia-lyase	amino acid metabolism
1.37	0.97	0.87	0.55	0.87	0.89	0.93	1.13	0.81	1.04	1.91	MW0009	serS	seryl-tRNA synthetase	protein synthesis
0.77	0.81	0.84	0.82	0.74	0.53	0.58	0.45	0.74	0.98	1.22	MW0010		hypothetical protein, similar to amino acid permease	transport/binding
1.01	0.62	0.55	0.68	0.65	0.45	0.55	0.48	0.62	1.08	1.49	MW0011		Conserved hypothetical protein	
0.83	0.92	1.07	1.52	0.97	0.84	0.83	0.48	0.94	0.97	1.08	MW0012		hypothetical protein, similar to homoserine-o-acetyltransferase	amino acid metabolism
0.85	0.81	0.95	1.28	0.99	0.72	0.72	0.47	0.83	0.99	1.18	MW0013		conserved hypothetical protein	
1.08	1.23	0.96	0.88	1.08	0.87	0.93	1.08	0.84	1.06	1.17	MW0014		conserved hypothetical protein	
1.12	0.84	0.91	0.89	1.05	0.84	0.77	0.91	0.81	0.81	1.16	MW0015	rplI	50S ribosomal protein L9	protein synthesis
0.89	0.93	1.01	0.74	1.04	0.93	0.80	1.08	0.71	1.00	1.17	MW0016	dnaC	replicative DNA helicase	DNA replication
0.74	0.85	1.14	0.88	0.98	0.82	0.82	0.91	0.87	0.99	0.71	MW0017	purA	adenylosuccinate synthase	[illegible]
0.84	0.86	1.10	1.39	1.06	1.27	0.94	0.89	0.98	1.07	0.75	MW0018	vicR	response regulator	RNA synthesis
0.93	1.22	1.10	1.56	1.08	1.14	0.86	0.98	1.10	1.01	0.97	MW0019	vicK	two-component sensor histidine kinase	sensor
0.91	1.13	1.00	1.23	0.91	0.98	0.91	1.02	1.10	0.97	0.98	MW0020		conserved hypothetical protein	
1.45	1.24	1.18	1.36	1.24	1.11	1.02	1.40	1.04	0.95	0.93	MW0021		conserved hypothetical protein	
1.17	1.21	1.24	1.05	1.11	1.14	0.94	1.33	1.07	1.01	0.91	MW0022		conserved hypothetical protein	
1.02	0.90	0.65	1.05	0.85	0.90	1.07	1.15	0.96	0.80	1.51	MW0023		hypothetical protein, similar to 5'-nucleotidase	[illegible]
0.90	1.08	1.17	1.35	1.15	1.07	0.88	1.16	1.13	1.02	1.86	MW0023n		hypothetical protein, similar to 5'-nucleotidase	[illegible]
1.04	0.95	1.21	1.35	1.10	1.04	0.92	0.86	1.00	1.02	0.81	MW0024	orfX	conserved hypothetical protein orfX	
0.90	0.94	1.06	1.40	1.07	0.91	0.83	1.05	1.08	1.07	0.97	MW0025		hypothetical protein	
1.03	0.93	0.94	1.01	0.79	0.80	0.83	0.87	1.09	0.97	1.11	MW0026		hypothetical protein	
1.16	1.43	1.15	0.91	1.41	1.29	1.00	1.45	0.85	0.88	1.17	MW0027		transposase for IS-like element	transposon and IS
1.04	0.72	0.87	0.78	1.07	0.92	1.09	1.08	1.36	0.81	1.10	MW0028		probable HMG-CoA synthase	carbohydrate metabolism
1.01	1.11	1.21	1.29	1.16	1.23	0.84	1.01	1.14	1.03	1.13	MW0028n		probable HMG-CoA synthase	carbohydrate metabolism
1.00	1.19	1.16	1.27	1.10	1.15	0.96	0.96	1.31	0.99	1.01	MW0029		glycerophosphoryldiester phosphodiesterase homologue	lipid metabolism
1.09	1.12	0.90	1.05	1.04	0.95	0.95	0.82	1.40	0.89	0.99	MW0030		conserved hypothetical protein	
2.05	1.12	1.01	1.11	1.77	1.16	1.42	0.89	1.36	0.89	0.70	MW0031	mecA	penicillin binding protein 2 prime	cell wall
1.01	0.90	0.92	0.69	1.11	0.76	1.24	1.18	1.02	0.93	0.76	MW0032	mecR1	methicillin resistance protein	sensor
1.43	0.50	0.63	0.67	0.93	0.59	1.57	0.66	0.93	0.70	0.77	MW0033	ncated h	tical protein, similar to type I restriction-modification system endc	DNA repair or modify
0.82	1.50	1.27	1.00	1.28	1.10	0.74	1.16	1.24	1.01	0.94	MW0034		hypothetical protein, similar to transposase	transposon and IS
0.91	0.94	1.20	1.63	1.27	1.08	1.00	0.60	1.23	1.14	1.07	MW0035		hypothetical protein	
0.83	0.99	1.08	1.24	0.98	0.85	0.92	0.70	1.03	1.12	0.98	MW0036		conserved hypothetical protein	
0.96	1.33	1.40	1.15	1.41	1.35	1.12	1.26	1.02	1.14	0.97	MW0037		hypothetical protein	
0.88	0.99	1.17	1.51	1.21	1.17	0.89	0.79	1.26	1.13	0.94	MW0037n		hypothetical protein	
0.81	0.92	0.93	0.67	1.11	0.85	1.01	1.21	0.99	1.11	1.16	MW0038	ccrB	cassette chromosome recombinase B	[illegible]
0.83	1.46	1.45	1.08	1.45	1.69	1.03	1.33	1.09	1.11	1.17	MW0039	ccrA	cassette chromosome recombinase A	[illegible]
1.08	1.60	1.33	1.02	1.19	1.29	1.35	1.63	1.06	1.06	1.08	MW0040		hypothetical protein	
0.96	1.44	1.22	1.11	1.09	1.47	1.00	1.65	0.83	1.02	1.03	MW0041		hypothetical protein	
1.01	1.02	1.01	0.90	0.95	0.99	0.96	1.01	1.01	0.98	0.84	MW0041n		hypothetical protein	
1.19	1.32	1.27	1.10	1.25	1.47	1.01	1.72	0.80	1.11	0.97	MW0042		hypothetical protein	
1.15	0.91	1.00	1.07	1.11	1.38	0.94	1.24	0.96	0.95	1.05	MW0043		hypothetical protein	
1.13	1.33	1.13	0.84	1.12	1.32	0.95	1.43	0.88	0.97	1.09	MW0045		hypothetical protein	
0.92	1.77	1.11	0.94	1.21	1.31	0.82	1.66	0.89	0.95	1.22	MW0046		truncated hypothetical protein	
1.32	0.81	0.97	1.07	1.07	0.93	0.90	1.42	0.79	1.03	1.15	MW0047		hypothetical protein	
1.00	1.31	1.09	0.87	0.94	0.95	0.93	1.00	1.02	1.00	0.78	MW0050		truncated transposase	transposon and IS
1.27	0.59	0.83	1.03	1.24	0.53	1.10	1.01	1.33	0.85	0.47	MW0051	seh	enterotoxin H	pathogenic factor
1.42	1.00	1.09	1.05	1.41	0.76	1.10	1.28	1.64	0.86	0.58	MW0052		hypothetical protein, similar to enterotoxin SEO	pathogenic factor
1.44	1.11	1.01	1.21	1.35	0.87	1.12	1.39	1.27	0.92	0.71	MW0053		conserved hypothetical protein	
1.23	1.41	1.21	1.31	1.47	0.97	1.30	1.50	1.32	1.14	0.77	MW0054		conserved hypothetical protein	
1.48	1.16	1.05	1.07	1.32	1.03	1.28	1.79	1.29	0.95	0.80	MW0054n		conserved hypothetical protein	
1.17	1.36	1.12	1.19	1.30	1.00	1.13	1.11	1.64	1.12	0.80	MW0055		conserved hypothetical protein	
1.37	1.01	1.14	1.15	1.32	1.05	1.10	1.06	1.39	1.05	0.94	MW0055n		conserved hypothetical protein	
1.09	1.57	1.18	1.23	1.32	1.21	1.26	1.31	1.23	1.07	0.81	MW0056		conserved hypothetical protein	
1.16	1.46	1.32	1.35	1.26	1.20	1.09	1.21	1.15	1.16	0.99	MW0056n		conserved hypothetical protein	
1.12	1.52	1.16	0.91	1.11	1.16	1.26	1.60	0.94	1.12	1.02	MW0057		conserved hypothetical protein	
0.96	1.14	1.07	1.10	1.02	0.90	1.03	1.36	1.10	1.09	1.01	MW0057n		conserved hypothetical protein	
0.97	1.39	1.09	1.22	1.09	1.40	1.33	1.37	1.24	1.07	0.94	MW0058		hypothetical protein, similar to homo sapiens CGI-44 protein, PRO1975 protei	miscellaneous
1.04	1.38	1.36	1.24	1.42	1.14	1.21	1.47	0.98	1.15	0.79	MW0059		conserved hypothetical protein	
1.32	0.86	1.07	0.81	1.21	1.06	1.31	1.53	0.86	1.08	0.91	MW0059n		conserved hypothetical protein	
0.93	1.18	1.14	0.93	1.04	1.27	1.10	1.70	0.89	0.99	1.00	MW0060		hypothetical protein	
1.05	1.08	1.03	1.03	1.08	1.10	1.01	1.17	0.94	1.03	1.05	MW0061		hypothetical protein	
0.89	1.40	1.21	1.35	1.07	1.32	0.96	1.06	1.17	1.10	1.15	MW0062		hypothetical protein, similar to macrolide-efflux determinant	transport/binding
0.95	1.14	1.30	1.26	1.13	1.30	1.03	1.19	0.97	1.03	1.22	MW0063		conserved hypothetical protein	
0.99	0.92	1.03	0.97	0.98	1.08	0.91	0.76	0.99	1.08	1.07	MW0064		hypothetical protein, similar to transcriptional regulator (LysR famil	RNA synthesis
0.87	1.43	1.19	1.26	1.07	1.28	0.91	1.07	0.36	1.12	1.16	MW0065		hypothetical protein	
0.97	1.26	1.27	1.16	1.00	1.34	1.03	1.18	0.93	1.12	1.11	MW0066		hypothetical protein, similar to transcriptional regulator	RNA synthesis
0.94	1.22	1.26	1.31	1.10	1.24	1.01	1.11	1.07	1.09	1.00	MW0067		hypothetical protein	
1.13	0.94	0.98	0.97	0.96	0.85	0.98	0.89	1.08	0.90	0.90	MW0069		hypothetical protein	
1.19	1.42	1.12	1.12	1.21	1.17	1.06	1.22	0.79	0.97	0.94	MW0070	plc	1-phosphatidylinositol phosphodiesterase precurosr	pathogenic factor
0.86	0.45	0.71	0.72	0.69	0.15	0.43	0.22	0.77	0.89	0.47	MW0071		hypothetical protein	
1.12	1.27	1.24	1.11	1.18	1.33	1.12	1.64	0.71	0.87	0.90	MW0071n		hypothetical protein	
1.04	1.36	1.35	1.47	1.13	1.45	1.07	1.12	1.20	1.07	0.79	MW0074		hypothetical protein	
1.24	1.09	1.27	0.92	1.16	1.22	1.36	1.75	0.94	1.14	0.95	MW0075		hypothetical protein	
0.93	1.21	1.28	1.35	1.16	1.25	1.04	1.36	1.08	1.01	1.13	MW0076		hypothetical protein	
0.89	1.08	1.12	0.94	0.91	1.23	1.38	1.43	1.11	1.12	1.15	MW0077		hypothetical protein, similar to transcription regulator AraC/XylS family	RNA synthesis
1.07	1.29	1.35	0.89	1.34	2.43	1.30	2.18	0.70	0.90	1.02	MW0078		hypothetical protein, similar to aminoacylase	amino acid metabolism
1.00	1.26	1.22	1.16	1.16	1.77	1.35	1.26	0.44	1.10	1.13	MW0079		hypothetical protein, similar to transmembrane efflux pump protei	transport/binding
1.07	1.15	1.19	0.83	1.06	1.55	1.42	1.93	0.80	1.00	0.94	MW0079n		hypothetical protein, similar to transmembrane efflux pump protein	transport/binding
0.99	0.86	0.94	1.22	0.84	0.56	0.95	0.88	0.86	0.93	1.51	MW0080		conserved hypothetical protein	
0.88	2.70	1.91	1.35	1.10	9.25	1.46	3.75	1.10	1.37	1.76	MW0080a		conserved hypothetical protein	
0.88	1.31	1.51	1.24	1.16	3.10	1.69	3.24	1.04	1.22	0.90	MW0081		67 kDa Myosin-crossreactive streptococcal antigen homologue	pathogenic factor
1.07	1.24	1.09	1.01	1.05	1.46	1.57	2.07	0.89	1.07	1.12	MW0082		hypothetical protein	
0.91	0.76	0.98	1.11	1.08	1.08	1.31	1.33	0.96	1.11	1.91	MW0083	lctP	L-lactate permease homologue	transport/binding
0.62	0.21	1.45	1.82	1.07	0.41	0.58	0.81	0.28	1.10	1.77	MW0084	spa	IMMUNOGLOBULIN G BINDING PROTEIN A PRECURSOR	pathogenic factor
0.72	0.15	1.16	1.06	0.93	0.39	0.53	0.62	0.26	1.00	1.64	MW0084n	spa	Immunoglobulin G binding protein A precursor	pathogenic factor
0.78	0.35	0.55	0.77	0.91	0.50	0.58	0.42	0.54	0.86	1.18	MW0085	arH1(sarS	staphylococcal accessory regulator A homologue	RNA synthesis
0.91	0.48	0.82	0.57	0.76	0.57	0.95	0.90	0.82	0.99	1.22	MW0086	sirC	lipoprotein	transport/binding
0.91	0.48	0.92	0.49	0.76	0.61	0.87	1.03	0.68	0.93	0.93	MW0087	sirB	lipoprotein	transport/binding
0.73	0.98	1.12	1.43	1.05	1.08	0.80	1.11	1.19	1.01	1.17	MW0088	sirA	lipoprotein	transport/binding
0.83	0.93	1.02	1.13	1.04	0.92	0.90	1.23	1.00	0.92	1.09	MW0088n	sirA	lipoprotein	transport/binding
0.55	1.21	1.06	1.26	1.05	1.14	0.87	1.10	1.05	1.08	0.89	MW0089		hypothetical protein, similar to cysteine synthase	amino acid metabolism
0.59	0.84	1.11	0.98	1.00	1.05	0.97	0.87	0.89	1.17	0.99	MW0090		hypothetical protein, similar to ornithine cyclodeaminase	amino acid metabolism

0.63	0.74	1.01	0.68	0.91	0.95	0.93	1.07	0.90	1.13	0.94	MW0091		conserved hypothetical protein	
0.68	0.85	1.20	1.32	0.99	1.06	1.01	0.85	0.99	1.16	0.78	MW0092		hypothetical protein, similar to multi-drug resistance efflux pump	transport/binding
0.72	0.95	0.91	0.42	0.68	0.91	1.05	1.18	0.79	0.95	0.71	MW0093		hypothetical protein, similar to rhizobactin siderophore biosynthesisprotein Rh	miscellaneous
0.67	1.43	1.30	0.95	1.23	1.67	0.97	1.50	0.95	1.03	0.91	MW0094		hypothetical protein, similar to rhizobactin siderophore biosynthesisprotein Rh	miscellaneous
0.69	0.95	1.21	1.18	1.03	1.24	0.89	1.00	1.25	1.09	0.82	MW0095		hypothetical protein, similar to various aldolase	aminoacid metabolism
0.60	1.16	1.12	1.19	1.06	1.32	0.98	1.38	1.07	1.09	0.75	MW0096		hypothetical protein, similar to diaminopimelate decarboxylase	aminoacid metabolism
0.58	1.10	1.17	1.02	0.99	1.12	0.81	1.12	0.94	1.12	0.87	MW0097		hypothetical protein	
0.69	1.09	1.07	1.35	1.01	1.22	0.88	0.91	0.98	1.11	0.94	MW0098		hypothetical protein	
0.76	0.89	1.14	1.22	0.91	1.02	0.95	0.95	1.00	1.17	0.92	MW0099		hypothetical protein	
1.34	0.45	0.76	0.79	0.94	0.59	0.76	0.55	0.93	1.27	0.38	MW0100	butA	acetoinreductase	carbohydrate metabolism
0.75	0.92	1.13	1.20	1.01	1.05	0.92	1.09	0.97	1.17	0.98	MW0101		hypothetical protein	
0.93	1.47	0.76	0.77	1.00	0.77	1.16	1.02	0.88	0.97	0.92	MW0101n		hypothetical protein	
0.74	1.40	1.21	1.04	1.17	1.35	1.04	1.40	0.94	1.04	0.82	MW0102		hypothetical protein, similar to UDP-glucose 4-epimerase (gale-1)	carbohydrate metabolism
0.72	1.02	1.07	1.05	1.03	1.24	0.95	1.23	0.99	1.11	0.69	MW0103		hypothetical protein, similar to glycosyltransferase TuaA	cell wall
0.48	1.39	1.19	1.23	1.09	1.26	0.83	1.15	1.05	1.14	0.91	MW0104		hypothetical protein, similar to Eps(Exopolysaccharide)G	cell wall
0.64	1.05	1.06	1.16	0.95	1.18	0.73	0.92	0.98	1.14	1.02	MW0105		hypothetical protein, similar to capsular polysaccharide synthesis protein 14H	transport/binding
0.96	0.71	0.95	0.96	1.02	0.66	0.89	0.79	1.16	0.99	1.42	MW0106		hypothetical protein, similar to capsular polysaccharide synthesis protein 14L	transport/binding
1.14	0.53	0.61	0.76	0.85	0.53	0.68	0.75	0.89	0.87	0.80	MW0107	sodM	superoxide dismutase	detoxification
1.18	0.40	0.51	0.54	0.60	0.52	0.73	0.58	0.82	0.73	0.69	MW0107n	sodM	superoxide dismutase	detoxification
0.74	1.02	1.26	1.32	0.92	1.46	1.00	1.95	0.85	1.29	0.79	MW0108		hypothetical protein	
0.79	1.03	1.11	0.91	0.99	1.48	0.92	1.51	0.79	1.12	0.91	MW0109		hypothetical protein, similar to trehalose operon transcriptional repressor	RNA synthesis
0.93	1.14	1.06	1.29	1.02	1.61	1.06	1.04	1.07	1.21	0.92	MW0110	pnp	purine nucleoside phosphorylase	[illegible]
0.86	0.91	1.10	1.06	1.12	1.16	1.06	0.99	0.33	1.09	0.93	MW0110n	pnp	purine nucleoside phosphorylase	[illegible]
0.82	1.17	1.12	1.34	1.06	1.55	1.10	1.29	1.13	1.18	0.89	MW0111		hypothetical protein, similar to tetracyclin resistance protein	detoxification
0.80	1.05	1.19	1.42	0.91	2.34	0.99	1.36	1.11	1.00	0.82	MW0112	dra	deoxyribose-phosphate aldolase	[illegible]
0.76	0.96	0.81	1.17	0.83	1.15	1.09	1.33	1.17	0.89	0.70	MW0113	drm	phosphopentomutase	[illegible]
0.85	1.45	1.24	1.08	1.19	1.65	1.04	1.90	0.99	0.97	0.87	MW0114		hypothetical protein, similar to phosphonates transport permease	transport/binding
0.69	1.28	1.21	1.11	1.14	1.47	0.98	1.53	0.90	1.10	0.84	MW0115		hypothetical protein, similar to phosphonates transport permease	transport/binding
0.91	0.87	0.96	1.03	0.95	1.14	1.27	1.14	1.15	1.00	1.04	MW0116		hypothetical protein, similar to transport system protein	transport/binding
0.72	1.29	1.22	1.38	1.11	1.48	0.98	1.16	1.05	1.14	0.93	MW0117		hypothetical protein, similar to alkylphosphonate ABC tranporter	transport/binding
0.74	1.09	1.17	1.23	1.01	1.22	1.08	1.16	1.15	1.11	0.87	MW0118		hypothetical protein	
0.86	0.83	0.82	1.03	0.91	0.84	1.09	1.03	1.07	0.92	0.65	MW0119		hypothetical protein, similar to lactococcal phosphatase homologue	phosphate metabolism
0.82	1.23	1.25	1.39	1.00	1.01	0.97	1.13	1.17	1.07	0.90	MW0120		truncated replication initiator protein	DNA replication
0.80	0.91	1.07	1.44	1.02	1.06	0.93	0.99	0.92	1.04	0.82	MW0121		truncated replication initiation protein	DNA replication
0.78	1.00	1.11	1.24	0.93	0.96	0.99	1.23	0.92	1.00	0.93	MW0122		hypothetical protein, similar to transposase	transposon and IS
0.84	0.49	0.94	1.75	0.60	0.51	2.13	3.19	0.64	0.91	0.24	MW0123	adhE	alcohol-acetaldehyde dehydrogenase	carbohydrate metabolism
0.81	1.31	1.16	1.45	0.96	1.26	1.29	1.76	0.95	1.08	0.84	MW0124	capA	capsular polysaccharide synthesis enzyme Cap5A	adaptation to atypical
0.82	1.22	1.38	1.37	1.00	1.37	1.30	1.57	1.10	1.19	0.92	MW0125	capB	capsular polysaccharide synthesis enzyme Cap5B	adaptation to atypical
0.82	1.24	1.24	1.35	0.95	1.43	1.42	1.74	1.26	1.18	0.90	MW0126	capC	capsular polysaccharide synthesis enzyme Cap8C	adaptation to atypical
0.90	0.99	1.06	1.29	0.89	1.32	1.59	1.87	1.26	1.08	0.77	MW0127	capD	capsular polysaccharide synthesis enzyme Cap5D	adaptation to atypical
0.97	1.81	1.44	1.08	1.23	1.98	1.36	2.76	0.92	1.08	0.89	MW0128	capE	capsular polysaccharide synthesis enzyme Cap8E	adaptation to atypical
0.76	1.70	1.38	1.05	1.15	1.84	1.27	2.21	1.00	1.15	0.80	MW0129	capF	capsular polysaccharide synthesis enzyme Cap5F	adaptation to atypical
0.71	1.57	1.46	1.19	1.00	1.55	1.30	1.80	0.94	1.21	0.95	MW0130	capG	capsular polysaccharide synthesis enzyme Cap5G	adaptation to atypical
0.79	1.89	1.47	1.57	1.07	1.98	1.19	1.64	1.16	1.26	1.14	MW0131	cap8H	capsular polysaccharide synthesis enzyme Cap8H	adaptation to atypical
0.86	1.56	1.49	1.53	1.04	1.68	1.28	1.39	1.12	1.18	1.11	MW0132	cap8I	capsular polysaccharide synthesis enzyme Cap8I	adaptation to atypical
0.84	1.48	1.50	1.49	1.00	1.53	1.29	1.29	1.07	1.15	0.93	MW0133	cap8J	capsular polysaccharide synthesis enzyme Cap8J	adaptation to atypical
0.78	1.59	1.03	1.00	0.87	1.37	0.98	1.71	1.05	1.08	1.21	MW0134	cap8K	capsular polysaccharide synthesis enzyme Cap8K	adaptation to atypical
1.08	1.51	1.17	0.79	1.06	1.35	1.39	2.00	1.03	1.13	1.03	MW0135	capL	capsular polysaccharide synthesis enzyme Cap5L	adaptation to atypical
0.88	1.38	1.09	1.10	1.11	1.48	1.26	1.26	1.02	1.17	0.90	MW0136	capM	capsular polysaccharide synthesis enzyme Cap5M	adaptation to atypical
0.79	1.17	1.19	1.44	1.01	1.37	1.06	1.18	0.95	1.19	1.08	MW0137	capN	capsular polysaccharide synthesis enzyme Cap5N	adaptation to atypical
0.76	0.91	1.20	1.58	0.99	1.65	1.05	1.03	1.07	1.24	0.95	MW0138	capO	capsular polysaccharide synthesis enzyme Cap8O	adaptation to atypical
0.81	0.80	1.02	0.90	0.91	1.15	1.03	1.04	1.00	1.22	1.05	MW0139	capP	capsular polysaccharide synthesis enzyme Cap5P	adaptation to atypical
0.92	0.36	0.75	0.77	0.63	0.59	0.78	0.92	0.69	0.98	0.84	MW0140		conserved hypothetical protein	
0.86	0.93	1.00	1.19	0.80	1.00	0.99	1.28	0.86	1.04	1.13	MW0141		conserved hypothetical protein	
0.76	1.56	1.32	1.15	1.09	2.32	1.14	1.16	1.04	1.52	1.04	MW0142	aldA	aldehyde dehydrogenase homologue	carbohydrate metabolism
0.70	1.44	1.33	1.56	1.06	1.50	0.99	1.07	1.14	1.20	1.23	MW0143		hypothetical protein, similar to cation-efflux system membrane protein CzcD	transport/binding
0.90	0.99	1.17	0.68	0.98	1.08	1.03	1.05	1.15	1.16	1.43	MW0144		hypothetical protein	
0.82	0.53	1.02	0.68	0.73	1.09	0.99	1.07	1.05	0.99	4.51	MW0145		hypothetical protein, similar to alpha-helical coiled-coil protein SrpF	
0.80	1.46	1.30	0.94	1.14	1.77	1.10	1.49	1.03	1.10	2.29	MW0146		hypothetical protein, similar to nitrate transporter	transport/binding
0.83	1.36	1.21	1.19	1.06	1.30	0.96	1.36	0.99	1.16	2.28	MW0147		hypothetical protein, similar to membrane lipoprotein SrpL	transport/binding
0.72	1.02	1.10	1.08	1.00	1.35	1.01	1.23	0.96	1.21	3.04	MW0148		hypothetical protein, similar to probable permease of ABC transporter	transport/binding
0.79	1.03	1.24	1.30	1.10	1.46	1.03	1.01	1.19	1.18	1.90	MW0149		hypothetical protein, similar to acyl-CoA dehydrogenase family protein	aminoacid metabolism
0.97	1.58	1.01	0.89	0.99	1.15	0.94	1.05	1.32	1.08	3.03	MW0150		conserved hypothetical protein	
1.02	1.41	1.10	0.87	0.93	1.08	0.81	0.94	1.48	1.04	2.43	MW0150n		conserved hypothetical protein	
0.86	1.11	0.77	0.82	0.78	1.17	1.01	1.03	1.11	0.95	1.43	MW0151	fdh	NAD-dependent formate dehydrogenase	carbohydrate metabolism
0.97	1.29	1.12	0.75	1.05	1.52	0.87	1.30	1.09	0.93	1.09	MW0152		hypothetical protein, similar to integral membrane protein LmrP	transport/binding
1.01	0.87	0.61	0.52	0.84	0.78	0.98	1.12	0.98	0.90	0.85	MW0153		hypothetical protein, similar to surfactin synthetase	antibiotic production
0.88	0.86	1.06	0.89	0.99	1.00	0.83	0.98	0.98	0.95	1.14	MW0154		conserved hypothetical protein	
0.88	0.72	1.06	1.31	0.91	0.66	1.09	0.90	1.10	1.20	0.82	MW0155		conserved hypothetical protein	
0.78	1.07	1.08	0.86	0.95	1.00	0.77	0.96	1.21	1.01	1.20	MW0156		hypothetical protein, similar to N-acetylglutamate 5-phosphotransferase	aminoacid metabolism
0.79	1.00	0.73	0.71	0.82	0.86	0.94	1.04	0.94	0.92	1.17	MW0157	argJ	arginine biosynthesis bifunctional protein homologue	aminoacid metabolism
0.85	1.07	1.15	0.77	1.07	1.13	0.89	1.61	0.92	0.93	1.22	MW0158	argC	N-acetylglutamate gamma-semialdehyde dehydrogenase	aminoacid metabolism
0.81	0.93	0.99	0.96	1.06	1.14	0.96	1.36	0.86	1.05	1.15	MW0159		ornithine aminotransferase	aminoacid metabolism
1.11	0.69	0.77	0.97	1.15	0.55	0.67	0.57	0.77	0.90	1.95	MW0160		hypothetical protein, similar to branched-chain amino acid transport system carrier pro	aminoacid metabolism
0.70	1.19	1.04	1.01	0.98	0.92	0.85	1.26	0.92	1.05	0.83	MW0161		hypothetical protein, similar to isochorismatase	coenzyme metabolism
0.71	1.05	0.97	1.10	0.98	1.12	0.90	1.41	1.18	1.10	0.85	MW0162		hypothetical protein, similar to indole-3-pyruvate decarboxylas	carbohydrate metabolism
0.60	1.06	0.83	0.98	0.92	1.00	0.71	2.64	1.32	0.87	0.38	MW0163	glcA	TS enzyme II (EC 2.7.1.69), glucose-specific, factor IIA homologu	transport/binding
0.59	0.72	0.58	0.85	0.77	0.70	0.77	2.16	1.03	0.83	0.36	MW0163n	glcA	PTS enzyme II (EC 2.7.1.69), glucose-specific, factor IIA homologue	transport/binding
0.72	1.78	1.18	0.97	1.20	4.10	0.92	2.34	1.01	0.97	0.73	MW0164		conserved hypothetical protein	
0.83	1.50	1.15	0.97	1.13	3.56	0.96	1.73	0.98	1.09	0.73	MW0165		conserved hypothetical protein	
0.72	1.73	1.27	1.22	1.19	2.76	0.98	1.34	1.02	1.13	0.82	MW0166		hypothetical protein, similar to sucrose phosphotransferase enzyme II	transport/binding
0.83	1.40	1.31	1.16	1.01	2.90	0.96	1.42	1.17	1.04	0.84	MW0167		hypothetical protein, similar to transcription regulator	RNA synthesis
0.95	1.03	0.99	0.97	0.95	1.45	1.06	1.31	1.03	1.02	1.04	MW0168		hypothetical protein	
0.81	0.94	0.77	0.90	0.87	1.16	0.87	0.76	0.86	1.04	1.16	MW0169	hsdR	probable type I restriction enzyme restriction chain	DNA repair or modify
0.72	0.90	0.85	0.92	0.96	1.38	0.87	1.07	0.71	1.05	1.17	MW0169a	hsdR	probable type I restriction enzyme restriction chain	DNA repair or modify
1.00	1.12	1.12	0.83	1.18	1.54	0.99	1.51	0.81	0.92	1.08	MW0170		hypothetical protein	
0.88	1.17	1.10	0.93	1.03	1.44	1.00	1.50	0.94	1.04	0.90	MW0171		conserved hypothetical protein	pathogenic factor
0.92	1.28	1.26	1.13	1.09	1.32	1.04	1.21	0.88	1.14	1.14	MW0172		hypothetical protein, similar to ABC transporter ATP-binding protein	
0.82	1.45	1.30	1.21	1.05	1.41	0.92	1.10	1.21	1.08	1.04	MW0174		hypothetical protein, similar to Enterococcus faecalis plasmid pPD1 bacI	pathogenic factor
1.56	1.25	1.01	0.80	0.85	0.77	1.35	0.94	1.87	1.10	1.29	MW0175		hypothetical protein	
1.21	3.89	1.17	1.24	1.09	1.17	1.21	2.14	1.45	0.93	1.29	MW0176		hypothetical protein	
1.30	1.61	1.08	0.84	1.03	1.19	1.00	1.39	1.14	0.88	1.26	MW0177		conserved hypothetical protein	
0.90	1.65	1.25	0.93	1.02	1.21	1.02	1.53	1.19	1.06	1.43	MW0178		hypothetical protein, similar to ABC transporter ATP-binding protein	transport/binding
0.96	1.23	1.13	1.00	0.79	0.98	1.23	1.15	1.17	1.11	1.24	MW0179		hypothetical protein	
0.90	1.50	1.25	1.14	0.93	1.07	1.12	1.23	0.89	1.19	1.23	MW0179n		hypothetical protein	
1.18	1.19	0.98	0.88	0.90	0.94	0.74	1.21	1.08	0.95	1.50	MW0180		hypothetical protein	
0.88	1.13	1.32	0.91	0.95	1.20	0.98	1.10	1.02	1.19	2.05	MW0181	oppF	oligopeptide transport ATP-binding protein	transport/binding
0.74	1.24	1.30	1.04	0.95	1.30	1.06	1.25	1.04	1.14	1.54	MW0182	oB#trunca	uncated hypothetical protein, similar to oligopeptide ABC transporter permea	transport/binding
0.76	1.00	1.06	1.09	0.90	1.14	1.27	1.24	1.03	1.04	1.33	MW0183		hypothetical protein, similar to dipeptide transporter protein dppC	transport/binding
0.86	1.60	1.23	0.72	0.99	1.36	1.14	1.75	0.86	1.21	1.79	MW0184	rlp	RGD-containing lipoprotein	transport/binding
0.98	1.22	1.34	1.05	1.30	2.19	1.15	1.76	0.99	1.17	1.07	MW0185		hypothetical protein, similar to gamma-glutamyltranspeptidase precursor	aminoacid metabolism
0.73	1.05	1.25	1.21	0.92	1.04	0.96	1.21	1.01	1.21	1.05	MW0186		hypothetical protein	
0.86	0.93	1.35	1.52	1.07	1.16	1.12	0.87	1.17	1.41	1.06	MW0187		NAD(P)H dehydrogenase homologue	membrane bioenergetics
0.91	1.89	1.37	1.20	1.44	1.86	0.91	1.85	0.87	1.09	1.16	MW0188		hypothetical protein, similar to lysostaphin precursor	cell wall
0.74	0.97	1.12	0.81	1.05	1.07	0.87	1.19	0.98	1.53	1.08	MW0189	msmX	multiple sugar-binding transport ATP-binding protein	transport/binding
0.47	1.28	1.17	1.04	0.95	1.45	1.20	1.46	0.83	1.58	0.90	MW0190a		hypothetical protein, similar to maltose/maltodextrin-binding protein	transport/binding
0.72	1.85	1.28	1.29	1.19	1.48	1.18	1.69	1.01	1.47	0.96	MW0190b		hypothetical protein, similar to maltose/maltodextrin-binding protein	transport/binding
0.62	1.22	1.39	1.13	1.12	1.66	1.05	1.63	0.89	1.48	0.87	MW0191		maltose/maltodextrin transport permease homologue	transport/binding
0.55	1.27	1.38	1.18	0.95	1.46	0.99	1.51	0.89	1.40	0.96	MW0192		maltose/maltodextrin transport permease homologu	transport/binding
0.62	1.15	1.49	1.67	1.20	1.53	1.03	1.01	1.07	1.36	0.76	MW0193		hypothetical protein, similar to NADH-dependent dehydrogenase	membrane bioenergetics
0.62	1.04	1.38	1.41	1.10	1.38	1.14	1.15	1.00	1.35	0.87	MW0194		hypothetical protein, similar to NADH-dependent dehydrogenase	membrane bioenergetics

0.61	1.05	1.24	1.00	1.03	1.38	0.94	1.30	0.99	1.25	0.91	MW0195		conserved hypothetical protein	
0.85	0.98	1.04	0.67	1.04	0.96	0.87	1.10	0.89	1.15	1.14	MW0196		conserved hypothetical protein	
0.66	1.53	1.65	1.21	1.06	1.75	1.07	1.43	1.11	1.32	1.18	MW0197	uhpT	hexose phosphate transport protein	transport/binding
0.81	1.44	1.47	1.23	1.00	1.67	1.06	1.44	1.31	1.21	1.20	MW0198		hypothetical protein, similar to two-component response regulator	RNA synthesis
0.89	1.66	1.31	0.80	1.18	1.42	1.08	1.72	0.91	0.98	1.08	MW0199		hypothetical protein, similar to two-component sensor histidine kinase	sensor
0.85	1.29	1.53	1.08	1.32	2.59	1.13	2.08	1.03	1.05	1.04	MW0200		hypothetical protein, similar to periplasmic-iron-binding protein BitC	transport/binding
1.11	4.12	3.44	2.07	2.12	15.38	3.00	8.99	1.65	1.67	0.68	MW0201	pflB	formate acetyltransferase	carbohydrate metabolism
1.20	2.93	3.33	2.69	2.16	15.10	2.79	7.05	2.04	1.50	0.60	MW0202	pflA	formate acetyltransferase activating enzyme	carbohydrate metabolism
0.99	1.61	1.62	1.36	1.27	2.53	1.41	1.85	1.47	1.17	0.91	MW0203		hypothetical protein	
0.82	1.28	1.50	1.04	1.13	1.91	1.09	1.25	1.21	1.15	1.16	MW0204		hypothetical protein, similar to glycerophosphodiester phosphodiesterase	lipid metabolism
1.11	1.04	0.85	0.85	0.84	1.15	0.80	1.08	0.99	0.92	1.29	MW0205		hypothetical protein	
1.21	1.06	1.05	0.54	1.14	1.63	0.92	1.27	0.71	0.90	1.34	MW0206	coa	staphylocoagulase precursor	pathogenic factor
0.77	1.33	1.39	0.77	1.27	1.57	1.16	1.53	0.97	1.12	0.90	MW0207		acetyl-CoA acetyltransferase homologue	carbohydrate metabolism
0.64	1.17	1.42	0.88	1.08	1.65	1.05	1.40	0.93	1.20	0.93	MW0208		hypothetical protein, similar to 3-hydroxyacyl-CoA dehydrogenase	lipid metabolism
0.84	1.12	1.50	1.29	1.29	1.65	1.12	1.13	1.22	1.25	0.81	MW0209		hypothetical protein, similar to glutaryl-CoA dehydrogenase	lipid metabolism
0.71	1.17	1.45	1.40	1.11	1.42	1.07	1.16	1.16	1.19	0.87	MW0210		hypothetical protein, similar to acid-CoA ligase	lipid metabolism
0.74	1.36	1.30	1.28	1.00	1.36	1.08	1.31	1.32	1.19	1.08	MW0211		conserved hypothetical protein	
0.72	1.16	1.12	1.11	0.93	1.16	1.17	1.24	1.00	1.06	0.97	MW0211n		conserved hypothetical protein	
1.13	1.49	1.24	0.94	1.35	1.35	0.93	1.60	0.99	0.89	2.63	MW0212		hypothetical protein	
1.14	1.49	1.27	1.36	1.26	0.97	1.07	2.05	1.02	0.98	0.58	MW0213		hypothetical protein, similar to nickel ABC transporter nickel-binding protein	transport/binding
1.16	1.03	1.13	1.28	1.08	0.90	0.98	1.43	0.96	0.97	0.53	MW0214		conserved hypothetical protein	
1.40	0.86	0.93	1.05	0.88	0.66	1.55	1.22	1.22	0.96	0.58	MW0215		hypothetical protein	
1.35	0.89	1.09	1.42	1.07	0.83	0.97	1.08	1.26	0.97	0.53	MW0215n		hypothetical protein	
1.02	1.03	1.27	1.89	1.05	1.12	0.97	1.38	1.05	0.93	0.41	MW0216		hypothetical protein, similar to flavohemoprotein	miscellaneous
1.04	0.72	1.28	1.08	1.14	0.38	1.26	0.49	0.95	1.50	1.36	MW0217	lctE	L-lactate dehydrogenase	carbohydrate metabolism
0.97	0.60	0.70	0.65	0.75	0.59	1.07	2.48	0.76	0.92	0.91	MW0218		PTS enzyme (EC 2.7.1.69), maltose- and glucose-specific, factor II hom	transport/binding
1.21	1.24	1.28	1.05	1.38	1.13	1.17	3.68	1.01	1.01	1.16	MW0218n		PTS enzyme (EC 2.7.1.69), maltose- and glucose-specific, factor II homologu	transport/binding
0.97	1.07	1.19	0.80	1.21	1.16	1.02	1.81	0.78	1.11	1.00	MW0219		hypothetical protein, similar to inosine-uridine preferring nucleoside hydrolase	nucleic acid metabolism
0.74	1.17	1.17	0.94	1.02	1.27	0.95	1.48	0.86	1.14	0.98	MW0220		hypothetical protein, similar to BglG antiterminator family	RNA synthesis
0.97	1.28	0.90	1.28	0.69	1.26	0.87	0.88	1.04	1.08	1.09	MW0221		hypothetical protein, similar to PTS fructose-specific enzyme IIBC component	transport/binding
0.84	1.13	1.21	0.86	1.28	1.40	0.96	1.76	0.84	1.03	1.02	MW0221a		hypothetical protein, similar to PTS fructose-specific enzyme IIBC component	transport/binding
0.96	1.16	1.09	1.07	1.03	1.00	0.94	1.16	1.16	1.10	1.09	MW0222		hypothetical protein, similar to PTS, galactitol-specific IIB component	transport/binding
0.92	1.08	1.16	1.06	0.99	1.09	1.05	1.08	1.12	1.07	0.91	MW0223	gatC	probable PTS galactitol-specific enzyme IIC component	transport/binding
1.10	1.07	1.17	0.87	1.63	1.33	1.14	1.80	0.69	0.94	1.02	MW0224		sorbitol dehydrogenase	carbohydrate metabolism
0.99	1.26	0.84	0.88	0.00	0.88	1.33	1.13	0.78	0.84	1.22	MW0225		hypothetical protein	
0.93	0.95	1.07	0.92	1.18	0.94	1.06	1.85	0.73	1.02	0.89	MW0225n		hypothetical protein	
0.83	1.05	1.24	1.16	1.20	1.20	1.03	1.15	0.90	1.12	0.94	MW0226		sorbitol dehydrogenase homologue	carbohydrate metabolism
1.14	0.96	1.07	1.10	0.85	0.99	0.95	1.07	0.86	1.02	1.23	MW0227		hypothetical protein, similar to 4-diphosphocytidyl-2C-methyl-D-erythritol synth	coenzyme metabolism
1.12	0.75	0.76	0.76	0.83	0.92	1.04	0.96	0.99	0.75	1.19	MW0228		hypothetical protein, similar to xylitol dehydrogenase	carbohydrate metabolism
1.21	0.90	1.03	0.96	0.90	0.77	1.05	0.94	1.00	1.01	1.33	MW0228n		hypothetical protein, similar to xylitol dehydrogenase	carbohydrate metabolism
0.86	0.70	0.79	0.71	0.79	0.67	0.91	0.74	0.89	0.89	1.43	MW0229		hypothetical protein, similar to teichoic acid biosynthesis protein B	cell wall
1.34	1.01	0.98	0.79	1.35	1.12	0.99	1.52	0.70	0.81	0.99	MW0230		hypothetical protein, similar to teichoic acid biosynthesis protein F	cell wall
1.35	0.79	0.84	0.82	0.85	0.68	0.89	1.16	0.69	0.77	0.73	MW0231		conserved hypotheticl protein	
1.39	0.46	0.69	0.92	0.72	0.52	1.16	0.81	1.05	0.59	0.74	MW0232		hypotheticl protein, similar to D-xylulose reductase	carbohydrate metabolism
1.16	0.84	0.87	1.01	0.98	0.69	1.05	0.97	0.81	0.87	0.80	MW0232n		hypotheticl protein, similar to D-xylulose reductase	carbohydrate metabolism
1.07	0.81	1.04	1.03	0.95	0.73	1.07	0.99	0.92	0.87	0.85	MW0233		hypothetical protein, similar to teichoic acid biosynthesis protein B	cell wall
0.91	0.93	1.03	1.09	1.05	0.79	0.95	0.86	0.93	1.08	0.86	MW0234		hypothetical protein, similar to beta-glycosyltransferase	cell wall
0.98	0.63	1.03	1.14	1.00	1.71	1.19	1.00	0.97	0.88	0.78	MW0235	scdA	cell division and morphogenesis-related protein	cell division
1.14	1.05	0.94	0.82	1.19	0.80	1.24	1.18	0.86	0.81	0.83	MW0236	lytS	two-component sensor histidine kinase	sensor
1.30	0.82	0.96	0.96	1.29	0.73	1.03	0.89	1.01	0.86	0.74	MW0237	lytR	two-component response regulator	RNA synthesis
0.74	1.09	0.91	0.93	0.72	0.68	0.98	0.64	0.84	1.25	0.59	MW0238	lrgA	holin-like protein LrgA	phage-related
0.72	1.26	0.98	1.19	0.94	0.70	1.15	0.51	0.98	1.31	0.61	MW0239	lrgB	holin-like protein LrgB	phage-related
1.05	1.11	1.06	1.14	0.98	0.84	0.91	0.70	0.94	1.04	1.11	MW0240		hypothetical protein, similar to transcription regulator GntR family	RNA synthesis
1.00	1.06	0.99	1.00	0.93	0.95	1.26	0.95	1.25	1.09	0.88	MW0241		hypothetical protein, similar to PTS beta-glucoside-specific enzyme II, ABC compo	transport/binding
0.98	1.04	0.92	0.79	0.98	0.92	1.03	0.83	1.05	1.05	1.01	MW0242	bglA	6-phospho-beta-glucosidase	carbohydrate metabolism
1.20	0.88	1.10	0.89	1.14	1.00	1.15	1.56	1.01	1.02	1.28	MW0243		conserved hypothetical protein	
0.81	1.24	1.24	0.96	1.10	1.14	0.95	1.17	0.87	1.08	1.04	MW0244	rbsK	probable ribokinase	carbohydrate metabolism
0.85	1.03	1.15	0.95	1.04	1.06	0.95	1.06	0.94	1.13	1.08	MW0245	rbsD	ribose permease	transport/binding
0.81	0.83	0.85	0.72	0.84	0.90	1.01	0.99	1.07	0.84	0.84	MW0246		hypothetical protein, similar to ribose transporter RbsU	transport/binding
0.74	0.83	1.25	1.25	1.14	1.33	1.03	0.85	1.08	1.21	0.94	MW0247		hypothetical protein, similar to rbs operon repressor RbsR	RNA synthesis
1.01	0.88	0.94	1.53	1.05	0.80	0.76	0.81	0.98	1.12	1.36	MW0248		truncated NADH dehydrogenase subunit	membrane bioenergetics
0.74	1.29	1.46	1.87	1.17	1.46	0.95	1.02	1.36	1.26	0.86	MW0250		hypothetical protein, similar to proton antiporter efflux pump	transport/binding
1.12	1.12	1.30	0.89	1.32	1.63	1.13	1.58	1.02	0.95	0.97	MW0251		hypothetical protein, similar to penicillin amidase (EC 3.5.1.11) V	detoxification
0.81	0.99	1.05	0.64	1.06	1.15	0.89	1.31	0.91	0.97	0.89	MW0252	lytM	peptidoglycan hydrolase	cell wall
0.74	1.10	1.17	0.94	0.97	1.15	0.98	1.16	0.86	1.07	0.89	MW0253		conserved hypothetical protein	
0.87	1.02	1.23	1.03	1.17	1.28	0.96	1.10	1.07	1.10	0.78	MW0254		hypothetical protein	
0.87	0.81	1.04	0.99	0.95	1.01	0.89	0.95	1.05	0.96	0.81	MW0255		hypothetical protein	
0.97	0.71	0.78	0.79	0.96	0.74	0.90	0.99	0.96	0.92	0.59	MW0256		hypothetical protein	
1.30	0.94	1.31	0.62	1.27	1.34	1.06	1.69	1.03	0.87	0.73	MW0257	ssaA	hypothetical protein, similar to secretory antigen precursor SsaA	pathogenic factor
1.32	0.72	1.59	0.86	0.86	0.94	0.99	2.15	1.21	1.00	0.34	MW0258		conserved hypothetical protein	
0.87	1.24	1.16	0.67	0.93	1.38	0.84	1.35	0.98	0.98	0.85	MW0259		hypothetical protein, similar to transmembrane protein Tmp7	transport/binding
1.13	0.97	1.35	0.97	1.20	1.27	0.95	1.18	1.18	1.02	0.95	MW0260		hypothetical protein	
1.11	1.01	1.18	1.01	1.10	1.02	1.18	1.22	1.16	1.01	1.07	MW0261		conserved hypothetical protein	
1.03	1.15	0.92	0.91	0.99	1.31	1.00	1.43	1.22	0.99	0.90	MW0262		conserved hypothetical protein	
1.21	1.32	1.38	0.66	1.13	1.84	1.08	2.16	1.00	1.09	0.91	MW0263		conserved hypothetical protein, similar to diarrheal toxin	pathogenic factor
1.41	1.34	1.34	0.86	1.40	1.45	1.11	1.94	0.95	0.94	0.95	MW0264		hypothetical protein	
1.27	1.10	1.30	0.81	1.19	1.41	1.15	1.64	0.94	1.05	0.88	MW0265		hypothetical protein	
1.04	1.29	1.33	0.99	1.05	1.26	0.96	1.44	0.97	1.08	1.00	MW0266		hypothetical protein	
1.22	1.08	1.35	1.02	1.09	1.33	1.14	1.34	1.11	1.26	1.00	MW0267		hypothetical protein	
1.14	1.08	1.10	1.06	0.89	0.97	1.21	1.14	1.17	1.02	0.98	MW0269		conserved hypothetical protein	
1.09	1.92	1.46	1.02	1.11	1.63	1.07	2.15	1.01	0.91	1.13	MW0270		hypothetical protein	
0.99	1.43	1.36	0.97	1.10	1.49	1.06	1.92	0.95	1.04	1.11	MW0271		hypothetical protein	
0.93	0.86	0.82	0.78	0.94	0.84	0.94	1.00	1.02	0.79	1.07	MW0273		hypothetical protein	
1.13	1.13	0.78	0.76	#NUM!	0.95	1.14	1.20	0.91	0.87	1.23	MW0273n		conserved hypothetical protein	
1.12	1.06	0.96	0.93	1.20	1.03	1.32	1.16	1.31	0.85	1.16	MW0274		conserved hypothetical protein	
1.09	1.56	0.95	0.95	0.80	0.96	1.16	1.15	0.94	0.84	1.14	MW0275		hypothetical protein	
1.05	0.94	0.88	1.11	0.87	0.91	1.05	0.86	1.16	0.94	1.12	MW0275n		conserved hypothetical protein	
0.99	1.22	1.01	0.89	1.11	0.91	1.35	1.27	1.28	0.83	0.96	MW0276		hypothetical protein	
1.19	1.16	1.14	0.79	1.29	1.05	1.08	1.51	0.77	1.00	1.02	MW0279		conserved hypothetical protein	
0.92	1.07	1.15	1.06	1.18	0.95	1.11	1.14	0.93	0.95	1.03	MW0280		hypothetical protein	
1.03	1.08	1.20	1.08	1.02	0.93	1.04	1.00	0.98	1.11	1.09	MW0281		hypothetical protein	
0.98	0.73	0.87	0.84	0.90	0.57	1.30	0.52	0.83	0.93	0.88	MW0282		hypothetical protein, similar to formate transporter NirC	transport/binding
1.16	1.23	1.29	0.81	1.00	0.69	1.14	0.84	1.45	1.14	1.10	MW0283		hypothetical protein, similar to branched-chain amino acid uptake carrier	transport/binding
1.08	0.71	0.93	0.80	0.83	0.73	1.17	1.43	1.02	0.83	1.15	MW0284		hypothetical protein, similar to outer membrane protein precursor	transport/binding
1.36	1.20	1.21	0.96	1.43	2.22	1.60	2.13	0.78	0.90	0.79	MW0285		conserved hypothetical protein	
0.98	0.81	0.88	1.01	0.80	1.36	1.87	1.14	1.18	0.84	0.70	MW0286		hypothetical protein, similar to ABC transporter ATP-binding protein	transport/binding
0.82	0.96	1.24	1.44	1.31	1.02	1.02	0.80	1.07	1.10	1.60	MW0287		hypothetical protein, similar to regulatory protein PfoR	RNA synthesis

0.78	1.09	1.28	1.25	1.24	1.29	0.96	1.20	0.94	1.25	0.91	MW0288		hypothetical protein, similar to carbohydrate kinase, PfkB family	carbohydrate metabolism
0.76	1.53	1.49	1.16	1.10	1.41	1.09	1.29	1.12	1.32	0.92	MW0289		conserved hypothetical protein	
0.79	0.84	1.17	0.76	0.89	1.29	1.34	1.41	0.92	1.26	0.86	MW0290		probable pyrimidine nucleoside transport protein	transport/binding
0.76	1.41	1.17	0.98	1.05	1.51	1.11	2.23	0.98	1.21	0.98	MW0291		hypothetical protein, similar to sodium-coupled permease	transport/binding
0.68	1.37	1.33	0.89	1.12	1.33	1.07	1.81	1.13	1.34	0.93	MW0292	nanA	N-acetylneuraminate lyase subunit	carbohydrate metabolism
0.69	1.19	1.22	1.43	1.17	1.29	0.90	1.26	1.13	1.29	0.99	MW0293		hypothetical protein, similar to glucokinase	carbohydrate metabolism
0.84	1.02	1.12	1.17	1.04	1.11	0.95	0.99	1.04	1.26	1.36	MW0294		conserved hypothetical protein	
0.84	1.21	1.21	1.08	1.04	1.12	1.05	1.30	1.24	1.14	1.15	MW0295		conserved hypothetical protein	
0.85	0.77	0.88	0.51	0.72	0.83	0.92	1.12	0.72	1.00	1.01	MW0296		conserved hypothetical protein	
0.76	0.98	0.83	1.05	1.17	0.85	0.73	0.53	0.96	1.05	2.01	MW0297	geh	glycerol ester hydrolase	pathogenic factor
0.76	1.15	0.93	1.09	0.97	0.90	0.79	0.79	1.25	0.94	1.45	MW0298		hypothetical protein	
0.57	0.94	1.07	1.23	1.06	0.97	0.94	0.91	0.93	1.14	1.31	MW0299		hypothetical protein, similar to trimethylamine dehydrogenase	carbohydrate metabolism
0.72	0.96	1.05	1.26	1.05	1.19	0.90	0.90	1.00	1.11	0.94	MW0300		hypothetical protein, similar to alkanal monooxygenase alpha chain	detoxification
0.90	0.84	0.94	0.80	1.07	1.00	0.94	1.12	1.08	1.00	1.11	MW0301		hypothetical protein, similar to glycine cleavage system H protein	amino acid metabolism
0.80	0.68	0.87	0.60	0.81	0.94	0.98	1.13	0.94	0.90	0.93	MW0302		conserved hypothetical protein	
0.93	1.49	1.17	1.22	1.26	1.67	1.09	1.49	1.04	0.94	1.04	MW0303		hypothetical protein	
0.87	1.01	0.66	0.99	0.83	1.12	1.11	1.03	0.86	0.82	1.01	MW0304		hypothetical protein, similar to lipoate-protein ligase	protein modification
0.75	0.87	1.07	0.89	1.05	1.15	1.03	1.38	0.85	1.09	1.01	MW0305		hypothetical protein, similar to dihydroflavonol-4-reductase	coenzyme metabolism
0.74	1.00	0.96	0.91	0.95	1.14	1.26	1.22	0.94	0.90	0.86	MW0306		hypothetical protein, similar to transport protein SgaT	transport/binding
0.79	1.07	1.12	1.05	1.16	1.24	0.98	1.15	1.02	1.16	1.06	MW0307		conserved hypothetical protein	
0.82	1.00	1.12	1.17	1.00	1.29	1.06	1.03	0.98	1.17	0.73	MW0308		hypothetical protein, similar to PTS fructose-specific enzyme IIBC component	transport/binding
0.67	1.18	1.14	0.96	0.92	1.36	0.90	1.40	1.04	1.30	1.19	MW0309		hypothetical protein, similar to transcription antiterminator BglG family	RNA synthesis
0.82	0.82	1.10	0.86	0.72	0.70	1.19	0.84	0.83	1.08	1.15	MW0310		hypothetical protein, similar to transcription regulator	RNA synthesis
0.74	1.26	1.32	0.82	1.15	1.59	1.04	1.53	0.87	1.11	1.11	MW0311	svrA	conserved hypothetical protein	RNA synthesis
0.84	1.09	1.18	0.89	1.05	1.23	1.04	1.43	0.81	1.16	0.95	MW0312		hypothetical protein	
0.78	1.19	1.26	0.98	1.08	1.41	1.20	1.32	0.91	1.29	0.95	MW0313	glpT	glycerol-3-phosphate transporter	transport/binding
0.84	1.05	1.19	1.07	0.99	2.00	1.08	1.02	1.08	1.21	0.97	MW0314		conserved hypothetical protein	
0.87	1.01	1.14	1.16	0.99	1.51	1.06	1.15	1.16	1.17	0.98	MW0315		conserved hypothetical protein	
0.83	1.10	0.86	1.04	0.74	1.26	1.11	0.97	0.96	0.94	0.87	MW0316		hypothetical protein, similar to NADH-dependent FMN reductase	coenzyme metabolism
0.95	1.04	1.10	1.02	1.07	1.41	1.03	1.50	0.82	0.94	1.15	MW0317		conserved hypothetical protein	
0.89	0.61	0.85	0.85	0.93	0.88	0.91	1.05	0.61	0.99	0.88	MW0318		hypothetical protein, similar to ribosomal-protein-serine N-acetyltransferase	protein modification
0.83	1.08	1.10	1.09	1.03	1.12	0.92	0.96	0.63	1.06	1.02	MW0319		conserved hypothetical protein	
0.96	0.86	1.24	1.11	1.07	1.26	1.04	0.93	1.04	1.14	0.84	MW0320		conserved hypothetical protein	
#NUM!	#NUM!	0.94	1.29	1.08	0.86	1.26	#NUM!	1.22	1.38	0.91	MW0321		conserved hypothetical protein	
0.80	0.81	0.87	0.67	0.92	0.75	1.04	0.69	1.05	0.81	1.90	MW0322		conserved hypothetical protein	
1.04	0.92	0.89	0.96	0.89	0.78	1.17	0.75	1.00	0.92	1.85	MW0322n		conserved hypothetical protein	
1.07	0.91	0.95	0.91	1.00	0.92	0.84	1.01	0.76	0.94	2.59	MW0323		conserved hypothetical protein	
1.00	1.20	0.87	0.81	0.99	1.11	0.89	1.06	0.66	1.02	1.78	MW0324		hypothetical protein	
1.18	1.02	0.93	0.70	1.24	1.19	0.63	1.12	0.82	0.98	1.28	MW0325		hypothetical protein, similar to transcriptional repressor	RNA synthesis
1.04	0.86	1.00	0.99	1.00	1.03	1.01	0.95	0.03	1.04	1.10	MW0325n		hypothetical protein, similar to transcriptional repressor	RNA synthesis
0.92	1.16	1.07	1.10	1.11	1.16	0.86	0.91	0.99	1.03	1.11	MW0327		hypothetical protein, similar to ABC transporter ATP-binding protein	transport/binding
0.97	1.00	0.97	1.14	0.95	0.97	0.86	0.93	1.16	0.98	1.26	MW0328		conserved hypothetical protein	
0.81	0.69	0.77	0.94	0.63	0.83	0.85	1.00	0.91	0.94	1.61	MW0329		hypothetical protein, similar to low temperature requirement A protein	
1.07	0.97	1.16	0.97	1.19	1.59	0.96	1.93	0.74	0.91	0.93	MW0330		acetyl-CoA C-acetyltransferase homologue	carbohydrate metabolism
0.82	0.98	0.98	0.70	1.00	0.96	0.81	1.32	0.71	1.08	0.92	MW0331		conserved hypothetical protein	
0.91	1.05	0.88	0.74	0.68	0.77	0.77	1.02	0.67	1.10	0.96	MW0332	metE	5-methyltetrahydropteroyltriglutamate-homocystei ne methyltransferase	amino acid metabolism
0.98	0.67	0.74	0.57	0.58	0.60	1.04	0.85	0.72	0.88	0.77	MW0333		conserved hypothetical protein	
0.88	1.16	1.25	0.92	0.94	0.97	0.91	0.99	0.94	1.08	0.87	MW0334		hypothetical protein, similar to cystathionine beta-lyase	amino acid metabolism
1.00	1.07	1.05	0.86	0.82	0.78	1.07	0.96	0.97	1.07	1.04	MW0335		hypothetical protein, similar to cystathionine gamma-synthase	amino acid metabolism
1.13	0.80	0.92	0.78	0.85	0.74	1.18	0.96	0.99	0.95	0.92	MW0336		hypothetical protein, similar to transcription terminator	RNA synthesis
1.33	1.22	0.94	0.79	1.24	1.13	0.94	1.19	0.80	0.78	1.04	MW0337		conserved hypothetical protein	
1.35	0.92	0.82	0.65	1.14	0.98	0.86	1.14	0.92	0.81	0.92	MW0338		conserved hypothetical protein	
1.36	0.99	0.99	0.93	1.09	0.87	1.15	1.08	0.78	0.92	0.86	MW0338n		conserved hypothetical protein	
1.14	0.88	1.00	0.95	0.99	0.78	1.01	0.93	0.77	1.12	0.94	MW0339		hypothetical protein, similar to GTP-binding protein	
1.22	0.97	0.99	0.96	0.85	0.70	1.08	0.80	0.92	1.07	0.65	MW0340		hypothetical protein	
0.82	0.86	0.91	0.75	0.81	0.28	0.81	0.56	1.03	1.02	0.58	MW0341	rpsF	30S ribosomal protein S6	protein synthesis
0.90	0.45	0.72	0.55	0.60	0.19	0.88	0.63	1.00	0.91	0.58	MW0342	ssb	single-strand DNA-binding protein of phage phi PVL	phage-related
0.88	0.88	0.78	0.76	0.83	0.30	0.60	0.52	1.08	0.90	0.53	MW0343	rpsR	30S ribosomal protein S18	protein synthesis
0.91	1.40	1.08	0.75	1.03	0.90	0.80	1.11	0.99	0.93	0.98	MW0344		hypothetical protein, similar to hypothetical protein virulence plasmid pXO1-38	
0.84	1.23	0.89	1.14	0.97	1.03	0.86	0.85	0.89	0.96	1.76	MW0345		hypothetical protein, similar to exotoxin 2	pathogenic factor
0.77	0.96	0.62	0.83	0.81	0.87	0.83	0.76	0.98	0.86	1.48	MW0346		conserved hypothetical protein	
0.85	0.95	0.92	1.19	0.87	1.02	0.92	0.76	0.91	1.01	1.06	MW0346n		conserved hypothetical protein	
2.00	1.44	0.80	0.86	0.81	1.92	3.27	1.71	1.28	1.01	1.17	MW0347		conserved hypothetical protein	
1.59	0.33	0.49	0.67	0.67	0.46	0.82	0.42	0.87	0.84	2.00	MW0348		hypothetical protein	
2.28	1.87	1.06	1.14	0.93	2.70	3.09	1.67	1.06	1.50	1.04	MW0349		conserved hypothetical protein	
0.93	1.18	0.99	0.82	0.97	0.98	1.07	0.96	0.82	1.06	0.95	MW0350		hypothetical protein	
0.94	0.98	1.03	1.15	1.08	1.01	1.01	0.94	0.97	1.08	1.15	MW0351		truncated hypothetical protein, similar to phosphoglycerate mutase; Gpm3p	carbohydrate metabolism
1.17	0.93	0.93	1.07	0.91	0.85	0.85	0.72	1.13	1.04	0.90	MW0352		conserved hypothetical protein	
1.09	1.14	1.05	0.96	1.04	1.05	0.99	1.84	0.66	1.00	0.99	MW0353		hypothetical protein	
1.10	0.81	0.89	0.79	0.83	0.83	0.84	0.95	1.14	1.01	1.13	MW0354		hypothetical protein	
1.43	0.96	0.95	0.94	0.98	0.97	1.16	1.56	0.83	1.06	1.21	MW0355		hypothetical protein	
1.08	1.03	0.93	0.91	1.04	1.12	0.82	1.07	0.95	0.90	0.93	MW0355n		hypothetical protein	
0.84	1.35	1.31	1.50	1.05	1.58	1.37	2.65	0.96	0.90	0.72	MW0356	ahpF	alkyl hydroperoxide reductase subunit F	membrane bioenergetics
0.75	0.76	1.05	1.28	0.85	1.29	1.19	1.92	0.85	0.83	0.57	MW0357	ahpC	alkyl hydroperoxide reductase subunit C	membrane bioenergetics
0.91	0.90	1.16	1.01	1.15	1.08	0.93	1.11	1.01	1.11	1.50	MW0358		hypothetical protein, similar to nitro/flavin reductase	membrane bioenergetics
0.90	1.04	1.24	1.00	1.13	1.12	1.00	0.99	1.15	1.21	8.26	MW0359		hypothetical protein, similar to proton/sodium-glutamate symport protein	transport/binding
1.21	1.03	1.00	1.00	1.22	1.21	1.08	1.11	0.93	0.97	1.34	MW0360		hypothetical protein	
1.01	0.69	0.62	0.86	0.71	0.60	1.07	0.67	0.81	0.85	0.78	MW0361		conserved hypothetical protein	
1.16	0.53	0.84	0.63	0.95	0.67	0.96	0.78	0.62	0.82	0.83	MW0362		hypothetical protein	
1.19	0.86	0.98	0.75	0.87	1.60	1.25	0.94	0.78	1.05	1.12	MW0363		hypothetical protein	
0.64	0.48	0.52	0.56	0.89	0.25	0.45	0.52	0.55	0.62	6.58	MW0364	xprT	xanthine phosphoribosyltransferase	nucleic acid metabolism
0.59	0.51	0.62	0.56	0.97	0.40	0.59	0.57	0.57	0.79	6.37	MW0365	pbuX	xanthine permease	transport/binding
0.71	0.50	0.58	0.58	0.96	0.32	0.56	0.43	0.58	0.78	3.66	MW0366	guaB	inositol-monophosphate dehydrogenase	nucleic acid metabolism
0.79	0.45	0.53	0.54	0.93	0.16	0.61	0.40	0.62	0.84	4.37	MW0367	guaA	GMP synthase(quaA)	nucleic acid metabolism
1.49	0.96	1.35	1.05	1.34	1.10	0.93	0.83	1.00	0.90	1.51	MW0368		hypothetical protein, similar to AbiD1,(Genomic island nu Sa alpha2)	
1.79	1.11	1.10	1.01	1.10	1.04	0.85	1.26	1.02	0.86	1.06	MW0369		hypothetical protein (Genomic island nu Sa alpha2)	
1.29	1.02	0.99	1.07	0.91	0.76	0.78	0.71	1.16	0.87	1.12	MW0370		hypothetical protein (Genomic island nu Sa alpha2)	
1.27	0.82	1.01	1.18	1.04	1.01	0.90	0.56	1.46	1.00	1.26	MW0371		hypothetical protein (Genomic island nu Sa alpha2)	
1.41	1.11	1.05	0.97	0.97	0.95	0.90	0.92	1.55	0.98	1.06	MW0372		hypothetical protein (Genomic island nu Sa alpha2)	
1.36	0.79	1.02	1.06	1.16	1.04	0.93	1.01	1.11	0.98	0.88	MW0373		hypothetical protein (Genomic island nu Sa alpha2)	
1.26	0.87	0.89	0.77	0.98	0.72	0.88	0.79	0.95	0.96	0.91	MW0374		hypothetical protein (Genomic island nu Sa alpha2)	
1.43	0.85	0.55	0.80	0.97	0.28	0.85	1.19	1.10	0.85	1.44	MW0374a		hypothetical protein (Genomic island nu Sa alpha2)	
1.18	1.21	0.91	0.79	1.24	1.06	0.82	1.14	1.05	0.87	1.29	MW0375		hypothetical protein (Genomic island nu Sa alpha2)	
1.24	1.09	1.02	0.87	1.16	1.02	1.03	1.05	0.73	1.00	1.08	MW0376		hypothetical protein (Genomic island nu Sa alpha2)	
0.96	1.21	1.07	1.08	1.02	1.01	1.09	1.12	0.00	1.00	1.06	MW0376n		hypothetical protein	
1.17	1.26	0.98	0.95	1.04	1.03	0.48	0.81	0.99	1.03	1.61	MW0377		conserved hypothetical protein (Genomic island nu Sa alpha2)	
0.96	1.17	0.99	0.95	1.20	1.25	0.77	0.87	1.03	1.01	1.12	MW0378		conserved hypothetical protein (Genomic island nu Sa alpha2)	

1.03	1.07	1.15	1.06	0.96	1.16	0.97	1.14	1.04	1.19	1.14	MW0380		conserved hypothetical protein	
0.95	1.11	1.24	0.99	1.03	1.15	0.98	1.05	1.19	1.07	0.94	MW0381		conserved hypothetical protein	
0.81	1.19	1.02	1.19	1.04	1.08	0.91	1.04	1.14	0.98	1.27	MW0382	set16	exotoxin homolog	pathogenic factor
0.68	1.88	1.42	1.08	1.40	1.54	0.84	1.33	1.11	1.10	1.03	MW0383	set17	exotoxin homolog	pathogenic factor
1.07	0.83	1.18	1.23	1.12	1.15	1.07	0.75	1.02	1.24	0.88	MW0385	set19	exotoxin homolog	pathogenic factor
0.90	1.37	1.28	1.00	1.30	1.45	1.03	2.07	0.58	1.09	1.03	MW0387	set21	exotoxin homolog [Genomic island nu Sa alpha2]	pathogenic factor
0.77	1.30	1.29	0.97	0.99	1.21	0.99	1.32	1.00	1.14	0.97	MW0390	set24	exotoxin homolog [Genomic island nu Sa alpha2]	pathogenic factor
0.73	1.27	1.35	1.08	1.18	1.52	0.96	1.32	1.02	1.14	1.17	MW0391	set25	exotoxin homolog [Genomic island nu Sa alpha2]	pathogenic factor
1.18	0.85	0.88	0.86	0.99	0.77	0.86	1.15	0.87	1.07	1.25	MW0393	hsdS	probable specificity determinant HsdS	DNA repair or modify
0.90	1.32	1.20	1.34	1.15	1.16	0.90	1.19	0.75	1.16	0.33	MW0394		exotoxin homolog [Genomic island nu Sa alpha2]	pathogenic factor
1.04	0.66	0.97	0.77	0.96	0.80	1.12	1.35	0.97	1.01	0.31	MW0395a		hypothetical protein	
1.45	0.70	0.88	0.70	1.23	0.84	0.89	1.47	0.70	0.95	0.79	MW0395b		hypothetical protein	
0.94	1.12	1.20	1.08	1.07	1.20	1.03	1.29	0.93	1.11	0.95	MW0397	lpl10	hypothetical protein (Genomic island nu Sa alpha2)	
0.95	1.04	1.12	1.52	0.92	0.92	1.35	1.10	0.78	1.12	0.86	MW0397n	lpl2	hypothetical protein	
0.98	1.10	1.15	1.42	1.04	0.95	0.86	1.27	0.88	1.07	1.04	MW0398	lpl11	hypothetical protein (Genomic island nu Sa alpha2)	
0.98	0.86	0.88	1.12	0.96	0.91	0.92	0.94	0.98	1.04	0.99	MW0399	lpl12	hypothetical protein (Genomic island nu Sa alpha2)	
1.09	0.95	1.14	0.83	1.05	1.17	1.08	1.28	1.02	0.98	0.97	MW0399n	lpl6	hypothetical protein	
0.72	1.07	1.18	0.95	1.07	0.86	0.92	1.11	1.06	1.00	0.89	MW0400	lpl13	hypothetical protein (Genomic island nu Sa alpha2)	
1.16	0.96	1.08	1.15	1.01	1.12	0.99	1.40	1.24	1.12	0.94	MW0401	lpl14	hypothetical protein (Genomic island nu Sa alpha2)	
1.03	1.01	0.90	0.98	0.99	0.95	0.85	1.32	0.94	0.98	0.80	MW0401n	lpl9	hypothetical protein	
1.12	0.92	0.92	0.60	0.97	0.84	1.07	1.49	0.90	1.08	0.54	MW0402		hypothetical protein	
1.22	1.03	1.28	0.95	1.13	1.15	1.07	1.53	1.09	1.00	0.69	MW0403		conserved hypothetical protein	
1.09	1.30	1.41	1.16	1.19	1.29	1.02	1.19	1.14	1.03	0.70	MW0404		hypothetical protein	
1.08	1.20	1.30	1.07	1.18	1.47	1.00	1.15	1.14	1.07	0.59	MW0405		hypothetical protein	
1.19	1.07	0.95	1.08	0.89	1.05	1.07	1.03	1.13	0.97	0.72	MW0405n		hypothetical protein	
0.89	1.56	1.62	1.23	1.33	1.51	1.01	1.74	1.04	1.16	0.18	MW0406		conserved hypothetical protein	
1.12	1.10	1.06	0.93	1.09	1.24	1.05	1.20	1.17	0.95	0.91	MW0406a	lpl3	hypothetical protein (Pathogenicity island SaPIn2)	
0.84	1.09	1.16	1.16	0.88	1.13	1.28	1.14	1.19	1.05	0.98	MW0407	ndhF	NADH dehydrogenase subunit 5	membrane bioenergetics
0.69	1.06	1.06	0.92	0.89	0.98	1.17	1.06	0.67	1.30	1.26	MW0408		conserved hypothetical protein	
0.89	0.92	1.09	1.19	0.86	0.74	0.98	0.80	1.02	1.12	1.07	MW0409		conserved hypothetical protein	
0.81	1.05	1.12	1.18	0.95	0.87	0.77	0.73	1.08	1.14	1.26	MW0410		conserved hypothetical protein	
0.81	0.99	1.20	0.96	1.04	0.96	0.90	0.80	1.02	1.16	1.43	MW0411		hypothetical protein, similar to carboxylesterase	aminoacid metabolism
0.92	0.98	1.15	0.91	1.04	0.94	0.95	0.94	0.90	1.17	0.98	MW0412		hypothetical protein	
0.85	1.10	1.23	1.18	0.98	0.97	0.89	0.86	1.00	1.22	1.38	MW0413		hypothetical protein, similar to sodium-dependent transporter	transport/binding
0.97	1.00	1.03	0.74	1.17	1.14	0.96	1.50	0.65	0.91	1.54	MW0414	cysM	cysteine synthase homologue	aminoacid metabolism
0.67	0.82	0.51	0.92	0.76	0.45	0.69	0.45	0.93	0.91	0.31	MW0415	metB	cystathionine gamma-synthase	aminoacid metabolism
0.68	0.67	0.62	0.41	0.89	0.49	0.68	0.61	0.51	0.92	1.48	MW0416		hypothetical protein, similar to ABC transporter ATP-binding protein	transport/binding
0.67	0.65	0.78	1.07	0.77	0.59	0.72	0.60	0.65	1.07	1.36	MW0417		hypothetical protein, similar to ABC transporter permease protein	transport/binding
0.66	0.68	0.57	0.49	0.65	0.43	0.57	0.42	0.69	0.95	1.75	MW0418		hypothetical protein, similar to lactococcal lipoprotein	transport/binding
1.06	0.84	1.20	0.91	1.45	0.42	1.07	0.27	0.90	0.76	1.52	MW0419		hypothetical protein, similar to autolysin (N-acetylmuramoyl-L-alanine amidas	cell wall
1.11	0.80	0.79	0.78	0.87	0.53	0.84	0.76	0.65	0.96	0.91	MW0420		hypothetical protein	
1.21	0.64	0.78	0.55	0.90	0.59	0.82	0.72	0.74	0.85	1.03	MW0421		conserved hypothetical protein	
1.17	0.71	0.78	0.58	1.00	0.50	0.89	0.92	0.70	0.92	1.32	MW0422		conserved hypothetical protein	
1.02	0.56	0.68	0.52	0.60	0.33	0.62	0.46	1.01	0.83	2.39	MW0423		conserved hypothetical protein	
0.80	0.69	0.69	0.55	0.72	0.43	0.63	0.51	0.42	0.90	1.18	MW0425	gltC	transcription activator of glutamate synthase operon	RNA synthesis
0.81	0.35	0.32	0.17	0.41	0.14	0.36	0.15	0.37	1.05	1.19	MW0426	gltB	glutamate synthase large subunit	aminoacid metabolism
0.81	1.12	1.31	1.23	0.87	0.90	1.19	0.90	1.52	1.31	1.09	MW0427	gltD	NADH-glutamate synthase small subunit	aminoacid metabolism
0.70	1.39	1.29	0.83	0.84	0.91	1.08	0.70	6.22	10.09	7.69	MW0428	treP	PTS enzyme II, phosphoenolpyruvate-dependent, trehalose-specific	transport/binding
0.92	1.53	1.36	0.77	1.06	1.09	1.21	1.14	3.56	2.56	2.50	MW0429	treC	alpha-glucosidase	carbohydrate metabolism
0.91	1.22	1.28	1.19	1.16	0.93	0.96	0.79	1.16	1.06	1.30	MW0430		hypothetical protein, similar to trehalose operon transcriptional repressor	RNA synthesis
0.99	0.87	0.83	0.94	1.55	0.86	1.34	1.20	1.08	0.82	1.03	MW0431		hypothetical protein	
0.64	1.32	1.29	1.32	1.12	1.18	0.89	0.76	1.78	1.42	1.10	MW0432		conserved hypothetical protein	
0.81	1.10	1.41	1.27	1.10	1.15	0.96	0.80	1.58	1.47	1.18	MW0433	dnaX	DNA polymerase III gamma and tau subunits	DNA replication
1.02	0.71	0.71	0.71	0.75	0.86	0.97	0.71	0.95	0.99	1.20	MW0434		conserved hypothetical protein	
1.08	0.66	1.11	0.87	0.76	0.63	1.21	0.77	1.15	1.10	1.27	MW0435	recR	recombination protein	[illegible]
0.97	1.14	1.40	1.21	1.02	1.18	1.17	1.10	1.22	1.26	1.05	MW0436		hypothetical protein, similar to lysine decarboxylase	aminoacid metabolism
1.06	1.23	1.18	1.47	1.09	1.04	1.09	0.81	1.29	1.16	1.01	MW0437	tmk	putative thymidylate kinase	nucleic acid metabolism
1.08	0.89	1.04	1.28	0.86	1.02	0.66	0.80	1.02	1.12	0.97	MW0438		conserved hypothetical protein	
1.08	1.03	1.22	1.22	1.01	0.91	0.96	0.80	1.39	1.11	1.03	MW0439	holB	probable DNA polymerase III, delta prime subunit	DNA replication
0.91	1.26	1.32	1.57	1.16	1.12	0.89	0.73	1.35	1.24	1.01	MW0440		hypothetical protein, similar to signal peptidase II homologue	protein secretion
1.01	1.16	1.07	1.04	1.15	0.98	0.96	1.05	1.07	1.13	1.05	MW0440n		hypothetical protein, similar to signal peptidase II homologue	protein secretion
1.11	1.10	1.13	1.10	1.16	1.11	0.84	0.97	1.08	1.09	1.04	MW0441		conserved hypothetical protein	
1.01	1.12	0.93	0.93	0.91	0.80	0.92	0.82	0.96	1.06	0.96	MW0442		conserved hypothetical protein	
1.02	1.09	1.12	1.02	0.93	0.98	0.96	0.96	1.19	1.11	1.07	MW0443		conserved hypothetical protein	
1.12	0.90	0.86	0.60	1.43	0.97	1.70	1.01	1.21	0.98	0.97	MW0444		conserved hypothetical protein	
0.92	0.92	0.96	0.88	1.12	0.97	0.87	1.36	0.63	0.98	1.46	MW0445	metS	methionyl-tRNA synthetase	protein synthesis
0.91	1.11	1.07	0.90	1.06	1.65	0.86	1.15	0.90	1.06	0.97	MW0446		conserved hypothetical protein	
1.45	0.84	0.99	0.92	1.05	0.96	1.03	1.07	0.91	0.89	1.51	MW0447		conserved hypothetical protein	
0.98	0.95	1.06	1.05	1.04	0.98	0.88	0.71	0.96	1.00	1.30	MW0448	ksgA	dimethyladenosine transferase(16S rRNA dimethylase) homologue	RNA modification
1.38	1.21	1.29	0.92	1.38	0.45	1.29	0.79	1.16	1.59	1.10	MW0449	veg	VEG protein homologue	
1.14	1.79	0.98	0.89	1.12	0.60	0.96	0.82	0.98	1.41	1.16	MW0450		hypothetical protein, similar to 4-diphosphocytidyl-2-C-methyl-D-erythritol kina	nucleic acid metabolism
1.02	1.54	1.00	1.08	1.02	1.91	1.17	0.97	0.86	1.27	0.88	MW0451	purR	pur operon repressor homologue	RNA synthesis
1.26	1.23	0.89	0.76	0.84	3.29	2.61	1.75	0.65	1.55	0.83	MW0452		translation initiation inhibitor homologue	protein synthesis
1.26	1.03	0.86	1.06	0.80	2.21	1.62	1.07	0.86	1.30	0.83	MW0453	spoVG	stage V sporulation protein G homologue	cell division
0.82	0.96	0.92	1.09	1.00	1.21	0.97	1.05	0.95	1.04	1.19	MW0454	gcaD	UDP-N-acetylglucosamine pyrophosphorylase homologue	cell wall
1.20	0.87	0.77	0.70	1.36	1.22	1.14	1.96	0.85	0.82	1.29	MW0455	prs	ribose-phosphate pyrophosphokinase	nucleic acid metabolism
1.00	1.20	0.88	0.71	1.19	0.59	0.74	1.09	1.07	0.88	0.83	MW0456	rplY	50S ribosomal protein L25	protein synthesis
0.98	0.92	0.80	0.75	0.99	0.91	0.84	1.13	0.72	0.90	1.24	MW0457	pth	peptidyl-tRNA hydrolase	protein synthesis
0.96	0.74	0.77	0.84	0.81	0.74	0.89	1.04	0.80	0.95	1.71	MW0458	mfd	transcription-repair coupling factor	RNA synthesis
0.82	1.25	0.89	0.69	1.10	0.96	0.77	1.13	0.84	0.90	1.58	MW0459		hypothetical protein, similar to low temperature requirement B protein	adaptation to atypical
0.91	1.20	0.87	0.95	0.88	0.84	0.70	0.75	0.90	0.98	1.31	MW0460		conserved hypothetical protein	
1.08	0.89	0.79	0.75	0.83	0.88	0.80	0.86	0.88	0.90	1.49	MW0461		conserved hypothetical protein	
1.10	1.03	0.83	0.79	0.94	0.85	0.76	0.94	0.75	0.92	1.51	MW0462		hypothetical protein, similar to cell-division initiation protein	cell division
0.86	0.95	0.79	0.95	0.95	0.55	0.77	0.92	0.63	1.03	1.57	MW0463		hypothetical protein, similar to polyribonucleotide nucleotidyltransferase	nucleic acid metabolism
0.90	1.34	1.04	1.27	1.15	1.00	0.79	0.91	1.09	0.86	0.83	MW0464		conserved hypothetical protein	
1.15	0.89	0.98	1.00	1.08	0.82	0.99	0.92	1.02	0.91	1.03	MW0465		hypoxanthine-guanine phosphoribosyltransferase homologue	nucleic acid metabolism
0.91	0.87	1.04	1.57	0.97	0.75	0.91	0.85	0.96	1.03	1.72	MW0466	ftsH	cell-division protein	cell division
0.89	1.29	1.27	0.72	1.20	1.34	1.19	1.40	1.13	1.20	1.29	MW0466a	ftsH	cell-division protein	cell division
0.85	1.24	1.08	1.16	1.08	1.06	0.93	1.00	1.10	1.03	1.22	MW0467		heat-shock protein HSP33 homologue	adaptation to atypical
0.89	1.65	0.98	1.30	1.13	1.70	1.06	1.67	1.05	0.93	6.73	MW0468	cysK	cysteine synthase (o-acetylserine sulfhydrylase) homologue	aminoacid metabolism
0.93	1.35	1.05	0.99	1.10	1.18	0.85	1.23	0.95	0.89	1.64	MW0469	folP	dihydropteroate synthase chain A synthetase	coenzyme metabolism
1.19	0.75	0.92	0.75	1.02	0.90	1.07	1.30	0.69	0.89	1.58	MW0470	folB	7,8-dihydroneopterin aldolase	coenzyme metabolism
0.77	1.08	1.02	1.00	1.02	0.97	0.80	0.82	0.93	0.94	1.75	MW0471	folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridin e pyrophosphokinase	coenzyme metabolism
0.74	1.05	0.94	0.99	1.05	0.91	0.83	0.97	0.82	0.98	1.58	MW0472	lysS	lysyl-tRNA synthetase	protein synthesis
0.83	1.28	1.60	1.51	1.17	1.22	1.33	1.36	1.14	1.28	1.15	MW0473		hypothetical protein, similar to transcription regulator GntR family	RNA synthesis
0.79	1.23	1.50	1.66	1.31	1.21	1.17	1.97	1.09	1.36	0.86	MW0474		conserved hypothetical protein	
0.83	1.05	1.37	1.40	1.10	1.22	1.01	1.52	1.26	1.20	0.98	MW0475		conserved hypothetical protein	

0.82	0.91	1.13	1.78	1.23	0.84	1.06	1.59	0.86	1.00	1.08	MW0476	nupC	pyrimidine nucleoside transport protein	transport/binding
0.98	1.02	0.92	1.38	0.82	1.57	1.06	1.06	1.21	0.93	0.41	MW0477	ctsR	transcription repressor of class III stress genes homologue	RNA synthesis
1.15	1.09	1.04	1.14	1.02	2.06	1.15	1.77	0.91	0.91	0.38	MW0478		conserved hypothetical protein	
0.88	1.10	1.07	1.39	1.14	1.86	0.97	1.29	1.02	0.95	0.33	MW0479		hypothetical protein, similar to creatine kinase	miscellaneous
1.11	1.06	0.90	1.26	1.09	1.33	1.01	1.21	0.91	0.89	0.67	MW0480	clpC	endopeptidase	adaptation to atypical
0.97	1.36	1.20	1.32	1.27	1.24	0.83	1.26	1.09	0.99	0.96	MW0481	radA	radA	DNA repair or modify
1.11	1.15	1.02	0.98	1.11	1.28	0.95	1.16	1.05	0.80	1.15	MW0482		conserved hypothetical protein	
0.89	1.01	0.96	0.88	1.12	1.26	0.78	1.26	0.88	0.85	1.20	MW0483	gltX	glutamyl-tRNA synthetase	protein synthesis
1.14	1.01	1.07	1.42	1.14	1.55	0.94	0.95	1.16	0.97	1.13	MW0484	cysE	Serine acetyltransferase homologue	aminoacid metabolism
1.17	1.20	1.04	0.84	1.18	1.65	0.97	1.58	1.11	0.90	1.13	MW0485	cysS	cysteinyl-tRNA synthetase	protein synthesis
1.10	1.21	1.05	1.21	1.07	1.29	0.97	1.13	1.19	0.93	1.23	MW0486		conserved hypothetical protein	
1.09	1.29	1.09	1.14	1.05	1.38	0.96	1.06	1.18	0.97	1.07	MW0487		hypothetical protein, similar to tRNA/rRNA methyltransferase	RNA modification
1.08	1.36	1.16	1.82	1.20	1.21	1.00	1.10	1.20	0.97	1.04	MW0488		conserved hypothetical protein	
0.86	1.34	0.96	1.14	0.94	1.02	0.90	1.15	1.25	0.91	1.09	MW0489	sigH	hypothetical protein	RNA synthesis
1.12	0.91	0.90	1.03	0.95	0.81	0.90	0.91	1.12	0.72	1.27	MW0490	secE	preprotein translocase subunit	protein secretion
0.91	1.24	1.01	0.86	1.24	1.08	0.73	1.28	0.94	0.72	1.12	MW0491	nusG	transcription antitermination protein	RNA synthesis
0.92	0.94	1.00	0.92	1.13	0.31	0.50	0.58	1.15	0.98	0.51	MW0492	rplK	50S ribosomal protein L11	protein synthesis
0.69	1.35	0.94	1.08	1.08	0.49	0.53	0.72	1.02	0.84	0.41	MW0493	rplA	50S ribosomal protein L1	protein synthesis
0.95	0.80	0.94	1.02	0.98	0.17	0.72	0.53	1.14	0.91	0.56	MW0494	rplJ	50S ribosomal protein L10	protein synthesis
1.04	0.82	0.82	0.66	1.09	0.25	0.71	0.56	1.07	0.78	0.50	MW0495	rplL	50S ribosomal protein L7/L12	protein synthesis
0.98	1.21	0.91	0.83	1.20	0.62	0.69	0.80	0.82	0.76	0.67	MW0496		conserved hypothetical protein	
0.91	1.34	0.97	0.85	1.51	0.74	1.04	0.70	1.28	0.74	1.09	MW0497	rpoB	RNA polymerase beta chain	RNA synthesis
0.94	1.00	0.87	0.81	1.30	0.63	0.80	0.68	1.14	0.78	1.15	MW0498	rpoC	RNA polymerase beta-prime chain	RNA synthesis
0.78	1.24	1.11	1.29	0.89	0.74	0.61	1.02	1.08	0.81	0.41	MW0500	rpsL	30S ribosomal protein S12	protein synthesis
0.64	1.00	0.86	1.01	1.00	0.48	0.70	1.04	1.23	0.76	0.38	MW0501	rpsG	30S ribosomal protein S7	protein synthesis
0.84	1.12	0.93	1.37	1.03	0.41	0.79	1.00	1.44	0.90	0.45	MW0502	fus	translational elongation factor G	protein synthesis
0.81	1.53	1.13	1.97	1.23	0.49	0.95	1.23	1.59	1.06	0.66	MW0503	tufA	translational elongation factor TU	protein synthesis
0.69	1.05	1.00	1.08	0.99	0.76	0.76	1.21	0.72	1.06	1.39	MW0504		hypothetical protein, similar to N-acyl-L-amino acid amidohydrolase	aminoacid metabolism
0.86	1.00	1.08	0.99	0.87	1.44	0.99	1.06	0.95	1.17	0.96	MW0505		hypothetical protein, similar to glycine C-acetyltransferase	aminoacid metabolism
0.69	1.24	1.08	1.26	0.96	1.26	0.85	0.89	1.02	1.14	0.84	MW0505n		hypothetical protein, similar to glycine C-acetyltransferase	aminoacid metabolism
0.92	1.84	0.91	1.44	0.73	0.95	1.19	1.58	1.19	1.22	2.16	MW0506		conserved hypothetical protein	
0.94	1.12	1.20	1.48	1.03	1.15	1.16	1.01	1.18	1.23	0.98	MW0507	araB	probable L-ribulokinase	carbohydrate metabolism
1.04	0.94	0.80	1.00	0.83	0.91	1.09	0.92	1.11	0.87	0.94	MW0508		hypothetical protein, similar to UDP-glucose 4-epimerase related protein	nucleic acid metabolism
1.02	0.44	0.43	0.54	0.69	0.31	0.82	0.58	0.92	0.69	0.95	MW0509	ilvE	branched-chain amino acid aminotroansferase homologue	aminoacid metabolism
0.87	0.66	0.51	0.53	0.78	0.42	0.72	0.56	0.93	0.67	1.09	MW0510		conserved hypothetical protein	
0.91	1.13	0.87	1.33	1.00	0.76	0.77	0.62	1.10	0.95	1.50	MW0511		hypothetical protein, similar to deoxypurine kinase	nucleic acid metabolism
1.16	0.88	0.99	0.80	1.01	0.62	0.92	0.86	1.00	1.05	1.46	MW0512		hypothetical protein, similar to deoxypurine kinase	nucleic acid metabolism
1.04	0.95	1.09	1.05	1.02	0.86	0.96	0.95	1.01	1.13	1.19	MW0513		hypothetical protein, similar to Cu binding protein (Mn oxidation	miscellaneous
0.84	1.09	1.14	1.51	1.14	0.90	1.07	0.88	1.12	1.21	1.08	MW0514		conserved hypothetical protein	
1.29	0.90	1.06	0.81	1.36	0.78	1.33	1.11	0.78	1.01	1.18	MW0515		conserved hypothetical protein	
1.43	1.08	1.06	1.43	1.13	1.09	1.87	1.09	1.21	1.24	0.91	MW0516	sdrC	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	pathogenic factor
0.89	1.24	1.56	1.12	1.31	1.36	1.22	1.19	1.15	1.34	1.52	MW0517	sdrD	Ser-Asp rich fibrinogen-binding bone sialoprotein-binding protein	pathogenic factor
0.69	1.27	1.26	1.42	1.15	1.01	1.01	0.87	1.07	1.10	1.43	MW0517n	sdrD	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	pathogenic factor
1.05	1.15	1.69	1.44	1.31	1.40	1.29	1.11	1.14	1.48	1.27	MW0518	sdrE	Ser-Asp rich fibrinogen-binding bone sialoprotein-binding protein	pathogenic factor
0.86	1.26	1.43	1.54	1.44	1.45	1.03	1.14	1.42	1.36	1.12	MW0518n	sdrE	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	pathogenic factor
0.94	1.04	1.16	1.38	1.10	1.14	0.90	0.90	0.98	1.02	0.91	MW0519		hypothetical protein, similar to poly (glycerol-phosphate) alpha-glucosyltransfer	cell wall
0.77	1.17	1.08	1.74	1.12	1.04	0.79	0.58	1.10	1.09	0.70	MW0520		ypothetical protein, similar to poly (glycerol-phosphate) alpha-glucosyltra	cell wall
1.00	0.76	0.63	1.06	0.68	0.91	1.02	0.81	1.01	0.85	0.60	MW0520n		hypothetical protein, similar to poly (glycerol-phosphate) alpha-glucosyltransfer	cell wall
1.15	0.89	0.84	0.75	1.30	0.86	0.94	1.15	0.90	0.88	1.27	MW0521		conserved hypothetical protein	
0.90	0.84	0.77	0.76	0.98	0.90	0.86	0.86	0.83	0.76	1.12	MW0522		conserved hypothetical protein	
0.89	1.00	0.80	1.03	0.97	0.81	0.89	0.83	0.80	0.89	1.26	MW0523		conserved hypothetical protein	
0.90	1.24	0.96	0.98	1.10	1.37	1.01	1.07	0.91	0.98	1.02	MW0524	nagB	probable glucosamine-6-phosphate isomerase	carbohydrate metabolism
1.08	0.91	0.88	1.01	0.90	1.72	1.24	1.32	0.90	0.99	1.02	MW0525		hypothetical protein, similar to hexulose-6-phosphate synthase	carbohydrate metabolism
0.93	1.00	1.00	1.34	1.01	2.02	1.21	1.59	1.00	0.95	1.08	MW0526		conserved hypothetical protein	
0.93	0.97	1.00	1.33	1.10	1.18	1.08	0.97	1.01	1.04	0.91	MW0527		hypothetical protein, similar to indigoidine systhesis protein	miscellaneous
1.24	0.91	1.12	0.79	0.88	1.21	2.07	1.36	1.01	1.15	0.56	MW0529		hypothetical protein	
0.75	1.48	1.30	1.34	1.14	1.36	1.08	1.06	1.04	1.21	0.95	MW0530	vraA	hypothetical protein, similar to long chain fatty acid CoA ligase	lipid metabolism
0.90	1.37	1.19	1.13	1.15	1.33	1.14	1.24	0.98	1.10	0.87	MW0531	vraB	acetyl-CoA c-acetyltransferase	lipid metabolism
0.91	1.13	1.21	1.21	1.05	1.15	1.21	1.06	1.11	1.29	1.00	MW0532	vraC	hypothetical protein	
0.95	1.16	1.28	1.35	0.98	1.10	1.17	1.17	1.07	1.21	1.11	MW0533		hypothetical protein	
1.32	0.58	0.84	1.26	0.90	0.62	4.84	0.67	0.90	1.47	0.48	MW0534		hypothetical protein	
1.29	0.61	0.82	1.32	0.93	0.56	3.84	0.58	0.94	1.40	0.48	MW0534n		hypothetical protein	
0.90	1.14	1.04	1.54	1.04	0.82	1.00	0.89	0.94	1.12	0.97	MW0535		hypothetical protein, similar to phosphomethylpyrimidine kinase, thiD homolog	coenzyme metabolism
0.93	1.12	0.98	1.24	0.99	0.86	0.89	0.72	1.13	0.96	0.89	MW0536	ung	uracil-DNA glycosylase	DNA repair or modify
0.83	1.21	0.94	1.29	0.96	0.85	0.92	0.85	1.21	0.99	0.97	MW0537		hypothetical protein	
0.96	1.01	0.77	0.98	0.78	0.65	1.10	0.77	1.01	0.89	0.94	MW0538		conserved hypothetical protein	
0.97	3.09	0.94	1.28	0.80	0.94	2.09	1.01	1.44	1.13	0.99	MW0539		hypothetical protein, similar to cationic amino acid transporter	transport/binding
1.26	1.06	0.87	0.81	1.04	0.91	1.41	0.99	0.90	1.00	1.35	MW0540		conserved hypothetical protein	
1.01	1.14	0.91	0.90	1.17	0.90	1.12	1.10	0.89	0.95	1.26	MW0541		conserved hypothetical protein	
1.19	1.22	1.11	1.89	1.33	0.87	1.07	1.34	1.16	0.92	1.03	MW0542		conserved hypothetical protein	
0.94	0.84	0.87	1.01	0.76	0.76	1.14	1.26	0.90	1.12	1.62	MW0543	pta	phosphotransacetylase	nucleic acid metabolism
0.97	1.58	0.89	1.19	1.22	1.05	0.91	1.49	1.07	0.88	1.49	MW0544		conserved hypothetical protein	
1.01	1.45	1.22	1.33	1.18	1.41	1.29	1.37	1.47	1.15	0.67	MW0545	mvaK1	mevalonate kinase	lipid metabolism
1.08	1.54	1.09	1.09	1.17	1.38	1.24	1.75	1.11	1.10	0.62	MW0545n	mvaK1	mevalonate kinase	lipid metabolism
1.12	1.49	1.19	1.17	1.05	1.33	1.40	1.68	1.57	1.13	0.69	MW0546	mvaD	mevalonate diphosphate decarboxylase	lipid metabolism
1.12	0.92	0.61	0.77	0.70	0.98	1.50	1.71	0.95	0.88	0.60	MW0547	mvaK2	phosphomevalonate kinase	lipid metabolism
1.24	0.94	1.01	1.01	1.04	0.87	1.07	1.02	1.28	1.03	0.85	MW0548		conserved hypothetical protein	
1.09	1.23	1.19	0.92	1.18	1.38	1.14	1.69	1.03	1.05	0.83	MW0549		mercuric reductase homologue	detoxification
1.07	1.21	1.21	1.03	1.05	1.15	0.96	1.19	1.15	1.04	0.89	MW0550		hypothetical protein	
1.10	1.06	1.14	1.32	1.06	1.25	1.06	1.13	1.36	1.03	0.98	MW0550n		hypothetical protein	
1.14	0.98	1.20	1.10	1.02	1.00	0.97	1.24	1.19	0.96	0.96	MW0552		hypothetical protein	
1.15	1.24	1.24	1.23	0.97	1.05	1.15	1.46	1.60	0.95	1.01	MW0553		conserved hypothetical protein	
1.33	1.13	1.26	0.95	1.12	1.14	1.10	1.44	1.38	1.01	0.98	MW0554		conserved hypothetical protein	
1.27	1.58	1.17	1.16	1.04	0.93	0.87	1.21	1.09	1.09	1.03	MW0555		conserved hypothetical protein	
1.00	1.02	0.87	1.12	0.95	0.80	1.17	1.21	0.99	0.97	1.09	MW0556		conserved hypothetical protein	
1.14	0.85	0.62	0.92	1.14	0.36	0.75	0.27	0.86	0.86	1.15	MW0556n		conserved hypothetical protein	
1.02	1.36	1.29	1.17	1.03	1.02	1.03	1.38	1.36	1.03	1.03	MW0557		conserved hypothetical protein	
1.04	0.85	1.04	0.93	1.13	0.92	1.01	1.20	1.26	0.93	1.03	MW0558		conserved hypothetical protein	
1.11	1.18	1.15	1.16	1.05	0.98	1.08	1.56	1.24	1.01	1.21	MW0559		conserved hypothetical protein	
1.18	1.10	1.12	0.84	0.95	0.93	1.03	1.42	1.12	1.06	1.22	MW0560		hypothetical protein	
1.13	1.10	0.91	0.78	#NUM!	0.99	0.97	1.22	1.12	0.98	1.24	MW0561		hypothetical protein	
0.94	1.15	1.17	1.64	1.02	0.80	1.05	1.15	0.86	1.17	1.05	MW0562		hypothetical protein	
0.85	1.18	1.04	1.32	1.12	1.10	0.81	0.92	1.02	0.95	0.98	MW0563		hypothetical protein, similar to oxidoreductase, ion channel	transport/binding
0.98	1.23	1.12	1.11	1.05	1.21	0.85	0.84	1.13	1.02	1.15	MW0564		conserved hypothetical protein	
0.85	0.83	0.74	0.81	0.84	0.79	0.64	0.75	0.76	0.73	1.22	MW0565		conserved hypothetical protein	
0.86	0.43	0.68	0.54	0.69	0.51	0.96	0.64	1.01	0.72	1.22	MW0566		conserved hypothetical protein	
0.98	0.82	0.73	0.72	1.01	0.65	0.71	0.91	0.77	0.86	1.45	MW0567		conserved hypothetical protein	

0.88	0.47	0.85	1.68	1.17	1.00	1.36	1.36	0.87	1.03	1.41	MW0568	adh1	alcohol dehydrogenase I	carbohydrate metabolism
1.48	0.86	0.88	0.88	0.99	0.92	0.94	0.99	1.09	0.82	1.46	MW0570		conserved hypothetical protein	
1.35	0.84	0.81	0.63	1.38	0.83	0.94	1.15	0.65	0.77	1.63	MW0571	argS	arginyl-tRNA synthetase	protein synthesis
0.96	1.27	0.86	0.71	1.12	1.06	0.91	1.12	0.80	0.91	1.30	MW0572		hypothetical protein, similar to endonuclease III	DNA repair or modify
0.84	0.94	0.84	0.95	1.03	0.93	0.61	0.74	0.80	0.82	1.24	MW0573		hypothetical protein, similar to iron-binding protein	transport/binding
0.84	1.68	1.72	1.22	1.29	1.28	1.06	1.53	1.49	1.04	0.50	MW0574		hypothetical protein, similar to iron(III) ABC transporter permease protein	transport/binding
0.95	1.04	0.90	1.18	0.94	1.22	0.83	1.01	1.10	0.87	1.10	MW0575		hypothetical protein, similar to L-2-haloalkanoic acid dehalogenase	carbohydrate metabolism
1.16	1.00	0.74	0.98	1.00	1.39	1.00	1.14	0.88	0.99	1.20	MW0576		hypothetical protein similar to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid hyd	miscellaneous
1.14	0.68	0.71	1.01	0.65	1.12	1.21	1.39	0.59	1.30	0.73	MW0577		hypothetical protein	
0.80	1.04	1.06	1.16	0.94	1.53	0.96	1.18	0.89	1.20	1.44	MW0578		hypothetical protein	
1.04	1.47	0.97	1.35	0.99	2.16	1.63	1.53	0.83	1.18	0.88	MW0579		hypothetical protein, similar to esterase/lipase	lipid metabolism
1.70	1.91	0.91	1.33	1.02	1.19	1.87	0.92	1.28	1.26	1.31	MW0580	sarA	staphylococcal accessory regulator A	RNA synthesis
1.16	1.60	1.04	0.87	1.09	1.48	1.28	1.63	0.98	0.97	1.25	MW0581		conserved hypothetical protein	
1.10	1.06	1.00	0.99	0.91	1.22	1.14	1.24	1.08	1.12	1.23	MW0582		hypothetical protein	
1.05	1.16	1.13	1.12	1.05	1.19	1.15	1.15	1.07	1.11	0.94	MW0583		hypothetical protein	
0.93	1.67	1.20	1.18	1.05	1.65	1.25	1.22	1.04	1.14	0.87	MW0584		hypothetical protein, similar to FimE recombinase	[illegible]
0.97	1.67	1.08	1.14	0.99	1.43	1.41	1.38	1.11	1.09	1.04	MW0585		hypothetical protein, similar to NADH dehydrogenase	membrane bioenergetics
0.99	1.57	0.99	1.00	0.82	1.12	1.66	1.33	1.09	0.97	0.99	MW0586		hypothetical protein, similar to Na+/H+ antiporter	membrane bioenergetics
0.98	1.37	1.15	0.95	0.91	1.14	1.74	1.33	1.09	1.04	0.89	MW0587		hypothetical protein, similar to Na+/H+ antiporter	membrane bioenergetics
1.16	1.07	1.09	1.07	1.04	1.12	1.33	1.16	0.99	1.19	1.16	MW0588		MnhD homologue, similar to Na+/H+ antiporter subunit	membrane bioenergetics
0.74	1.13	1.12	1.12	0.93	1.04	1.22	1.12	0.88	1.21	1.09	MW0588a		MnhD homologue, similar to Na+/H+ antiporter subunit	membrane bioenergetics
0.81	1.78	1.04	1.35	1.00	1.34	1.17	0.96	1.19	1.02	0.95	MW0589		hypothetical protein, similar to Na+/H+ antiporter	membrane bioenergetics
1.03	1.41	1.12	1.26	1.08	1.30	1.14	1.04	1.16	1.15	1.04	MW0590		hypothetical protein, similar to Na+/H+ antiporter	membrane bioenergetics
0.86	1.17	1.01	1.39	1.10	1.27	1.11	0.94	1.17	1.10	1.00	MW0591		conserved hypothetical protein	
0.89	0.95	0.74	0.84	0.72	0.74	1.13	1.15	0.97	0.97	1.28	MW0592		conserved hypothetical protein	
0.61	0.80	0.84	2.77	0.53	0.56	0.72	0.85	0.70	1.33	8.79	MW0593		ORFID:MW0593~lipoprotein, Streptococcal adhesin PsaA homologu	pathogenic factor
0.62	0.99	0.97	3.44	0.62	0.57	0.70	0.78	0.85	1.36	6.65	MW0593n		lipoprotein, Streptococcal adhesin PsaA homologue	pathogenic factor
0.48	0.93	0.96	3.52	0.66	0.70	0.63	0.82	0.63	1.32	10.16	MW0594		conserved hypothetical protein	
0.86	0.76	1.18	1.86	0.84	0.86	0.79	0.64	0.82	1.37	1.66	MW0596		hypothetical protein, similar to iron dependent repressor	RNA synthesis
0.90	0.97	0.92	1.03	0.88	0.98	0.86	1.05	0.76	1.20	1.29	MW0597		hypothetical protein	
0.91	0.98	0.99	1.19	1.02	1.05	0.72	0.81	0.99	1.15	1.38	MW0598	tagA	teichoic acid biosynthesis protein	cell wall
1.01	1.04	0.95	1.43	0.89	0.89	0.85	0.80	1.27	1.02	1.07	MW0599	tagH	teichoic acid translocation ATP-binding protein	cell wall
1.05	0.97	0.77	1.09	0.88	0.76	0.97	0.87	1.41	0.89	1.20	MW0600	tagG	teichoic acid translocation permease protein	cell wall
1.11	0.90	0.79	0.88	0.88	0.95	1.01	1.01	1.10	0.98	0.91	MW0601	tagB	teichoic acid biosynthesis protein B	cell wall
1.07	1.64	0.94	0.88	1.07	1.46	0.79	1.08	1.04	0.92	0.92	MW0601n	tagB	teichoic acid biosynthesis protein B	cell wall
1.12	0.92	0.81	0.71	0.74	0.87	1.02	0.86	1.17	0.98	0.91	MW0602	tagX	teichoic acid biosynthesis protein X	cell wall
1.11	1.44	0.94	1.04	1.12	1.57	0.82	1.30	1.00	0.94	0.95	MW0602n	tagX	teichoic acid biosynthesis protein X	cell wall
1.35	1.05	0.90	0.92	0.94	0.92	0.86	0.97	0.90	0.98	1.03	MW0603	tagD	teichoic acid biosynthesis protein D	cell wall
0.95	1.31	1.00	1.14	1.03	0.86	0.78	0.62	1.19	1.00	1.16	MW0604	pbp4	penicillin binding protein 4	cell wall
1.18	1.42	1.04	1.05	0.99	1.05	0.81	0.79	1.54	1.19	1.27	MW0605		ATP-binding cassette transporter A	transport/binding
1.76	0.00	0.55	0.00	1.00	0.00	1.46	0.91	0.00	1.06	1.42	MW0606		hypothetical protein	
1.19	1.19	1.12	1.57	1.19	0.78	0.84	0.84	1.09	1.18	1.61	MW0607		hypothetical protein, similar to pyrimidine nucleoside transporter	transport/binding
0.89	0.59	0.73	1.11	0.95	0.59	0.72	0.49	1.00	0.83	0.77	MW0608		conserved hypothetical protein	
0.95	0.65	0.87	1.16	1.00	0.59	0.76	0.46	1.09	0.91	0.86	MW0608n		conserved hypothetical protein	
0.70	0.61	0.62	0.89	0.76	0.43	0.77	0.55	0.93	0.74	1.24	MW0609	fhuA	ferrichrome transport ATP-binding protein	transport/binding
0.77	0.76	0.65	0.81	0.81	0.48	0.83	0.58	0.94	0.83	1.32	MW0610	fhuB	ferrichrome transport permease	transport/binding
0.77	0.60	0.75	0.79	0.74	0.46	1.02	0.62	1.01	0.87	1.29	MW0611	fhuG	ferrichrome transport permease	transport/binding
0.88	1.20	0.99	0.97	1.18	1.42	0.90	1.20	0.89	1.05	0.99	MW0612		hypothetical protein, similar to dihydroxyacetone kinase	carbohydrate metabolism
0.79	1.40	0.99	1.23	1.16	1.35	0.93	1.03	0.99	1.05	0.94	MW0613		conserved hypothetical protein	
0.88	1.04	0.95	0.94	0.98	1.15	0.90	1.04	0.88	1.11	1.10	MW0614		conserved hypothetical protein	
1.10	1.40	0.95	1.00	1.06	0.94	0.94	0.81	1.11	1.06	0.83	MW0615		hypothetical protein	
0.88	1.58	0.99	1.06	1.01	0.66	0.95	0.68	1.56	0.87	0.85	MW0616		conserved hypothetical protein	
0.86	1.39	1.04	0.77	1.06	0.88	0.78	0.83	0.93	1.02	0.90	MW0616n		conserved hypothetical protein	
0.94	1.10	0.92	1.02	0.98	0.85	0.84	0.85	0.99	0.98	1.17	MW0617		hypothetical protein, similar to lipase LipA	pathogenic factor
1.10	1.13	0.97	0.98	0.86	0.84	0.92	0.92	1.01	0.92	1.93	MW0618		hypothetical protein	
1.15	0.92	0.93	0.79	0.80	0.85	1.07	0.87	0.90	0.98	1.05	MW0619		conserved hypothetical protein	
1.09	1.20	1.06	1.04	1.05	1.15	0.90	0.90	1.01	1.00	1.21	MW0620		hypothetical protein	
0.96	0.99	0.98	1.05	1.05	1.15	0.97	0.93	0.89	1.04	1.35	MW0621		hypothetical protein, similar to two-component response regulator	RNA synthesis
1.25	0.70	0.75	0.71	0.76	0.82	1.10	0.90	0.98	0.82	1.07	MW0622		hypothetical protein, similar to two-component sensor histidine kinas	sensor
1.48	1.16	1.02	0.79	1.25	1.08	1.04	1.34	0.70	0.89	1.15	MW0623	vraF	ABC transporter ATP-binding protein	transport/binding
1.05	1.01	1.23	1.12	1.19	0.94	0.99	1.01	1.03	1.09	1.24	MW0624	vraG	ABC transporter permease	transport/binding
1.06	0.91	1.17	1.09	1.58	1.02	0.95	1.29	1.14	0.69	0.86	MW0625		conserved hypothetical protein	
0.94	1.23	1.37	1.48	2.02	1.04	1.00	1.49	1.19	0.79	0.93	MW0626		hypothetical protein, similar to low-affinity inorganic phosphate transporter	transport/binding
1.53	0.66	0.91	0.67	1.23	0.39	1.06	0.59	0.62	0.82	1.36	MW0627	ssaA	secretory antigen SsaA homologue	pathogenic factor
1.47	1.30	1.05	1.23	1.18	0.82	1.22	0.77	1.19	1.31	1.87	MW0628		conserved hypothetical protein	
1.00	0.42	1.00	#NUM!	1.00	#NUM!	1.00	0.00	0.27	1.00	1.00	MW0629		hypothetical protein, similar to AraC/XylS family transcriptional regulator	RNA synthesis
1.29	0.86	0.92	0.75	1.29	0.75	1.27	0.87	1.17	1.23	2.05	MW0629a		hypothetical protein, similar to AraC/XylS family transcriptional regulator	RNA synthesis
1.19	1.32	0.96	1.01	0.95	0.97	0.80	0.97	0.96	1.01	1.98	MW0630		hypothetical protein	
1.09	0.95	0.73	1.03	0.83	0.78	0.91	1.02	1.11	0.91	1.24	MW0631		conserved hypothetical protein	
0.77	1.14	0.81	1.08	0.97	0.83	0.74	0.95	0.81	0.89	1.21	MW0631n		conserved hypothetical protein	
1.22	0.87	0.80	0.74	1.13	0.88	0.89	1.12	0.94	0.95	1.56	MW0632		conserved hypothetical protein	
1.09	1.60	0.98	0.84	1.06	1.54	1.20	2.13	0.67	0.93	1.04	MW0632n		conserved hypothetical protein	
0.89	0.73	0.69	0.96	0.78	0.86	0.69	0.70	0.67	0.78	0.61	MW0633		conserved hypothetical protein	
1.09	1.04	0.74	1.01	1.16	1.37	0.80	1.02	0.83	0.71	0.58	MW0634		RFID:MW0634~hypothetical protein, similar to LysR family transcriptional	RNA synthesis
0.93	0.79	0.62	0.95	0.75	0.84	0.94	0.79	0.90	0.79	0.60	MW0634n		hypothetical protein, similar to LysR family transcriptional regulator	RNA synthesis
0.95	0.95	0.87	1.01	1.10	1.12	0.92	0.91	1.01	0.90	0.73	MW0635		hypothetical protein, similar to sugar efflux transpoter	transport/binding
1.53	0.88	0.81	0.66	1.10	1.22	1.13	1.32	0.97	0.85	0.80	MW0636		conserved hypothetical protein	
1.04	0.88	1.05	1.15	0.98	0.98	0.96	0.97	0.85	1.14	1.24	MW0637		conserved hypothetical protein	
0.97	1.01	0.93	1.00	0.97	1.28	0.85	0.94	0.89	1.03	1.12	MW0638		hypothetical protein	
1.40	1.21	1.05	0.89	1.17	1.35	1.00	1.47	0.88	0.91	1.04	MW0639		conserved hypothetical protein	
1.12	1.04	1.02	1.04	0.93	1.18	0.97	0.97	0.99	0.97	1.09	MW0639n		conserved hypothetical protein	
1.41	1.04	0.94	0.87	1.07	1.48	1.32	1.69	0.85	1.06	0.77	MW0640		hypothetical protein	
1.13	1.02	0.77	0.84	0.82	1.05	1.17	1.06	1.19	0.87	0.65	MW0641		conserved hypothetical protein	
1.21	1.15	0.83	0.87	0.72	1.09	1.90	1.08	0.87	0.87	0.84	MW0642		conserved hypothetical protein	
1.16	0.95	0.81	0.87	0.74	1.27	1.73	1.12	0.84	0.87	0.76	MW0643		conserved hypothetical protein	
1.04	1.38	1.04	1.44	0.97	2.98	1.19	1.09	1.01	1.12	0.66	MW0644		conserved hypothetical protein	
1.21	0.62	0.79	0.56	0.77	0.77	1.22	0.91	0.87	1.05	1.26	MW0645	bacA	bacitracin resistance protein (putative undecaprenol kinase) homologue	cell wall
1.05	1.32	0.90	0.98	1.05	1.05	1.02	1.34	0.78	0.99	1.21	MW0646		hypothetical protein, similar to ABC transporter required for expression of cytochro	transport/binding
1.19	1.40	0.82	0.84	1.17	1.07	1.10	1.49	0.87	1.09	1.22	MW0647		hypothetical protein, similar to ABC transporter required for expression of cytochro	transport/binding
1.04	0.66	0.87	0.91	0.82	0.30	0.83	0.50	0.98	1.36	1.70	MW0648	mgrA	conserved hypothetical protein, similar to transcriptional regulator	RNA synthesis
1.29	1.03	0.98	0.93	0.97	0.53	1.14	0.67	1.34	1.17	1.26	MW0649		hypothetical protein, similar to cobalamin synthesis related protein	coenzyme metabolism
0.97	0.86	0.68	0.93	0.91	0.58	0.95	0.65	0.89	0.86	0.72	MW0650		hypothetical protein, similar to aryl-alcohol dehydrogenase	carbohydrate metabolism
1.00	1.03	1.10	1.41	1.18	0.76	0.92	0.86	0.94	1.10	0.76	MW0651		hypothetical protein	
0.89	0.89	0.94	1.20	1.03	0.96	0.88	0.80	1.01	0.94	0.54	MW0652		conserved hypothetical protein	
0.89	0.66	0.63	0.72	0.89	0.89	0.91	0.85	0.86	0.79	0.49	MW0653		hypothetical protein, similar to deoxyribodipyrimidine photolyase	[illegible]
1.14	1.22	1.00	1.15	0.86	0.97	1.18	1.27	0.85	1.12	1.26	MW0654		hypothetical protein	
1.34	0.89	0.92	1.15	1.22	0.87	0.94	0.64	0.96	0.97	1.13	MW0655		conserved hypothetical protein	

1.28	0.92	0.92	1.00	1.13	0.90	0.96	0.67	1.04	1.04	1.15	MW0656		conserved hypothetical protein	
1.43	1.13	1.02	1.02	1.39	0.99	1.39	0.63	1.08	1.02	1.38	MW0657	norA	quinolone resistance protein	detoxification
1.57	0.18	0.37	0.19	0.63	0.18	1.09	0.24	0.86	0.67	0.99	MW0658		hypothetical protein	
1.82	0.84	0.86	1.10	0.96	0.85	1.29	0.88	1.09	1.11	0.95	MW0659		hypothetical protein, similar to transcription regulation protein	RNA synthesis
4.71	1.39	1.36	1.69	1.26	1.30	1.21	1.04	1.29	2.45	3.54	MW0660		hypothetical protein, similar to transcription repressor of fructose operon	RNA synthesis
5.83	1.39	1.26	1.93	1.25	1.19	1.38	1.17	1.49	3.01	4.12	MW0661	fruB	fructose 1-phosphate kinase	carbohydrate metabolism
7.16	0.85	0.95	1.34	0.81	1.06	1.78	1.06	1.10	3.00	4.47	MW0662	fruA	fructose specific permease	transport/binding
1.36	0.73	0.64	0.92	0.78	0.79	1.27	0.97	0.93	1.03	1.01	MW0663	nagA	probable N-acetylglucosamine-6-phosphate deacetylase	carbohydrate metabolism
0.87	0.37	0.83	0.56	0.82	0.60	1.19	0.83	1.00	0.92	0.92	MW0664		hypothetical protein, similar to hemolysin homologue	pathogenic factor
0.92	1.21	0.99	1.38	1.21	1.42	1.02	1.22	0.80	0.99	0.84	MW0665		hypothetical protein, similar to plant-metabolite dehydrogenases	carbohydrate metabolism
1.14	1.09	0.91	1.15	1.06	1.13	1.29	1.50	0.95	0.97	0.98	MW0666		hypothetical protein, similar to CsbB stress response protein	adaptation to atypical
1.33	0.61	0.62	0.48	1.44	0.39	0.84	0.41	0.84	0.78	2.40	MW0667	saeS	histidine protein kinase	sensor
1.40	0.37	0.53	0.36	1.58	0.39	0.81	0.52	0.59	0.70	2.50	MW0668	saeR	response regulator	RNA synthesis
1.26	0.49	0.56	0.39	1.38	0.23	0.72	0.38	0.69	0.70	2.11	MW0669		hypothetical protein	
0.93	0.37	0.55	0.63	1.19	0.24	0.67	0.24	0.95	0.71	2.10	MW0669n		hypothetical protein	
1.40	0.77	0.79	0.53	1.29	0.82	0.94	0.88	1.51	0.65	1.02	MW0671		hypothetical protein	
1.12	0.88	0.76	0.56	1.38	0.79	0.79	0.93	1.55	0.61	1.15	MW0672		coenzyme PQQ synthesis homologue	coenzyme metabolism
1.03	0.71	0.69	0.56	1.54	0.73	0.65	0.97	1.24	0.63	1.09	MW0673		6-pyruvoyl tetrahydrobiopterin synthase homologue	coenzyme metabolism
0.78	0.87	0.72	0.82	1.04	0.57	0.72	0.62	1.34	0.75	1.08	MW0674		conserved hypothetical protein	
0.88	1.02	0.95	1.08	1.06	0.87	0.79	0.77	1.15	0.88	1.15	MW0675		hypothetical protein, similar to anthranilate synthase component II	aminoacid metabolism
0.86	1.12	1.00	1.16	1.08	0.93	0.80	0.74	1.21	0.94	1.08	MW0676		hypothetical protein, similar to para-aminobenzoate synthase component I	carbohydrate metabolism
0.87	1.05	1.12	1.17	1.00	0.90	0.81	0.79	1.09	0.93	1.23	MW0677		hypothetical protein, similar to para-aminobenzoate synthase component I	carbohydrate metabolism
0.93	1.05	1.03	1.05	0.98	0.91	0.96	0.83	1.07	0.83	1.34	MW0678		hypothetical protein	
1.00	1.00	0.93	0.95	1.07	0.91	0.80	0.85	1.01	0.86	1.48	MW0679		hypothetical protein, similar to urea amidolyase	aminoacid metabolism
1.03	1.13	1.00	1.21	1.08	0.95	0.80	0.73	1.15	0.89	1.16	MW0680		conserved hypothetical protein	
1.30	0.79	0.88	0.72	0.99	0.77	1.11	1.29	0.92	0.96	0.94	MW0681		hypothetical protein, similar to anion-binding protein	transport/binding
1.28	0.88	1.18	0.79	1.63	0.45	1.44	0.25	1.35	0.91	1.42	MW0682		hypothetical protein, similar to ABC transporter ATP-binding protein	transport/binding
1.33	1.14	0.82	0.56	1.11	0.67	1.13	0.88	0.85	1.12	1.15	MW0683	recQ	probable DNA helicase	DNA recombination
0.94	1.04	0.78	0.71	0.96	0.75	0.99	0.73	0.84	0.94	1.06	MW0683n	recQ	probable DNA helicase	DNA recombination
1.11	0.95	0.79	0.98	0.78	0.96	0.95	0.96	1.02	1.05	2.01	MW0684		hypothetical protein, similar to choline transport ATP-binding protein	transport/binding
0.93	1.24	0.91	1.00	0.95	0.95	0.99	0.85	0.86	1.04	1.89	MW0685		hypothetical protein, similar to choline transporter	transport/binding
0.72	0.89	0.76	1.19	0.84	0.75	0.68	0.48	0.71	1.00	1.14	MW0686		hypothetical protein, similar to histidinol-phosphate aminotransferase	aminoacid metabolism
1.06	0.77	0.74	0.89	0.83	0.55	0.71	0.42	0.86	0.93	1.21	MW0687		conserved hypothetical protein	
0.93	1.12	0.97	1.21	0.89	1.34	1.47	0.71	0.84	1.07	1.07	MW0688		hypothetical protein, similar to multidrug resistance protein	detoxification
0.64	0.51	0.81	0.66	0.88	0.32	0.57	0.37	0.50	1.22	2.33	MW0689		hypothetical protein, similar to di-tripepride ABC transporter	transport/binding
1.06	0.63	0.76	0.70	0.96	0.44	0.72	0.42	0.92	0.88	1.40	MW0690		conserved hypothetical protein	
0.92	0.90	0.86	0.87	0.97	0.53	0.80	0.54	0.94	0.97	1.36	MW0691		conserved hypothetical protein	
0.70	0.65	0.69	0.74	0.73	0.48	0.63	0.28	0.54	1.02	1.26	MW0692	nrdI	NrdI protein involved in ribonucleotide reductase function	nucleic acid metabolism
0.77	0.59	0.78	0.62	0.80	0.37	0.68	0.34	0.52	1.11	1.62	MW0692n	nrdI	NrdI protein involved in ribonucleotide reductase function	nucleic acid metabolism
0.86	0.74	0.69	0.76	0.81	0.35	0.55	0.38	0.54	1.10	1.84	MW0693	nrdE	hypothetical protein, similar to comF operon protein 3	nucleic acid metabolism
0.90	0.59	0.71	0.60	0.78	0.24	0.67	0.34	0.62	1.04	1.67	MW0694	nrdF	ribonucleoside-diphosphate reductase minor subunit	nucleic acid metabolism
0.74	0.95	1.19	2.89	1.05	0.70	0.99	0.92	1.25	0.98	1.23	MW0695		hypothetical protein, similar to ferrichrome ABC transporter permease	transport/binding
0.82	0.76	1.08	1.26	0.92	0.70	0.85	0.85	1.07	0.94	1.00	MW0696		hypothetical protein, similar to ferrichrome ABC transporter permease	transport/binding
0.90	0.95	1.18	1.77	0.99	0.65	1.11	1.23	1.22	0.91	1.29	MW0697		hypothetical protein, similar to ferrichrome ABC transporter ATP-binding prote	transport/binding
0.95	0.25	1.11	1.40	0.72	0.51	0.96	1.39	0.85	0.92	1.36	MW0698		lipoprotein, similar to ferrichrome ABC transporter	transport/binding
1.11	0.80	0.95	1.22	0.98	0.77	0.96	0.92	1.32	0.83	1.02	MW0699		conserved hypothetical protein	
0.91	1.04	1.01	1.22	1.00	0.87	1.02	0.94	1.33	0.85	0.93	MW0700		hypothetical protein, similar to UDP-N-acetylenolpyruvoylglucosamine reducta	cell wall
1.07	0.82	0.94	0.99	0.82	0.71	1.16	1.01	1.13	0.88	1.11	MW0701		conserved hypothetical protein	
1.08	1.01	0.92	1.01	0.90	0.92	0.93	0.97	1.21	0.86	1.04	MW0702		hypothetical protein	
1.73	1.02	0.97	0.68	0.96	1.36	1.29	1.14	0.99	0.89	1.43	MW0703		conserved hypothetical protein	
1.24	0.94	0.87	0.72	1.14	1.22	1.07	1.64	0.65	0.96	0.92	MW0704		hypothetical protein, similar to glycerate kinase	carbohydrate metabolism
1.06	0.99	0.90	0.93	1.15	0.96	0.78	1.17	0.80	0.87	0.94	MW0705	pepT	aminotripeptidase	protein modification
0.99	0.92	0.92	0.87	0.94	0.99	0.74	1.14	0.86	1.01	1.00	MW0706		conserved hypothetical protein	
0.88	1.17	0.92	0.96	1.00	1.08	0.84	1.01	0.98	0.95	0.98	MW0707		conserved hypothetical protein	
0.94	1.25	0.97	0.83	1.06	1.08	0.77	1.17	0.99	0.88	0.88	MW0708		conserved hypothetical protein	
0.78	0.96	0.90	0.66	0.77	0.90	0.84	0.94	0.83	1.02	1.46	MW0709	llm	lipophilic protein affecting bacterial lysis rate and methicillin resistance level	cell wall
0.86	0.96	1.09	1.10	0.95	0.93	0.92	0.93	0.95	1.08	1.23	MW0710		conserved hypothetical protein	
0.77	0.87	1.04	1.12	1.01	0.91	0.85	0.83	0.84	1.12	1.10	MW0711		conserved hypothetical protein	
0.88	1.53	1.02	0.92	1.05	1.28	0.80	1.33	0.89	0.86	0.97	MW0712	ORFID:MW0712~hypothetical protein, similar to comF operon protei		transformation/competence
0.71	1.00	0.99	1.28	0.89	1.07	0.88	0.88	1.12	0.98	0.93	MW0712n	comFA	hypothetical protein, similar to comF operon protein 1	transformation/competence
0.81	0.92	0.76	0.73	0.71	0.85	0.89	0.78	1.03	0.96	1.18	MW0713	comFC	hypothetical protein, similar to comF operon protein 3	transformation/competence
1.15	0.97	1.05	0.90	1.22	0.76	0.94	0.95	0.79	0.90	1.57	MW0714		conserved hypothetical protein	
0.73	0.96	0.75	0.72	0.90	0.63	0.78	0.70	1.09	0.84	1.18	MW0715	secA	preprotein translocase subunit	protein secretion
0.91	0.86	0.72	0.80	1.01	0.69	0.77	0.81	0.71	0.81	1.48	MW0716	prfB	peptide chain release factor 2	protein synthesis
0.72	0.82	0.80	0.92	0.93	0.78	0.83	0.72	0.87	0.93	1.28	MW0717		conserved hypothetical protein	
1.11	0.81	0.77	0.51	0.86	0.52	0.86	0.58	0.84	0.93	1.48	MW0718		conserved hypothetical protein	
1.15	0.87	1.25	1.43	0.87	0.79	0.80	0.85	0.64	0.79	1.17	MW0719		hypothetical protein	
1.28	1.00	1.01	1.15	1.05	1.47	1.01	0.96	0.84	1.02	0.63	MW0720	uvrB	exinuclease ABC subunit B	DNA repair or modify
1.23	0.96	0.71	0.88	1.05	1.29	1.20	1.03	0.94	1.15	0.86	MW0721	uvrA	exinuclease ABC subunit A	DNA repair or modify
0.94	0.91	0.97	0.89	0.92	1.11	1.10	0.83	1.22	0.91	1.18	MW0722	hprK	HPr kinase/phosphatase	RNA synthesis
0.97	0.94	0.76	0.90	0.81	0.93	1.17	0.94	1.03	0.74	1.24	MW0723	lgt	prolipoprotein diacylglyceryl transferase	protein modification
1.31	1.05	0.93	0.90	1.09	1.01	1.12	1.00	0.88	0.83	1.31	MW0724		hypothetical protein, similar to O-acetyltransferase	carbohydrate metabolism
0.86	1.18	0.86	0.83	0.81	0.96	0.97	1.10	1.17	0.86	1.03	MW0725		conserved hypothetical protein	
1.03	0.98	0.97	0.83	0.93	1.39	0.97	1.83	0.84	0.99	1.41	MW0726	trxB	thioredoxine reductase	membrane bioenergetics
0.95	1.31	0.89	0.97	0.89	2.59	1.12	1.05	0.98	0.94	0.95	MW0727		conserved hypothetical protein	
1.28	0.81	0.57	0.45	0.65	3.72	1.87	1.28	0.58	0.93	1.04	MW0728		conserved hypothetical protein	
1.12	1.04	1.01	1.13	0.91	1.94	1.85	1.34	0.84	1.21	1.04	MW0729		conserved hypothetical protein	
1.17	1.08	0.88	1.18	0.85	0.94	1.05	1.16	1.29	0.95	1.03	MW0730	clpP	clpP	adaptation to atypical
1.02	0.96	0.89	0.91	0.75	0.89	1.48	1.15	1.07	1.15	0.88	MW0731		hypothetical protein, similar to cell-division inhibitor	cell division
1.58	1.40	0.92	0.95	1.21	1.82	1.90	1.28	0.96	0.85	1.27	MW0732		conserved hypothetical protein	
0.73	0.43	0.34	0.95	0.80	0.38	1.18	1.12	0.47	0.54	1.40	MW0733	gapR	glycolytic operon regulator	RNA synthesis
0.57	0.41	0.35	1.42	0.64	0.32	1.22	2.26	0.44	0.55	1.10	MW0734	gap	glyceraldehyde-3-phosphate dehydrogenase	carbohydrate metabolism
0.63	0.43	0.45	1.25	0.67	0.44	1.46	3.13	0.38	0.59	1.37	MW0735	pgk	phosphoglycerate kinase	carbohydrate metabolism
0.58	0.53	0.46	1.59	0.51	0.42	1.21	2.72	0.52	0.65	1.32	MW0736	tpi	triosephosphate isomerase	carbohydrate metabolism
0.64	0.47	0.54	1.74	0.58	0.45	1.51	3.48	0.42	0.67	1.24	MW0737	pgm	2, 3-diphosphoglycerate-independentphosphoglycer ate mutase	carbohydrate metabolism
0.60	0.71	0.63	1.87	0.68	0.67	1.19	2.47	0.60	0.90	1.34	MW0738	eno	enolase	carbohydrate metabolism
0.74	0.59	0.92	0.98	1.10	0.98	0.94	0.49	0.80	1.07	1.44	MW0739		hypothetical protein	
0.97	0.70	0.85	0.82	0.90	0.72	0.83	0.52	0.90	1.14	1.47	MW0740	secG	probable protein-export membrane protein	protein secretion
1.07	0.82	0.78	0.91	0.86	0.60	0.77	0.62	0.94	1.03	1.31	MW0741		carboxyesterase precursor homologue	lipid metabolism
1.06	0.89	0.71	0.63	0.78	0.72	0.92	0.63	0.96	0.90	1.06	MW0743	ssrP	ssrA-binding protein	protein synthesis
1.20	1.18	1.02	0.91	1.17	1.04	0.84	1.18	0.75	0.86	0.82	MW0746		hypothetical protein (Genomic island nu Sa alpha3mw)	
1.33	0.74	0.84	0.66	0.84	0.73	0.89	0.65	0.68	1.06	0.70	MW0748		hypothetical protein (Genomic island nu Sa alpha3mw)	
1.24	0.58	0.95	0.85	0.85	0.76	0.85	0.82	0.70	0.92	0.77	MW0749		hypothetical protein (Genomic island nu Sa alpha3mw)	
1.23	0.71	0.99	0.71	0.94	0.89	0.87	0.92	0.67	1.01	0.74	MW0750		hypothetical protein (Genomic island nu Sa alpha3mw)	
1.09	0.48	1.00	0.54	1.08	0.66	1.09	0.95	0.43	1.19	0.74	MW0751		putative primase (Genomic island nu Sa alpha3mw)	DNA repair or modify
1.14	0.65	1.06	0.94	0.88	0.65	0.97	0.62	0.74	1.05	0.77	MW0752		hypothetical protein (Genomic island nu Sa alpha3mw)	
1.33	0.53	0.99	0.70	0.83	0.73	0.91	0.70	0.72	1.03	0.80	MW0753		hypothetical protein (Genomic island nu Sa alpha3mw)	

1.00	0.78	1.14	1.07	0.96	0.79	0.79	0.75	0.65	0.97	0.67	MW0754		hypothetical protein (Genomic island nu Sa alpha3mw)	
1.13	0.89	1.02	0.95	1.00	0.83	0.82	0.82	0.71	0.95	0.66	MW0755		hypothetical protein (Genomic island nu Sa alpha3mw)	
1.39	0.56	0.96	0.72	0.83	0.63	1.19	0.84	0.64	1.27	1.12	MW0756		hypothetical protein (Genomic island nu Sa alpha3mw)	
0.98	0.81	1.06	1.19	1.12	0.75	0.95	0.63	1.04	1.00	1.14	MW0757		hypothetical protein (Genomic island nu Sa alpha3mw)	
1.01	1.07	1.12	1.04	1.02	1.06	0.79	0.75	1.05	1.00	1.12	MW0758	ear	Ear (Genomic island nu Sa alpha3mw)	pathogenic factor
1.87	2.71	1.32	0.73	1.35	2.79	0.90	0.55	3.33	0.96	2.06	MW0759	sec4	ENTEROTOXIN TYPE C PRECURSOR	pathogenic factor
1.74	2.77	1.32	0.62	1.26	3.09	0.82	0.29	3.74	0.93	1.91	MW0759n	sec3	enterotoxin typeC3	pathogenic factor
1.22	0.74	1.07	1.15	1.01	0.82	1.15	0.64	1.17	0.92	0.69	MW0760	sel	extracellular enterotoxin L	pathogenic factor
1.12	1.06	1.21	0.95	1.18	1.15	0.92	1.32	1.17	0.92	0.43	MW0761		conserved hypothetical protein	
0.94	1.04	1.34	1.19	1.15	1.17	1.20	1.18	1.02	1.16	0.97	MW0762		hypothetical protein	
1.10	0.86	1.14	1.03	1.06	1.47	1.33	0.94	1.10	1.18	1.02	MW0763		conserved hypothetical protein	
1.09	1.32	1.52	1.34	0.96	4.84	2.11	1.73	1.07	1.37	0.85	MW0764	clfA	fibrinogen-binding protein A, clumping factor	pathogenic factor
0.87	1.43	1.28	1.51	1.26	1.23	1.05	1.11	1.14	1.17	0.81	MW0765		truncated secreted von Willebrand factor-binding protein VWbp	pathogenic factor
0.71	1.53	1.34	1.40	1.21	1.39	0.92	1.16	1.16	1.23	1.51	MW0767	ssp	extracellular ECM and plasma binding protein	pathogenic factor
1.00	0.92	1.00	1.04	0.82	0.94	1.23	1.39	1.04	1.14	1.51	MW0767n	ssp	extracellular ECM and plasma binding protein	pathogenic factor
0.58	1.36	1.15	1.21	1.03	1.06	0.72	1.17	1.09	0.98	0.81	MW0768		hypothetical protein, similar to extracellular matrix and plasma bindi	pathogenic factor
0.89	1.26	0.90	1.06	0.88	0.79	1.09	1.20	1.06	1.06	0.94	MW0768n		hypothetical protein, similar to extracellular matrix and plasma binding	pathogenic factor
1.26	0.91	0.69	0.65	0.85	0.52	0.53	1.10	0.70	0.74	1.08	MW0769		staphylococcal nuclease	pathogenic factor
1.02	0.92	1.24	1.33	0.72	0.31	1.00	0.39	0.91	2.11	1.32	MW0770	cspC	cold-shock protein C	adaptation to atypical
1.00	0.88	0.73	0.48	0.60	0.70	1.07	1.01	0.74	1.01	1.26	MW0771		hypothetical protein	
1.10	1.15	0.95	1.05	0.97	1.06	1.07	1.17	0.89	0.99	1.34	MW0772		hypothetical protein	
0.58	0.65	1.42	2.60	1.17	0.70	0.72	2.21	0.81	1.07	0.62	MW0773		conserved hypothetical protein	
1.40	1.12	0.85	0.99	0.98	1.07	1.33	1.14	1.08	1.08	1.08	MW0774		hypothetical protein	
1.27	0.99	0.73	0.81	0.78	0.85	1.33	0.83	1.00	0.94	1.04	MW0775		hypothetical protein	
1.41	1.75	1.14	1.63	0.83	4.25	3.83	1.87	1.19	1.21	1.02	MW0776		hypothetical protein	
1.25	1.80	0.95	1.14	0.78	3.97	2.59	2.96	1.12	1.20	1.20	MW0777		hypothetical protein	
1.13	1.06	0.88	1.03	0.85	1.01	1.12	1.01	1.07	1.09	1.24	MW0778		hypothetical protein, similar to phosphoglycerate mutase	carbohydrate metabolism
0.96	1.32	1.04	1.30	0.89	0.87	0.92	0.52	1.16	1.11	1.14	MW0779		conserved hypothetical protein	
0.97	0.37	0.57	0.92	0.74	0.29	0.70	0.20	0.64	1.31	1.18	MW0780		hypothetical protein, similar to lactococcal prophage ps3 protein 05	phage-related
2.02	1.00	0.90	1.39	1.07	0.57	1.06	0.88	0.87	1.00	1.08	MW0780a		hypothetical protein, similar to lactococcal prophage ps3 protein 05	phage-related
1.28	1.38	0.79	1.17	0.71	2.19	1.91	1.41	0.99	0.98	0.66	MW0781		hypothetical protein, similar to general stress protein 170	adaptation to atypical
0.94	1.24	0.86	1.09	0.86	0.97	1.07	0.96	1.07	0.91	0.94	MW0782		hypothetical protein, similar to 3-dehydroquinate dehydratase	amino acid metabolism
0.94	0.77	0.79	1.28	0.92	0.77	1.02	0.63	1.15	0.96	1.14	MW0783		conserved hypothetical protein	
1.35	1.35	0.91	0.75	1.02	0.97	1.02	1.29	0.90	1.02	1.41	MW0784		hypothetical protein, similar to thioredoxin	membrane bioenergetics
1.21	0.48	0.63	0.87	0.74	0.80	0.64	0.70	0.60	0.71	0.70	MW0785		hypothetical protein, similar to arsenate reductase	detoxification
1.24	0.65	0.69	0.88	0.97	0.79	0.61	0.88	0.61	0.79	0.50	MW0786		glycine cleavage system protein H homologue	amino acid metabolism
1.03	1.29	0.93	0.92	1.17	1.24	0.94	1.70	0.77	0.86	0.56	MW0787	uncated-S	conserved hypothetical protein	
1.23	1.07	0.90	0.70	1.10	1.12	0.95	1.05	0.82	0.80	0.94	MW0788		conserved hypothetical protein	
1.16	1.19	0.81	0.70	1.17	1.04	0.90	1.20	0.88	0.81	1.04	MW0789		hypothetical protein, similar to thioredoxin	membrane bioenergetics
1.16	0.65	0.62	0.41	1.41	0.58	0.71	0.39	0.51	0.71	1.37	MW0790		ABC transporter ATP-binding protein homologue category	transport/binding
1.02	0.65	0.49	0.39	0.87	0.27	0.65	0.29	0.74	0.83	1.71	MW0791		conserved hypothetical protein	
1.10	0.74	0.49	0.38	0.86	0.28	0.78	0.28	0.89	0.76	1.38	MW0792		conserved hypothetical protein	
2.79	2.30	1.36	1.06	0.66	8.07	5.20	1.66	1.43	2.84	1.00	MW0793		conserved hypothetical protein	
2.55	2.15	1.33	1.01	0.63	9.77	5.09	1.59	1.38	2.81	1.00	MW0793n		conserved hypothetical protein	
1.45	2.25	1.01	1.11	0.86	1.51	2.23	0.84	1.38	1.38	1.09	MW0794		conserved hypothetical protein	
1.29	2.21	1.24	1.02	1.04	2.76	2.21	1.69	0.96	1.21	0.58	MW0795		ABC transporter ATP-binding protein homologue	transport/binding
1.04	1.87	1.10	0.97	1.03	1.99	2.10	1.53	1.10	1.08	0.60	MW0796		conserved hypothetical protein	
0.92	2.84	1.10	1.21	1.11	2.54	1.91	1.62	1.07	1.01	0.64	MW0797	nifS	aminotransferase NifS homologue	coenzyme metabolism
1.19	1.85	0.86	0.94	1.00	1.96	2.17	1.62	0.91	0.92	0.62	MW0798		hypothetical protein, similar to nitrogen fixation protein NifU .	miscellaneous
0.96	1.92	0.92	1.18	0.88	1.64	2.05	1.30	1.24	1.02	0.75	MW0799		conserved hypothetical protein	
0.98	1.19	1.01	0.93	1.05	1.29	1.16	0.96	1.00	0.94	1.22	MW0800		hypothetical protein	
0.93	1.08	0.83	1.06	0.91	1.57	1.38	1.08	0.85	0.95	1.03	MW0801		hypothetical protein	
0.95	1.30	1.07	0.86	1.02	2.61	1.50	1.33	1.07	0.96	1.10	MW0802		hypothetical protein, similar to hemolysin	pathogenic factor
1.09	1.52	1.09	1.05	1.15	2.99	1.49	1.66	1.08	1.00	1.06	MW0803		hypothetical protein, similar to 2-nitropropane dioxygenase	detoxification
1.06	1.47	1.00	0.88	1.04	1.59	1.23	1.75	0.88	0.98	0.94	MW0804		conserved hypothetical protein	
1.05	1.64	1.00	0.98	1.12	1.63	1.07	1.70	1.00	0.83	0.94	MW0805		conserved hypothetical protein	
0.76	1.19	1.06	1.06	1.00	1.17	1.04	1.12	0.95	0.90	0.89	MW0806		conserved hypothetical protein	
0.82	1.12	0.94	1.32	1.24	1.01	0.89	0.97	1.02	0.97	1.16	MW0807	lipA	lipoic acid synthetase	lipid metabolism
1.03	0.92	0.90	0.92	1.02	0.85	0.94	1.04	1.02	0.92	1.13	MW0808		conserved hypothetical protein	
0.95	0.83	0.94	1.12	0.88	0.80	0.82	0.73	0.90	0.91	1.31	MW0809		conserved hypothetical protein	
1.13	0.80	0.79	0.89	1.02	0.97	0.76	1.33	0.76	0.78	0.98	MW0810		conserved hypothetical protein	
0.86	0.89	0.92	1.02	1.07	0.89	0.76	0.93	0.82	0.86	0.99	MW0811		hypothetical protein, similar to N-acetyl-glucosamine catabolism homologue	carbohydrate metabolism
0.89	1.07	0.93	1.11	1.02	0.78	0.77	0.95	0.84	0.88	0.96	MW0812		hypothetical protein, similar to glycerate dehydrogenase	carbohydrate metabolism
1.23	0.61	0.74	0.63	0.91	0.60	0.79	0.71	0.68	0.62	1.31	MW0813		hypothetical protein	
0.97	0.67	0.73	0.70	1.00	0.53	0.58	0.37	0.95	0.65	1.48	MW0813n		hypothetical protein	
0.94	0.64	0.80	0.81	0.87	0.48	0.65	0.52	0.84	0.83	1.71	MW0814	dltA	D-alanine-D-alanyl carrier protein ligase	cell wall
0.73	1.05	1.14	0.96	1.01	0.62	0.56	0.49	1.09	0.86	1.88	MW0815	dltB	DltB membrane protein	transport/binding
1.02	0.69	0.80	0.67	0.79	0.29	0.62	0.42	1.14	0.75	1.64	MW0816	dltC	D-alanyl carrier protein	cell wall
0.79	0.74	0.76	0.58	0.78	0.29	0.59	0.64	0.85	0.96	1.99	MW0817	dltD	poly D-alanine transfer protein	transport/binding
1.11	0.68	0.88	0.92	0.92	0.62	1.05	0.62	1.16	1.09	1.78	MW0818	nifU	hypothetical protein, similar to nitrogen fixation protein NifU	miscellaneous
0.82	0.72	0.87	1.06	1.00	0.73	0.81	0.67	1.00	1.03	1.05	MW0819		conserved hypothetical protein	
1.00	0.90	0.91	0.91	1.00	0.77	0.79	0.72	0.97	1.00	1.06	MW0819n		conserved hypothetical protein	
0.79	1.05	1.14	1.10	1.10	1.08	0.91	0.77	1.11	1.12	0.90	MW0820		hypothetical protein, similar to NADH dehydrogenase	membrane bioenergetics
1.22	0.77	0.89	0.84	0.91	0.74	0.92	0.66	0.90	1.08	1.20	MW0821		conserved hypothetical protein	
1.11	0.92	0.93	1.07	0.93	0.77	0.95	0.78	1.16	1.12	1.10	MW0822		conserved hypothetical protein	
0.94	1.21	0.94	1.27	0.95	1.61	1.07	1.28	1.27	0.91	1.03	MW0823		hypothetical protein, similar to NADH dehydrogenase .	membrane bioenergetics
0.80	0.92	0.97	1.06	0.95	1.03	0.97	1.07	1.14	1.04	1.14	MW0824	ampA	probable cytosol aminopeptidase	protein modification
0.74	1.36	0.97	1.12	1.02	0.98	0.89	0.92	1.28	0.89	0.51	MW0825		conserved hypothetical protein	
0.97	1.00	0.91	1.06	0.97	0.77	0.93	0.87	0.95	0.95	0.59	MW0826		conserved hypothetical protein	
0.68	1.09	1.00	1.16	1.03	0.81	0.83	0.84	1.15	1.02	0.10	MW0827		hypothetical protein	
0.92	0.92	0.79	0.89	1.00	0.64	0.79	0.63	1.11	0.89	1.25	MW0828	mnhG	Na+/H+ antiporter subunit	membrane bioenergetics
0.90	0.89	0.80	0.90	0.97	0.43	0.90	0.60	1.06	0.92	1.50	MW0829	mnhF	Na+/H+ antiporter subunit	membrane bioenergetics
0.95	0.55	0.55	0.37	0.68	0.23	0.72	0.47	0.63	0.82	1.32	MW0830	mnhE	Na+/H+ antiporter subunit	membrane bioenergetics
0.72	0.84	0.64	0.69	0.81	0.43	0.83	0.67	0.83	0.81	1.45	MW0831	mnhD	Na+/H+-antiporter subunit	membrane bioenergetics
0.71	1.00	0.79	0.96	0.96	0.53	0.79	0.54	1.21	0.72	1.12	MW0832	mnhC	Na+/H+ antiporter subunit	membrane bioenergetics
0.71	0.75	0.77	0.97	0.95	0.49	0.92	0.68	1.06	0.84	1.26	MW0833	mnhB	Na+/H+ antiporter subunit	membrane bioenergetics
0.52	1.07	0.96	1.29	1.03	0.93	0.68	0.58	1.01	0.83	1.22	MW0834	mnhA	Na+/H+ antiporter subunit	membrane bioenergetics
0.81	0.76	0.79	0.98	0.75	0.82	0.86	0.67	1.03	0.81	1.10	MW0835		conserved hypothetical protein	RNA synthesis
0.92	0.86	0.77	1.08	0.78	0.80	0.83	0.78	1.16	0.81	1.14	MW0836		peptidyl-prolyl cis-trans isomerase homologue	protein folding
1.31	1.04	1.04	1.00	1.03	1.07	0.78	0.70	1.36	1.07	1.89	MW0837		hypothetical protein, similar to polyribonucleotide nucleotidyltransfer	[illegible]
1.50	0.87	0.92	0.95	0.80	0.69	1.06	0.72	1.17	1.06	1.68	MW0837n		hypothetical protein, similar to polyribonucleotide nucleotidyltransferase	[illegible]
1.00	1.13	1.09	1.00	0.92	1.37	1.02	1.13	0.94	1.06	1.45	MW0838		hypothetical protein, similar to NADH-dependent flavin oxidoreductase	membrane bioenergetics
0.78	1.62	1.01	0.91	0.97	2.89	0.73	1.09	0.79	0.97	0.77	MW0839	rocD	ornithine aminotransferase	amino acid metabolism
0.85	1.37	1.10	0.86	1.07	4.18	0.84	1.66	0.89	1.07	0.82	MW0840	gudB	NAD-specific glutamate dehydrogenase	amino acid metabolism
0.92	1.75	1.34	0.99	1.29	4.49	1.22	2.18	1.21	1.05	0.79	MW0841	glpQ	glycerophosphoryl diester phosphodiesterase	lipid metabolism
0.87	1.68	1.15	1.06	1.16	7.53	1.07	1.55	1.13	1.04	0.72	MW0842	argH	argininosuccinate lyase	amino acid metabolism
0.85	1.66	1.11	1.13	1.17	13.00	0.98	1.43	1.16	0.91	0.63	MW0843	argG	argininosuccinate synthase	amino acid metabolism

0.96	1.20	0.82	1.44	1.12	1.52	0.83	2.14	0.89	0.80	1.16	MW0844	pgi	glucose-6-phosphate isomerase A	carbohydrate metabolism
1.36	0.80	0.90	1.01	1.21	0.95	1.26	1.30	0.92	0.91	1.40	MW0845		conserved hypothetical protein	
1.13	0.91	0.86	0.90	1.15	0.87	1.05	1.02	0.92	0.83	1.24	MW0846	spsA	type-I signal peptidase	protein secretion
0.91	0.92	0.84	1.10	0.99	0.76	0.85	0.59	1.07	0.93	1.33	MW0847	spsB	type-1 signal peptidase 1B	protein secretion
0.92	1.03	1.08	1.00	0.97	1.55	0.97	1.26	1.02	0.93	1.04	MW0848		hypothetical protein, similar to ATP-dependent nuclease subunit B	DNA repair or modify
0.91	1.05	0.97	0.91	0.94	1.39	1.02	1.36	0.90	1.00	1.10	MW0849		hypothetical protein, similar to ATP-dependent nuclease subunit A	DNA repair or modify
0.70	1.19	0.79	1.00	0.79	0.98	0.70	0.97	0.78	0.92	0.88	MW0850		hypothetical protein, similar to 5-oxo-1,2,5-tricarboxilic-3-penten acid decarboxy	aminoacid metabolism
0.95	1.06	0.93	1.03	1.00	1.16	0.77	1.06	1.07	1.01	0.90	MW0851		conserved hypothetical protein	
0.74	1.27	0.96	1.38	1.11	1.21	0.83	1.02	0.97	1.05	1.72	MW0852	cdr	coenzyme A disulfide reductase	coenzyme metabolism
0.91	1.25	1.01	1.07	0.95	1.26	0.95	1.14	0.86	1.11	1.19	MW0853		conserved hypothetical protein	
1.08	0.72	0.86	1.10	1.03	0.70	0.89	0.50	1.19	1.09	1.21	MW0854		conserved hypothetical protein	
1.14	0.94	0.93	1.20	0.91	0.68	0.90	0.70	1.11	0.99	1.32	MW0855		hypothetical protein	
1.60	0.67	0.82	0.95	0.85	0.44	0.88	0.70	1.15	1.03	1.26	MW0855n		hypothetical protein	
0.83	0.91	1.04	1.18	1.03	1.49	1.05	1.18	1.05	1.18	1.19	MW0856		hypothetical protein, similar to lipopolysaccharide modification acyltransferas	cell wall
0.80	1.35	1.19	1.48	1.08	3.16	1.36	1.10	0.85	1.17	0.23	MW0857	clpB	clpB	adaptation to atypical
0.70	1.47	1.25	1.33	1.05	1.92	1.10	1.19	1.03	1.24	0.93	MW0858		hypothetical protein, similar to transcription regulator LysR family	RNA synthesis
0.64	1.20	1.18	1.51	1.12	1.33	1.09	0.97	1.11	1.17	1.04	MW0859		hypothetical protein, similar to 2-isopropylmalate synthase	aminoacid metabolism
0.60	1.19	1.31	1.45	1.02	1.31	1.00	1.20	1.11	1.10	1.12	MW0860		conserved hypothetical protein	
0.77	1.21	1.16	1.04	0.96	1.26	1.07	1.19	0.62	1.09	1.31	MW0861		hypothetical protein	
0.78	1.38	1.14	1.29	0.99	1.09	0.85	1.09	1.19	0.99	1.04	MW0862		conserved hypothetical protein	
0.74	1.68	1.56	1.24	0.86	1.95	1.04	1.86	0.00	1.32	1.36	MW0862n		conserved hypothetical protein	
0.88	0.90	0.96	1.20	1.03	0.93	0.86	1.05	1.06	0.93	0.71	MW0863		hypothetical protein, similar to cell surface protein Map-w	pathogenic factor
1.03	0.78	0.90	1.21	0.94	0.69	0.69	0.76	1.13	0.92	1.06	MW0864		hypothetical protein	
0.81	1.09	1.05	1.35	0.85	0.77	0.77	1.09	1.26	0.86	0.51	MW0865	FabH	FabH	lipid metabolism
0.71	1.10	1.19	1.57	0.95	0.69	0.84	0.96	1.26	0.93	0.66	MW0866	fab	3-oxoacyl- synthase	lipid metabolism
0.74	0.74	0.80	1.32	0.76	0.40	0.65	0.45	0.75	0.94	0.87	MW0867		hypothetical protein	
0.50	0.42	0.44	0.64	0.53	0.21	0.21	0.13	0.39	0.79	0.59	MW0868	oppB	oligopeptide transport system permease protein	transport/binding
0.57	0.52	0.56	0.52	0.61	0.22	0.22	0.09	0.41	0.76	0.62	MW0869		hypothetical protein, similar to oligopeptide transport system permease protein C	transport/binding
0.65	0.35	0.50	0.35	0.54	0.16	0.30	0.15	0.35	1.05	0.76	MW0870	oppD	oligopeptide transport system ATP-binding protein OppD homologue	transport/binding
0.60	0.44	0.63	0.90	0.62	0.18	0.29	0.09	0.48	0.96	0.68	MW0871	oppF	ligopeptide transport system ATP-binding protein OppF homologu	transport/binding
0.73	0.45	0.57	0.44	0.55	0.15	0.30	0.10	0.38	0.95	0.67	MW0871n	oppF	oligopeptide transport system ATP-binding protein OppF homologue	transport/binding
0.82	0.17	0.35	0.08	0.38	0.03	0.26	0.05	0.21	1.08	0.61	MW0872		hypothetical protein, similar to peptide binding protein OppA	transport/binding
0.53	0.97	0.92	0.95	0.89	0.45	0.70	0.58	0.93	1.01	0.97	MW0873		hypothetical protein, similar to oligopeptide ABC transporter oligopeptide-binding p	transport/binding
0.65	1.21	1.04	1.12	0.82	0.62	0.89	0.68	1.08	1.03	1.14	MW0874		oligopeptide ABC transporter ATP-binding protein homologue	transport/binding
0.76	0.91	0.97	0.90	0.85	0.62	0.97	0.71	1.09	1.05	1.07	MW0875	appF	oligopeptide transport system ATP-binding protein AppF homologue	transport/binding
0.71	0.87	0.85	0.51	0.83	0.56	0.83	0.63	0.76	1.00	1.17	MW0876	oppB	probable oligopeptide transport system permease protein OppB	transport/binding
0.73	1.07	0.89	1.14	0.96	0.79	0.87	0.69	1.08	0.93	1.14	MW0877		Hypothetical protein, similar to oligopeptide transport system permease protein C	transport/binding
0.77	0.67	0.63	0.98	0.74	0.63	0.73	0.52	0.97	0.78	1.70	MW0878	trpS	tryptophanyl-tRNA synthetase	protein synthesis
1.02	0.51	0.80	1.04	0.87	0.47	0.81	0.16	1.01	1.46	0.89	MW0879		conserved hypothetical protein	
1.08	0.72	0.53	0.56	0.79	0.47	0.90	0.50	0.97	0.98	1.39	MW0880		hypothetical protein, similar to negative regulator of genetic competence MecA	
0.97	0.40	0.58	0.39	0.71	0.62	0.97	0.72	0.99	0.73	1.00	MW0881		hypothetical protein, similar to transcription factor	RNA synthesis
1.04	0.58	0.46	0.65	0.58	0.62	0.91	1.01	0.96	0.66	1.59	MW0882		thimet oligopeptidase homologue	aminoacid metabolism
1.04	1.11	0.85	1.28	0.93	1.34	0.87	0.76	1.19	0.94	1.10	MW0883		conserved hypothetical protein	
1.21	0.81	0.64	0.92	0.84	1.34	1.07	0.75	1.12	0.65	0.93	MW0883n		conserved hypothetical protein	
1.20	0.55	0.62	0.72	0.70	1.47	1.12	0.87	1.12	0.73	0.96	MW0884		conserved hypothetical protein	
1.00	0.50	0.59	0.40	0.69	0.79	0.85	0.71	0.85	0.63	0.66	MW0885		conserved hypothetical protein	
0.97	0.52	0.47	0.70	0.56	0.88	0.81	0.69	0.72	0.59	0.74	MW0886		conserved hypothetical protein	
0.90	0.68	0.61	0.91	0.74	0.99	0.92	0.74	0.88	0.61	0.75	MW0887	relA	GTP pyrophosphokinase	nucleic acid metabolism
1.05	0.86	0.77	1.20	0.81	1.00	0.83	0.72	1.12	0.81	0.91	MW0888		conserved hypothetical protein	
0.73	0.83	0.92	0.99	0.88	1.00	0.91	0.81	0.97	1.08	0.97	MW0889		conserved hypothetical protein	
1.09	0.76	0.70	0.81	0.66	0.80	1.12	0.74	0.99	0.67	0.91	MW0890		hypothetical protein, similar to Mg2+ transporter	transport/binding
1.01	1.05	0.76	0.69	1.00	0.77	0.87	1.00	0.78	0.86	1.34	MW0891		Na+/H+ antiporter homologue	membrane bioenergetics
0.86	1.27	0.81	0.79	1.09	1.03	0.72	0.90	0.94	0.84	1.36	MW0892	fabI	trans-2-enoyl-ACP reductase	lipid metabolism
0.82	0.91	0.89	1.16	1.11	0.84	0.85	0.92	0.93	0.91	1.39	MW0893		conserved hypothetical protein	
0.66	0.76	0.62	0.66	0.81	0.52	0.47	0.60	0.41	1.09	1.06	MW0894		hypothetical protein, similar to Na+/H+-dependent alanine carrier protein	transport/binding
0.94	1.03	0.88	0.91	0.85	0.94	0.72	0.69	0.84	0.86	1.04	MW0895		conserved hypothetical protein	
1.04	1.44	1.25	1.42	1.26	1.33	0.88	1.08	1.20	1.08	0.29	MW0896		conserved hypothetical protein	
0.94	1.71	1.03	1.07	1.17	1.00	0.83	1.11	1.22	0.90	1.58	MW0897		hypothetical protein, similar to multidrug resistance protein-related protein	detoxification
1.03	1.42	0.94	1.00	1.00	0.93	0.86	1.17	0.96	0.91	1.32	MW0898		hypothetical protein, similar to cell wall synthesis protein	cell wall
0.73	1.36	1.00	1.16	1.04	1.03	0.86	0.75	1.15	1.03	1.16	MW0899	murE	UDP-N-acetylmuramoylalanyl-D-glutamate—2, 6-diaminopimelate ligase	cell wall
1.04	1.11	0.95	0.94	1.12	1.08	0.92	0.90	1.15	0.96	1.69	MW0900		hypothetical protein	
0.86	1.38	1.07	1.06	1.11	0.97	0.80	0.90	1.25	1.00	1.24	MW0901	prfC	peptide chain release factor 3	protein synthesis
1.15	1.75	1.37	1.24	1.24	0.95	1.00	1.03	1.61	1.35	1.53	MW0902		toxic anion resistance protein homologue	detoxification
0.79	1.19	0.91	1.06	1.12	0.90	0.80	1.05	0.94	0.94	1.46	MW0904		hypothetical protein, similar to Na+-transporting ATP synthase	membrane bioenergetics
0.80	1.24	0.97	1.19	1.11	0.99	0.88	0.85	1.15	0.98	0.88	MW0905		hypothetical protein, similar to nucleotidase	phosphate metabolism
0.90	1.53	1.04	1.04	1.10	0.96	0.85	1.00	1.24	1.03	1.09	MW0906		hypothetical protein, similar to competence transcription factor	transformation/competence
0.81	0.09	0.35	0.42	0.73	0.13	0.35	0.05	0.25	1.03	0.21	MW0907		hypothetical protein	
1.09	0.60	0.62	0.49	0.74	0.53	0.92	1.01	0.99	0.75	0.63	MW0908		lipoate-protein ligase homolog	protein modification
1.75	0.86	0.98	0.67	0.70	0.47	1.38	0.79	1.34	1.09	1.17	MW0909		conserved hypothetical protein	
1.11	0.94	1.05	0.90	1.07	0.54	1.09	0.61	1.61	1.03	1.08	MW0909n		conserved hypothetical protein	
1.15	1.26	1.19	1.32	1.17	0.83	0.92	0.75	1.82	0.95	1.14	MW0910		hypothetical protein	
0.95	1.29	1.23	1.02	1.16	1.28	1.09	1.22	1.03	1.24	1.01	MW0912		hypothetical protein, similar to lactococcin 972	pathogenic factor
0.67	1.00	0.00	0.00	0.24	1.00	2.63	9.75	1.00	0.88	2.64	MW0914		hypothetical protein, similar to lactococcin 972 immunity factor	transport/binding
0.76	1.14	1.13	1.23	1.11	1.07	0.82	0.92	1.04	1.03	1.18	MW0915		conserved hypothetical protein	
0.66	1.60	1.35	1.22	1.20	1.25	0.94	1.21	1.02	1.05	0.97	MW0916		conserved hypothetical protein	
0.90	1.08	1.35	1.51	1.29	1.20	1.09	0.96	1.21	1.00	1.40	MW0917		hypothetical protein	
0.83	0.94	1.21	1.29	1.18	1.00	1.04	0.73	1.08	1.13	1.27	MW0918		hypothetical protein	
0.96	0.95	1.15	0.98	1.21	1.29	0.97	1.09	1.16	1.04	1.71	MW0919		pothetical protein, similar to UDP-glucose:polyglycerol phosphate glucosyltransferase	
1.53	0.75	0.99	0.63	1.22	0.53	0.65	0.48	0.91	0.69	5.07	MW0920		conserved hypothetical protein	
0.92	1.11	1.24	1.14	1.28	1.30	1.19	1.15	1.38	1.10	1.02	MW0921		hypothetical protein, similar to ferrichrome ABC transporter	transport/binding
0.97	1.25	1.30	1.24	1.19	1.25	1.17	1.17	1.06	1.13	0.91	MW0921n		hypothetical protein, similar to ferrichrome ABC transporter	transport/binding
1.27	1.08	1.10	1.04	0.95	1.86	1.57	1.13	1.18	1.22	0.91	MW0922		hypothetical protein	
0.92	1.05	0.99	0.96	1.00	0.98	0.89	1.01	1.09	0.98	1.03	MW0923		hypothetical protein	
0.97	1.09	0.98	1.09	0.88	0.91	1.02	1.16	1.17	0.95	1.07	MW0923n		hypothetical protein	
1.06	0.86	0.81	0.89	1.31	1.00	1.34	1.29	1.30	0.71	0.71	MW0924		conserved hypothetical protein	
0.92	0.86	1.03	0.92	1.25	0.77	1.02	0.88	1.40	1.04	1.49	MW0925		hypothetical protein, similar to 1,4-dihydroxy-2-naphthodate octaprenyltransfer	coenzyme metabolism
1.34	1.40	1.33	1.04	0.90	1.79	1.38	2.40	1.17	0.86	0.67	MW0926		hypothetical protein, similar to menaquinone-specific isochorismate synthase	coenzyme metabolism
1.22	1.83	1.22	1.28	1.26	1.40	1.61	2.67	1.30	0.92	1.01	MW0927	menD	menaquinone biosynthesis protein	coenzyme metabolism
0.82	1.49	1.20	1.04	1.00	1.26	1.35	1.46	1.18	1.05	0.89	MW0928		hypothetical protein, similar to prolyl aminopeptidase	protein modification
0.81	1.67	1.24	1.34	1.31	2.66	1.22	1.83	1.16	1.02	0.91	MW0929	menB	naphthoate synthase	coenzyme metabolism
0.94	1.26	1.22	0.99	1.12	1.21	1.12	1.27	0.96	1.04	1.05	MW0930	sspC	cysteine protease	pathogenic factor
1.25	0.57	0.73	0.85	1.15	0.49	1.47	0.65	0.94	0.85	3.08	MW0931	sspB	cysteine protease precursor	pathogenic factor
1.01	1.09	1.11	1.09	1.26	1.47	1.13	1.29	1.18	1.02	0.94	MW0931a	sspB	cysteine protease precursor	pathogenic factor
0.90	1.17	1.12	0.92	1.29	1.20	1.06	1.69	0.77	1.00	1.15	MW0932	sspA	serine protease; V8 protease; glutamyl endopeptidase	pathogenic factor
0.96	0.50	0.57	0.60	0.67	0.36	0.95	0.39	1.04	0.75	1.31	MW0933	hisC	HisC homolog	aminoacid metabolism
0.92	1.02	0.98	0.66	1.03	0.70	0.93	1.11	0.87	0.95	1.20	MW0934		conserved hypothetical protein	
0.93	1.07	0.98	0.96	1.17	0.82	1.05	0.52	1.19	0.91	1.73	MW0935	atlR	hypothetical protein, probable ATL autolysin transcription regulator	RNA synthesis

1.64	0.67	0.80	0.39	1.27	0.29	1.95	0.20	0.90	0.80	1.26	MW0936	atl	autolysin	cell division
0.95	1.16	1.03	1.12	0.99	0.81	0.83	0.82	1.32	0.92	0.72	MW0937		conserved hypothetical protein	
0.89	0.97	0.77	0.86	0.98	0.59	0.69	0.74	0.94	0.79	0.73	MW0938		conserved hypothetical protein	
0.80	0.94	0.67	0.77	0.80	0.52	0.75	0.41	1.03	0.74	1.34	MW0939		conserved hypothetical protein	
0.98	1.02	0.93	0.82	0.90	0.88	0.73	0.80	1.18	0.87	1.01	MW0940	fmtA	FmtA, autolysis and methicillin resistant-related protein	pathogenic factor
0.91	0.92	0.95	0.93	1.15	0.49	1.25	0.80	1.28	0.82	1.43	MW0941		hypothetical protein, similar to quinol oxidase polypeptide IV QoxD	membrane bioenergetics
0.74	0.81	1.08	0.78	1.21	0.83	1.17	0.69	1.22	1.00	1.58	MW0942	qoxC	Quinol oxidase polypeptide III QoxC	membrane bioenergetics
0.81	0.87	1.45	1.24	1.19	0.86	1.16	1.21	1.17	1.13	1.61	MW0943	qoxB	Quinol oxidase polypeptide I QoxB	membrane bioenergetics
0.77	0.77	1.05	0.58	0.91	0.90	1.04	0.99	0.95	0.88	1.38	MW0944		hypothetical protein, similar to quinol oxidase polypeptide II QoxA	membrane bioenergetics
1.37	1.07	0.97	1.00	1.22	1.16	1.29	0.69	1.03	0.77	1.28	MW0945		hypothetical protein, similar to chitinase B	miscellaneous
0.97	1.15	0.88	0.83	0.80	1.14	0.87	1.14	0.77	1.05	0.52	MW0946	folD	FolD bifunctional protein	coenzyme metabolism
0.91	0.92	1.14	1.48	0.99	1.12	0.96	0.76	1.15	1.12	0.98	MW0947		hypothetical protein, similar to phosphoribosylaminoimidazole carboxylase Pur	[illegible]
0.80	1.05	1.15	1.42	1.16	1.70	0.99	1.07	1.40	1.08	1.16	MW0948	purK	phoribosylaminoimidazole carboxylase carbon dioxide-fixation chain PurK hon	[illegible]
0.99	1.37	1.09	1.06	1.02	1.26	1.22	1.21	1.37	1.10	1.57	MW0949	purC	phosphoribosylaminoimidazolesuccinocarboxamide synthetase homolog	[illegible]
1.10	1.12	1.08	0.97	1.08	1.13	1.00	1.35	1.00	1.04	1.49	MW0950		conserved hypothetical protein	
0.90	0.95	1.11	1.10	1.04	1.38	1.01	1.12	1.16	1.11	1.42	MW0951	purQ	phosphoribosylformylglycinamidine synthase I PurQ	[illegible]
1.08	0.41	0.81	0.43	0.59	0.95	1.14	1.56	0.94	0.93	1.78	MW0952	purL	phosphoribosylformylglycinamidine synthetase PurL	[illegible]
1.06	1.46	1.17	1.00	1.20	1.82	1.17	1.75	1.05	0.94	2.23	MW0953	purF	phosphoribosylpyrophosphate amidotransferase PurF	[illegible]
1.14	1.16	0.72	0.89	1.00	1.11	1.27	1.06	1.04	0.84	1.63	MW0954	purM	phosphoribosylformylglycinamidine cyclo-ligase PurM	[illegible]
1.00	1.16	1.10	0.89	1.10	1.24	0.98	1.32	0.89	1.00	2.17	MW0955	purN	phosphoribosylglycinamide formyltransferase	[illegible]
0.98	1.04	1.20	0.98	0.94	1.26	1.24	1.14	1.04	1.17	2.16	MW0956	purH	bifunctional purine biosynthesis protein PurH	[illegible]
1.15	0.55	0.73	0.39	0.67	0.72	1.02	0.98	0.57	0.98	1.73	MW0957	purD	phosphoribosylamine--glycine ligase PurD	[illegible]
1.04	0.84	0.75	0.73	0.86	0.79	0.98	0.82	0.93	0.97	1.85	MW0957n	purD	phosphoribosylamine--glycine ligase PurD	[illegible]
0.83	1.01	0.92	0.78	0.79	0.73	1.13	1.59	1.01	1.02	0.64	MW0958		conserved hypothetical protein	[illegible]
0.98	0.75	0.27	0.13	0.63	0.11	0.29	0.08	0.40	0.79	1.25	MW0959		hypothetical protein, similar to cation ABC transporter	transport/binding
0.74	1.03	0.86	1.16	0.91	0.87	0.71	0.73	0.85	1.04	0.57	MW0960		conserved hypothetical protein	
1.05	1.21	1.00	1.17	0.88	1.21	2.11	1.14	1.26	1.01	1.04	MW0961		hypothetical protein	
0.97	1.35	0.96	1.10	0.92	1.19	1.36	1.16	0.86	1.07	0.79	MW0961n		hypothetical protein	
0.66	1.36	1.26	0.87	0.98	0.83	1.07	0.81	3.45	8.51	9.73	MW0962		hypothetical protein	
0.90	1.14	1.19	1.06	0.99	0.99	1.14	0.88	2.75	2.35	2.25	MW0963		conserved hypothetical protein	
1.14	1.91	1.00	1.21	0.87	5.64	1.99	1.42	0.74	1.25	0.73	MW0964		hypothetical protein	
0.95	0.82	0.77	1.36	1.09	1.60	1.35	2.18	0.78	0.86	0.83	MW0965	ptsH	phophocarrier protein HPR	protein modification
0.88	0.98	0.91	1.15	0.91	1.16	1.28	1.77	0.82	0.97	0.93	MW0966	ptsI	phosphoenolpyruvate-protein phosphatase	protein modification
0.89	0.99	0.94	1.11	0.86	0.72	0.73	0.73	1.10	0.93	1.12	MW0967		conserved hypothetical protein	
0.74	1.66	1.01	0.91	1.15	0.84	0.92	1.03	1.20	0.89	0.67	MW0968	cydA	cytochrome D ubiquinol oxidase subunit 1 homolog	membrane bioenergetics
0.71	1.26	0.92	1.17	1.03	0.74	0.71	0.58	1.38	0.96	0.87	MW0970		conserved hypothetical protein	
1.11	0.87	1.09	1.00	0.94	0.77	1.13	0.89	1.25	1.12	0.95	MW0971		hypothetical protein	
1.14	0.73	0.69	0.49	1.05	0.62	0.91	1.42	0.92	0.89	1.41	MW0972		conserved hypothetical protein	
1.17	1.20	0.79	0.94	0.89	0.69	0.89	0.81	1.21	1.14	1.03	MW0973		conserved hypothetical protein	
1.26	0.84	0.76	0.85	0.94	0.84	0.83	0.90	1.22	1.02	0.95	MW0973n		conserved hypothetical protein	
1.24	1.22	0.83	0.76	1.17	1.07	0.83	1.42	0.90	0.84	1.24	MW0974	pdf1	formylmethionine deformylase homolog	aminoacid metabolism
1.33	0.94	0.64	0.58	1.05	0.85	0.72	1.00	0.76	0.82	1.26	MW0975		conserved hypothetical protein	
1.05	1.34	1.07	1.16	0.99	1.73	1.15	4.07	1.05	1.09	1.10	MW0976	pdhA	pyruvate dehydrogenase E1 component alpha subunit	carbohydrate metabolism
0.97	2.09	1.09	1.47	1.24	2.82	1.01	3.63	1.20	0.77	1.07	MW0977	pdhB	pyruvate dehydrogenase E1 component beta subunit	carbohydrate metabolism
1.04	1.49	0.98	0.93	1.26	2.02	1.10	3.98	1.15	0.81	1.16	MW0978	pdhC	olipoamide S-acetyltransferase component of pyruvate dehydrogenase comp	carbohydrate metabolism
0.85	1.82	0.99	1.57	1.27	1.52	1.02	2.32	1.23	0.98	1.27	MW0979	pdhD	dihydrolipoamide dehydrogenase component of pyruvate dehydrogenase E3	carbohydrate metabolism
1.14	1.07	0.88	1.08	0.85	1.00	0.86	0.90	1.23	0.85	1.05	MW0980		conserved hypothetical protein	
1.19	0.95	0.81	0.64	0.98	0.88	0.64	0.90	0.86	0.71	0.75	MW0981		conserved hypothetical protein	
1.09	1.08	0.86	0.65	1.11	0.85	0.70	0.99	0.83	0.73	0.73	MW0982	potA	spermidine/putrescine ABC transporter, ATP-binding protein homolog	transport/binding
1.18	0.69	0.80	0.50	1.18	0.70	0.78	0.94	0.61	0.81	0.69	MW0983	potB	potB	transport/binding
1.03	0.78	0.86	0.69	0.84	0.58	0.79	0.71	0.83	0.85	0.84	MW0984	potC	spermidine/putrescine ABC transporter homolog	transport/binding
0.82	0.94	0.84	0.57	1.06	0.91	0.74	0.79	0.75	0.76	0.67	MW0985	potD	spermidine/putrescine-binding protein precursor homolog	transport/binding
1.11	1.34	0.93	0.52	1.11	0.99	0.86	0.87	1.34	0.85	2.35	MW0986		conserved hypothetical protein	
1.40	0.96	0.85	0.81	0.94	0.84	0.91	1.04	0.79	0.87	2.03	MW0987		hypothetical protein	
0.90	0.38	0.65	0.32	0.62	0.46	0.85	0.71	0.64	0.97	1.61	MW0988		hypothetical protein, similar to Mn2+-transport protein	transport/binding
0.79	1.11	1.08	1.15	0.95	0.95	0.77	0.82	0.96	0.86	1.04	MW0989		conserved hypothetical protein	
0.98	0.91	0.94	1.26	0.93	1.05	0.77	0.80	0.73	1.09	0.77	MW0990		myo-inositol-1(or 4)-monophosphatase homolog	carbohydrate metabolism
0.83	0.77	1.32	3.18	1.07	0.90	0.82	1.05	0.92	1.14	0.68	MW0991		hypothetical protein	
0.73	1.16	1.27	2.00	1.01	0.85	0.93	1.26	0.91	1.12	0.29	MW0992		GTP-binding elongation factor homolog	protein synthesis
1.11	0.76	0.86	0.84	0.81	0.60	0.79	0.55	0.86	1.03	1.00	MW0993		conserved hypothetical protein	
0.97	0.72	0.91	1.10	0.85	0.67	0.89	0.66	0.63	0.97	0.97	MW0993n		conserved hypothetical protein	
0.96	0.94	0.93	1.19	0.98	0.77	0.77	0.70	0.80	0.97	0.97	MW0994		conserved hypothetical protein	
0.95	0.52	0.71	0.80	0.79	0.42	0.54	0.46	0.83	0.89	0.80	MW0995		conserved hypothetical protein	
0.86	0.98	0.91	1.00	0.94	0.54	0.67	0.64	1.25	1.00	1.60	MW0996		conserved hypothetical protein	
0.93	0.93	0.96	1.36	1.00	0.66	0.60	0.57	1.03	1.06	1.53	MW0996n		conserved hypothetical protein	
0.82	0.68	0.76	0.65	0.89	0.57	0.55	0.58	0.68	0.91	2.03	MW0997	pycA	pyruvate carboxylase	carbohydrate metabolism
1.11	1.29	1.18	0.87	1.29	0.89	0.92	0.96	0.98	1.00	1.18	MW0998		hypothetical protein, similar to heme synthase	membrane bioenergetics
0.77	0.89	1.33	1.00	1.51	1.10	1.11	0.92	1.22	1.07	1.25	MW0999	ctaB	cytochrome caa3 oxidase (assembly factor) homolog	membrane bioenergetics
1.13	0.76	1.22	0.85	1.36	0.71	1.18	0.70	1.32	1.00	1.25	MW1000		conserved hypothetical protein	
1.06	0.68	0.76	0.77	0.92	0.73	1.08	0.77	1.27	0.68	0.91	MW1001		conserved hypothetical protein	
1.10	1.18	1.00	1.12	1.08	0.94	0.93	0.95	1.09	1.00	1.24	MW1002		conserved hypothetical protein	
1.03	1.16	1.04	1.19	1.03	0.89	0.89	0.96	1.10	1.06	1.24	MW1003		hypothetical protein, similar to glycerophosphoryl diester phosphodiesterase	lipid metabolism
1.04	0.94	1.01	1.16	0.83	0.78	0.84	0.92	1.16	0.92	1.18	MW1004		conserved hypothetical protein	
0.86	0.96	0.97	1.13	1.02	0.84	0.87	0.94	1.18	0.94	1.06	MW1005		conserved hypothetical protein	
1.04	1.09	1.10	1.14	0.96	0.94	0.89	1.00	1.26	0.98	1.16	MW1006		conserved hypothetical protein	
0.98	1.20	1.19	1.28	1.04	0.96	1.03	1.02	1.11	1.08	1.21	MW1007		phosphopantetheine adenyltransferase homolog	coenzyme metabolism
0.95	1.14	1.05	1.15	1.10	1.05	0.81	0.99	1.23	0.95	0.91	MW1008		conserved hypothetical protein	
0.73	0.99	0.85	0.66	1.00	0.32	0.53	0.52	1.06	0.80	0.65	MW1009		conserved hypothetical protein	
1.04	0.71	0.71	0.79	0.80	0.38	0.55	0.44	1.16	0.80	0.67	MW1010	rpmF	ribosomal protein L32	protein synthesis
1.04	0.72	0.67	0.77	0.89	0.32	0.60	0.42	1.05	0.81	0.83	MW1010n	rpmF	ribosomal protein L32	protein synthesis
0.94	1.03	1.03	1.30	0.97	0.86	0.88	0.88	1.23	1.01	1.18	MW1011	isdB	conserved hypothetical protein	
0.78	0.55	1.10	2.76	0.79	0.51	0.71	0.92	1.36	0.86	2.73	MW1012	isdA	cell surface protein	pathogenic factor
0.84	0.81	1.00	2.38	0.85	0.78	0.69	1.00	1.35	0.82	1.32	MW1013	isdC	conserved hypothetical protein	
1.09	0.66	0.99	1.72	0.84	0.76	0.74	0.98	1.06	0.87	1.05	MW1014	isdD	conserved hypothetical protein	
1.06	0.70	1.12	1.82	0.81	0.75	1.03	1.04	1.43	0.82	0.97	MW1015	isdE	hypothetical protein, similar to ferrichrome ABC transporter	transport/binding
0.94	1.17	1.45	2.46	1.10	1.06	0.82	1.21	1.66	1.14	1.07	MW1016	isdF	hypothetical protein, similar to ferrichrome ABC transporter	transport/binding
1.24	0.76	0.95	0.84	0.70	0.77	0.92	0.97	0.76	0.92	1.09	MW1016n	isdF	hypothetical protein, similar to ferrichrome ABC transporter	transport/binding
1.03	0.80	1.06	1.50	0.89	0.64	0.76	1.07	1.25	0.90	1.12	MW1017	srtB	NPQTN specific sortase B	
0.91	1.03	1.10	1.39	1.16	0.77	0.79	0.99	1.11	0.89	1.16	MW1018	isdG	conserved hypothetical protein	
1.01	0.92	1.19	1.50	0.88	0.83	0.92	1.15	1.33	1.05	1.07	MW1018n	isdG	conserved hypothetical protein	
1.00	1.09	0.91	0.91	0.85	0.81	0.94	1.13	1.20	0.95	1.20	MW1019		hypothetical protein	
0.90	1.14	0.99	1.13	0.93	0.76	1.12	0.95	1.15	1.00	0.97	MW1020		hypothetical protein, similar to rRNA methylase	RNA modification
1.07	1.42	1.10	1.08	1.22	1.19	0.91	1.75	1.16	0.85	0.58	MW1021	pheS	Phe-tRNA synthetase alpha chain	protein synthesis
0.88	1.03	1.10	1.16	1.06	0.87	1.00	1.77	0.84	1.19	0.58	MW1022	pheT	Phe-tRNA synthetase beta chain	protein synthesis
1.07	1.63	1.06	0.84	1.28	1.51	0.88	1.88	0.95	0.87	1.08	MW1023		hypothetical protein, similar to ribonuclease HIII	RNA modification
1.07	1.51	1.02	0.86	1.07	1.28	1.06	1.55	0.75	0.91	1.02	MW1024		conserved hypothetical protein	
1.32	1.42	0.98	0.80	0.90	1.19	0.96	1.92	1.14	1.09	1.23	MW1025		conserved hypothetical protein	

1.01	0.94	1.01	0.65	0.82	1.15	1.34	1.44	1.04	1.09	0.89	MW1026		DNA-dependent DNA polymerase beta chain	DNA replication
0.55	1.12	0.71	1.04	0.93	1.29	0.61	0.79	0.91	0.88	1.00	MW1027	mutS2	MutS-like protein	DNA repair or modify
1.99	1.22	1.15	1.01	0.88	1.14	1.29	1.59	0.89	1.02	1.90	MW1028	trxA	thioredoxin	membrane bioenergetics
1.05	1.68	1.24	0.64	1.01	2.40	1.19	1.48	0.91	1.36	0.83	MW1029	uvrC	excinuclease ABC subunit C	DNA repair or modify
1.02	1.81	1.67	0.82	1.00	2.47	1.15	1.70	0.92	1.87	0.73	MW1030	sdhC	succinate dehydrogenase cytochrome b-558	carbohydrate metabolism
0.91	1.17	1.17	0.65	1.05	2.96	1.44	2.50	0.75	1.50	0.74	MW1031	sdhA	succinate dehydrogenase flavoprotein subunit	carbohydrate metabolism
1.13	1.03	1.10	0.76	1.28	1.43	1.46	1.58	0.67	1.20	0.75	MW1032	sdhB	succinate dehydrogenase iron-sulfur protein subunit	carbohydrate metabolism
0.93	0.75	0.84	0.83	0.88	1.00	1.09	1.00	0.84	0.90	1.25	MW1033	murI	glutamate racemase	cell wall
1.09	0.91	0.92	0.97	1.23	1.00	1.03	0.83	0.81	0.77	1.20	MW1034		conserved hypothetical protein	
1.12	0.58	0.79	0.55	1.07	0.77	1.17	1.04	0.87	0.82	1.33	MW1035		conserved hypothetical protein	
1.06	0.86	0.89	0.92	0.91	0.73	1.11	0.89	1.02	0.87	1.46	MW1036		hypothetical protein	
0.95	0.88	0.91	0.67	0.88	1.14	0.88	1.55	0.73	0.99	0.56	MW1036n		hypothetical protein	
0.79	0.23	0.69	0.67	1.45	0.21	0.93	0.51	0.39	0.69	0.99	MW1037		hypothetical protein, similar to fibrinogen-binding protein	pathogenic factor
1.11	0.67	0.71	0.59	0.88	0.50	0.88	0.64	1.09	0.78	1.00	MW1038		hypothetical protein	
0.94	1.10	1.01	1.06	1.12	1.29	0.76	0.83	1.12	0.73	0.82	MW1038n		hypothetical protein	
0.78	0.52	0.90	1.23	1.16	0.40	0.71	0.56	0.71	0.91	1.53	MW1040		hypothetical protein, similar to fibrinogen-binding protein	pathogenic factor
0.94	0.62	0.76	1.00	0.94	0.36	0.54	0.33	0.64	0.86	1.65	MW1041		hypothetical protein, similar to fibrinogen-binding protein	pathogenic factor
1.31	0.93	1.25	0.93	1.19	0.90	1.17	1.03	1.16	0.87	1.80	MW1042		hypothetical protein	
1.57	0.67	0.91	0.99	1.14	0.80	1.19	0.80	1.04	0.83	1.61	MW1043		hypothetical protein	
1.69	1.22	1.14	0.77	1.48	1.25	1.01	1.14	1.71	0.72	1.86	MW1044	hla	Alpha-Hemolysin precursor	pathogenic factor
0.91	0.62	0.70	0.36	1.00	0.69	0.92	0.63	0.42	0.98	1.26	MW1045		hypothetical protein	
0.98	0.87	1.07	1.19	1.13	1.06	0.90	0.73	1.06	1.02	1.25	MW1045n		hypothetical protein	
0.95	1.41	1.04	1.01	1.06	0.91	1.08	1.15	1.26	0.97	1.15	MW1047		hypothetical protein, similar to exotoxin 1	pathogenic factor
0.91	1.08	1.02	0.87	1.06	0.91	0.98	0.88	1.12	1.03	1.11	MW1047n		hypothetical protein, similar to exotoxin 1	pathogenic factor
0.85	1.24	1.04	1.11	1.02	1.35	1.16	1.37	1.39	1.03	1.09	MW1048		hypothetical protein, similar to exotoxin 4	pathogenic factor
1.07	1.05	1.07	1.34	1.00	1.09	1.13	1.04	0.97	1.05	1.10	MW1048n		hypothetical protein, similar to exotoxin 4	pathogenic factor
1.04	1.10	1.06	1.04	0.98	1.44	1.33	1.78	1.22	0.95	1.00	MW1049		hypothetical protein, similar to exotoxin 3	pathogenic factor
1.00	0.85	0.72	0.75	0.89	0.76	0.74	0.59	1.04	0.86	1.22	MW1049n		hypothetical protein, similar to exotoxin 3	pathogenic factor
0.86	1.26	1.54	1.37	1.17	4.10	1.12	3.14	1.34	1.23	0.99	MW1050	argF	ornithine carbamoyltransferase	amino acid metabolism
0.92	2.00	1.63	1.62	1.30	4.88	1.16	3.65	1.32	1.22	1.03	MW1051		hypothetical protein, similar to carbamate kinase	nucleic acid metabolism
1.05	1.15	1.28	1.25	1.23	4.05	1.56	5.01	1.04	1.21	1.24	MW1052		conserved hypothetical protein	
0.97	1.77	1.66	1.24	1.16	4.33	1.26	3.04	1.18	1.36	1.12	MW1052n		conserved hypothetical protein	
1.34	0.91	1.13	1.34	1.17	0.82	0.85	0.79	1.33	0.93	1.93	MW1053		hypothetical protein	
1.09	1.26	1.58	1.84	1.24	1.27	1.21	1.23	1.48	1.14	0.94	MW1054		conserved hypothetical protein	
1.02	1.14	1.31	1.21	0.96	0.94	1.15	1.16	1.07	1.10	1.00	MW1055		hypothetical protein	
28.58	12.76	4.13	0.44	0.58	0.74	0.46	0.65	39.45	1.41	0.38	MW1056		hypothetical protein, similar to antibacterial protein	pathogenic factor
30.97	11.91	4.20	0.44	0.60	0.62	0.57	0.84	35.40	1.42	0.46	MW1057		hypothetical protein, similar to antibacterial protein	pathogenic factor
1.20	1.47	1.29	1.25	0.90	1.20	1.01	0.97	1.45	1.17	0.93	MW1058		conserved hypothetical protein	
1.22	0.82	0.93	1.01	0.84	1.26	0.85	0.73	0.86	1.08	0.44	MW1059		conserved hypothetical protein	
0.93	1.03	1.05	1.29	0.97	1.39	1.00	1.07	1.24	1.18	1.25	MW1060		conserved hypothetical protein	
0.98	0.85	0.89	1.05	0.76	1.74	1.04	0.81	1.05	1.11	1.60	MW1061		conserved hypothetical protein	
0.83	0.99	1.00	1.20	0.97	2.09	1.04	0.98	1.11	1.06	1.53	MW1062		conserved hypothetical protein	
1.09	0.72	0.67	0.62	0.89	1.25	0.97	1.12	1.00	0.93	1.33	MW1063	ftsL	cell division protein	cell division
1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	7.24	1.00	MW1064	pbpA	penicillin-binding protein 1	cell wall
1.01	1.26	0.92	0.91	0.83	0.99	0.97	1.15	1.33	0.92	1.16	MW1065	mraY	phospho-N-muramic acid-pentapeptide translocase	cell wall
1.03	0.94	0.89	0.69	0.68	0.92	1.10	1.14	1.16	0.88	0.97	MW1066	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	cell wall
1.44	0.76	0.74	0.44	0.66	0.76	0.97	1.47	0.84	0.83	1.02	MW1067	div1b	cell division protein, FtsQ homolog	cell division
1.00	1.09	1.02	1.64	0.91	1.40	0.95	1.00	1.14	0.78	0.96	MW1068	ftsA	cell division protein	cell division
0.91	1.11	0.94	1.41	0.88	1.03	1.00	1.08	1.13	0.85	1.23	MW1069	ftsZ	cell division protein	cell division
1.16	1.10	0.86	0.90	0.98	1.19	0.86	1.04	0.98	0.70	1.40	MW1070		conserved hypothetical protein	
1.01	0.97	1.04	1.04	1.09	1.67	0.93	0.94	0.86	0.89	0.90	MW1071		conserved hypothetical protein	
1.00	0.95	1.04	0.87	0.96	1.34	1.02	1.21	0.81	0.85	0.96	MW1072		conserved hypothetical protein	
1.28	1.19	0.93	0.96	1.05	0.93	0.97	1.10	1.01	0.79	0.92	MW1073		conserved hypothetical protein	
1.06	1.24	0.85	0.97	1.09	1.00	0.82	0.92	0.94	0.83	1.00	MW1074		hypothetical protein, similar to cell-division protein	cell division
0.85	1.00	1.30	3.37	1.01	1.24	0.91	2.42	0.68	1.00	0.46	MW1074n		hypothetical protein, similar to cell-division protein	cell division
0.76	0.95	0.87	1.40	1.00	0.95	0.74	0.60	0.87	0.98	1.08	MW1075		hypothetical protein, similar to cell-divisio initiation protein	cell division
0.79	0.98	0.67	0.58	0.91	1.00	0.87	1.26	1.15	0.91	1.50	MW1076	ileS	Ile-tRNA synthetase	protein synthesis
0.97	1.21	1.11	0.96	1.04	1.15	0.90	1.55	1.02	0.84	1.08	MW1077		conserved hypothetical protein	
1.08	0.93	1.16	0.87	1.04	1.05	1.03	1.62	0.93	0.95	0.93	MW1078	ncated#	truncated transposase	transposon and IS
0.78	1.05	1.05	0.87	0.93	0.90	0.77	1.10	1.10	0.81	0.52	MW1079	lsp	lipoprotein signal peptidase	protein modification
0.72	1.09	1.02	1.48	0.97	0.87	0.79	1.31	1.03	0.83	0.52	MW1080		conserved hypothetical protein	
0.65	0.86	1.75	8.53	0.92	0.88	0.88	2.03	1.19	0.86	0.13	MW1081	pyrR	pyrimidine operon repressor chainA	RNA synthesis
0.54	0.87	1.60	7.03	0.92	0.96	1.00	2.72	0.81	1.01	0.10	MW1082	pyrP	uracil permease	transport/binding
0.50	1.01	1.49	6.52	0.86	1.16	0.91	2.24	1.00	0.91	0.09	MW1083	pyrB	aspartate transcarbamoylase chain A	nucleic acid metabolism
0.50	0.92	1.85	13.93	0.78	1.09	1.00	2.21	1.34	0.88	0.10	MW1084	pyrC	dihydroorotase	nucleic acid metabolism
0.51	0.87	2.08	13.61	0.92	1.15	1.04	2.88	0.89	0.92	0.10	MW1085	pyrAA	carbamoyl-phosphate synthase small chain	nucleic acid metabolism
0.69	0.68	1.87	9.82	0.83	0.94	1.18	2.44	1.05	1.07	0.14	MW1086	pyrAB	carbamoyl-phosphate synthase large chain	nucleic acid metabolism
0.88	1.03	1.82	11.89	0.87	0.94	1.36	3.68	0.77	1.04	0.11	MW1086a	pyrAB	carbamoyl-phosphate synthase large chain	nucleic acid metabolism
0.73	0.88	2.03	10.16	1.07	1.09	1.09	1.43	0.98	1.02	0.17	MW1087	pyrF	orotidine-5-phosphate decarboxylase	nucleic acid metabolism
0.82	0.70	1.61	5.98	0.97	0.95	1.01	1.45	0.87	1.05	0.30	MW1088	pyrE	orotate phosphoribosyltransferase	nucleic acid metabolism
0.88	0.72	1.42	5.20	0.89	0.92	0.98	1.25	0.53	1.00	0.37	MW1089		hypothetical protein	
0.92	0.70	1.17	1.96	0.98	0.76	1.21	1.16	0.85	1.08	0.90	MW1090		conserved hypothetical protein	
0.79	0.78	1.16	1.39	1.03	0.90	0.90	0.97	0.89	1.05	1.14	MW1091		hypothetical protein, similar to fibrinogen binding protein	pathogenic factor
0.75	0.88	0.92	0.71	0.76	1.00	0.75	0.75	0.60	1.06	1.77	MW1092	gmk	guanylate kinase homolog	nucleic acid metabolism
0.88	0.64	0.73	0.81	0.86	0.75	0.68	0.64	0.60	1.02	1.68	MW1093		conserved hypothetical protein	
0.93	0.95	0.97	0.91	0.92	1.00	0.88	1.04	0.73	1.03	1.32	MW1094		pantothenate metabolism flavoprotein homolog	coenzyme metabolism
0.80	1.13	1.08	1.20	1.06	1.20	0.94	1.09	0.99	1.07	1.06	MW1095	priA	PriA, primosomal protein	DNA replication
0.95	1.17	1.14	1.24	1.00	1.24	0.94	1.02	1.19	1.02	1.02	MW1096		hypothetical protein	
1.49	1.06	0.94	0.91	0.86	2.55	1.77	1.21	1.06	1.01	0.94	MW1097		conserved hypothetical protein	
1.08	1.17	1.23	1.29	1.06	1.05	0.92	0.96	1.17	0.98	0.99	MW1098		hypothetical protein, similar to polypeptide deformylase	protein modification
1.01	1.09	1.09	1.67	0.98	1.08	0.94	0.65	1.16	0.96	0.96	MW1099		methionyl-tRNA formyltransferase	protein synthesis
0.99	0.90	1.06	0.97	0.90	1.10	1.00	0.96	1.27	0.95	1.12	MW1100		hypothetical protein, similar to RNA-binding Sun protein	RNA modification
1.18	1.71	1.32	1.11	1.31	1.37	1.02	1.28	1.23	0.76	1.06	MW1101		conserved hypothetical protein	
1.12	1.29	1.17	1.23	1.00	0.91	1.05	0.92	1.54	0.91	1.15	MW1102		conserved hypothetical protein	
1.12	0.92	0.96	0.75	0.92	0.77	0.93	1.04	1.23	0.98	1.32	MW1103		protein kinase	protein modification
1.17	1.45	1.09	1.09	1.19	1.25	0.94	1.39	1.11	0.87	0.99	MW1104		conserved hypothetical protein	
1.24	1.17	1.05	0.94	1.17	1.36	1.00	1.39	1.05	0.87	1.08	MW1104a		conserved hypothetical protein	
1.04	1.10	0.89	1.26	0.86	0.99	0.99	1.03	1.28	0.86	1.04	MW1105	cfxE	ribulose-5-phosphate 3-epimerase homolog	carbohydrate metabolism
0.96	0.94	1.04	0.88	0.79	0.85	0.92	0.97	1.16	1.08	1.21	MW1106		conserved hypothetical protein	
1.77	0.53	0.81	0.44	0.92	0.26	1.81	0.33	1.57	1.14	3.22	MW1107	rpmB	50S ribosomal protein L28	protein synthesis
1.24	0.93	0.96	0.88	0.95	1.00	0.87	1.04	1.30	0.93	0.59	MW1108		conserved hypothetical protein	
0.88	0.97	0.94	0.96	1.11	0.79	0.88	1.45	0.78	1.07	1.45	MW1109		conserved hypotehtical protein	
1.01	1.12	0.91	1.07	1.12	1.00	0.89	1.24	0.97	0.97	1.44	MW1109a		conserved hypotehtical protein	
0.97	1.02	1.12	1.05	0.86	0.97	1.19	1.41	1.15	1.07	1.21	MW1110	recG	ATP-dependent DNA helicase	[illegible]
0.91	0.98	1.00	1.16	0.71	1.12	1.02	1.28	1.24	0.75	0.40	MW1111		conserved hypothetical protein	
1.07	1.00	0.76	1.17	0.57	0.98	1.17	1.77	1.21	0.81	0.52	MW1112	plsX	fatty acid/phospholipid synthesis protein	lipid metabolism
1.16	1.28	1.07	1.32	0.71	1.09	1.29	1.55	1.42	0.77	0.49	MW1113	fabD	malonyl CoA-acyl carrier protein transacylase	lipid metabolism

0.88	0.63	1.00	0.70	0.71	0.80	1.25	1.64	1.16	0.89	0.56	MW1114	fabG	3-oxoacyl- reductase	lipid metabolism
1.40	0.55	0.75	0.55	0.61	0.44	1.12	1.08	0.98	0.80	0.85	MW1115	hmrB	HmrB protein	lipid metabolism
1.19	0.99	0.82	1.13	0.79	1.06	1.10	1.25	1.04	0.84	0.87	MW1116	rnc	RNase III	RNA modification
1.26	1.12	0.99	0.92	0.89	1.15	1.20	1.37	1.37	0.84	0.97	MW1117	smc	chromosome segregation SMC protein	DNA packaging
0.92	1.36	0.92	1.10	0.92	1.25	0.94	1.43	1.41	0.97	1.01	MW1118	ffh	signal recognition particle	protein secretion
1.15	0.99	0.92	0.80	0.77	0.84	1.24	1.26	1.17	1.01	0.87	MW1119		conserved hypothetical protein	
1.12	1.72	1.32	1.12	1.13	1.68	1.00	1.87	1.10	1.09	0.85	MW1120	ffh	signal recognition particle homolog	protein secretion
1.33	0.65	0.80	0.44	0.91	0.33	0.73	0.69	0.71	0.83	0.82	MW1121	rpsP	30S ribosomal protein S16	protein synthesis
1.13	1.00	1.06	0.79	1.15	0.85	0.79	1.48	0.71	0.90	0.86	MW1122	rimM	probable 16S rRNA processing protein	RNA modification
1.03	1.21	1.05	0.74	0.98	0.83	0.95	1.27	0.95	0.95	0.83	MW1123	trmD	tRNA	RNA modification
1.11	1.14	1.34	1.14	1.11	0.28	0.89	0.61	1.17	1.09	0.56	MW1124	rplS	50S ribosomal protein L19	protein synthesis
0.98	1.33	1.17	0.78	1.19	1.71	1.30	2.34	1.05	1.08	1.14	MW1125		conserved hypothetical protein	
1.18	1.08	1.07	0.74	1.14	1.66	1.03	1.69	0.77	0.78	0.94	MW1126		conserved hypothetical protein	
1.00	1.02	1.01	0.78	0.97	1.53	1.03	1.44	1.08	0.88	0.88	MW1127	rnhB	RNase HII	DNA replication
0.81	1.51	1.12	1.02	1.13	4.29	1.15	1.91	1.08	0.95	0.60	MW1128	sucC	succinyl-CoA synthetase	carbohydrate metabolism
0.98	1.22	1.22	0.87	1.17	2.73	1.17	2.10	0.93	1.00	0.62	MW1129	sucD	succinyl-CoA synthetase	carbohydrate metabolism
0.96	1.11	1.13	0.98	1.27	1.33	1.17	1.58	0.86	1.06	0.83	MW1130	lytN	LytN protein	cell wall
0.90	1.09	0.97	0.90	1.00	1.24	0.98	1.17	1.10	0.93	0.85	MW1131	fmhC#epr	FmhC protein	cell wall
0.99	1.30	0.98	1.23	1.06	1.17	0.91	1.24	1.06	0.93	0.92	MW1132		hypothetical protein, similar to DNA processing Smf protein	DNA packaging
0.85	0.95	0.94	0.64	0.94	1.27	0.99	1.15	0.76	0.83	0.82	MW1133	topA	DNA topoisomerase I topA homolog	DNA replication
0.98	1.05	0.94	0.76	1.02	0.97	1.19	1.29	0.81	0.95	1.19	MW1134	gid	glucose-inhibited division protein gid	cell division
1.01	1.34	1.24	1.16	1.12	1.43	0.86	0.99	1.43	0.86	0.73	MW1135	xerC	site-specific recombinase XerC homolog	phage-related
1.16	1.07	1.18	1.04	1.12	1.49	1.02	1.02	1.39	0.81	0.74	MW1136	clpQ	heat shock protein HslV	adaptation to atypical
1.07	1.96	1.52	1.13	0.96	1.31	1.38	1.31	1.00	0.82	0.91	MW1137	clpY	heat shock protein HslU	adaptation to atypical
0.90	1.40	1.37	1.36	1.04	1.13	1.04	1.27	1.48	0.95	0.74	MW1138	codY	transcription pleiotropic repressor codY	RNA synthesis
0.89	0.85	0.79	0.71	0.86	0.42	0.59	0.74	0.93	0.89	0.40	MW1139	rpsB	30S ribosomal protein S2	protein synthesis
0.87	0.96	0.92	1.02	1.00	0.70	0.74	1.16	1.06	0.78	0.62	MW1140		elongation factor TS	protein synthesis
1.17	1.41	0.94	1.02	1.09	0.79	0.81	1.28	1.10	0.81	0.79	MW1141	smbA	uridylate kinase	[illegible]
1.08	1.02	1.05	0.84	0.93	0.67	0.77	1.19	1.12	0.83	0.88	MW1142	frr	ribosome recycling factor	protein synthesis
0.96	1.05	1.04	1.09	0.99	0.67	0.77	0.73	1.21	0.81	0.95	MW1143	uppS	undecaprenyl pyrophosphate synthetase	cell wall
1.06	1.16	1.04	1.02	0.98	0.71	0.81	0.81	1.26	0.84	1.30	MW1144	cdsA	phosphatidate cytidylyltransferase	lipid metabolism
0.83	1.22	0.96	1.00	0.97	0.82	0.71	0.72	1.19	0.83	1.26	MW1145		conserved hypotehtical protein	
0.72	1.29	1.04	1.43	1.01	0.72	0.78	0.87	1.08	0.93	1.26	MW1146	proS	proline-tRNA ligase	protein synthesis
0.93	0.86	0.96	1.27	0.85	0.87	1.01	0.82	1.08	1.02	1.44	MW1147	polC	DNA polymerase III, alpha chain PolC-type	DNA replication
1.15	0.86	1.15	0.98	0.94	1.20	0.87	0.92	1.35	0.97	1.15	MW1148		conserved hypotehtical protein	
1.17	1.39	1.18	1.44	1.11	1.52	0.94	0.99	1.44	1.03	0.93	MW1149	nusA	transcription termination-antitermination factor	RNA synthesis
1.00	2.20	0.25	1.00	0.20	#NUM!	1.00	0.55	1.31	0.70	0.70	MW1150		conserved hypotehtical protein	
1.50	0.90	1.06	0.95	0.99	1.23	0.89	1.11	1.47	0.90	1.02	MW1151		hypothetical protein, similar to ribosomal protein L7AE family	protein synthesis
0.87	1.31	0.98	1.01	0.91	1.00	0.84	1.05	1.18	0.86	0.95	MW1152	infB	translation initiation factor IF-2	protein synthesis
1.30	1.00	0.88	0.97	0.94	0.72	0.90	0.76	1.41	0.90	0.91	MW1153	rbfA	ribosome-binding factor A (rbfA)	protein synthesis
1.08	0.87	0.92	0.80	0.81	0.88	1.25	1.05	1.13	1.00	0.92	MW1154	truB	tRNA pseudouridine 5S synthase	RNA modification
1.24	0.70	0.80	0.69	0.76	0.83	1.04	0.98	0.84	0.87	1.01	MW1155	ribC	riboflavin kinase / FAD synthase ribC	coenzyme metabolism
0.86	0.89	1.10	1.03	0.86	0.39	0.76	0.66	1.31	0.95	0.55	MW1156	rpsO	30Sribosomal protein S15	protein synthesis
0.85	1.22	1.09	1.09	1.17	1.04	0.89	1.08	0.96	0.97	1.22	MW1157	pnpA	polyribonucleotide nucleotidyltransferase	nucleic acid metabolism
0.97	1.09	1.01	0.82	0.85	1.09	1.16	1.32	1.17	1.16	1.47	MW1158		conserved hypotehtical protein	
1.12	0.78	0.66	0.52	0.72	0.73	1.26	1.19	1.18	0.82	1.42	MW1159	spoIIIE	sporulation-related protein SpoIIIE homolog	sporulation
1.27	1.11	0.76	0.73	0.00	0.76	1.28	1.55	1.28	0.82	1.24	MW1160		hypothetical protein, similar to transcription regulator GntR family	RNA synthesis
1.34	1.43	1.05	0.88	1.02	1.05	1.22	1.57	1.13	0.99	1.56	MW1161		hypothetical protein, similar to processing proteinase homolog	aminoacid metabolism
1.11	1.35	0.89	0.99	0.88	0.99	1.10	1.32	1.54	0.97	1.36	MW1162		hypothetical protein, similar to precessing proteinase	aminoacid metabolism
1.14	0.85	0.68	0.49	0.71	0.71	0.95	1.03	1.12	0.77	1.01	MW1163		hypothetical protein, similar to 3-oxoacyl- acyl-carrier protein reductase homolog	lipid metabolism
0.90	0.70	0.52	0.77	0.53	0.68	0.83	0.89	0.95	0.77	1.00	MW1164		conserved hypothetical protein	
1.17	0.86	0.75	0.76	0.82	0.79	0.78	1.15	0.78	0.92	1.07	MW1165		conserved hypotehtical protein	
1.18	0.77	0.69	1.00	0.79	0.70	1.17	1.10	1.16	0.84	1.16	MW1166	pgsA	phosphatidylglycerophosphate synthase	lipid metabolism
1.16	1.17	1.00	0.88	1.02	1.12	1.21	1.29	1.00	0.92	1.08	MW1167	cinA	competence-damage inducible protein cinA	
1.26	0.87	1.02	0.92	1.08	1.13	1.33	1.10	0.87	1.13	1.29	MW1168	recA	RecA protein	[illegible]
1.29	0.96	1.05	0.88	1.34	1.70	0.94	1.27	0.96	0.92	1.17	MW1169		conserved hypothetical protein	
1.03	1.13	0.93	0.73	1.13	1.22	0.97	0.89	1.10	0.91	1.09	MW1170		hypothetical protein	
1.11	0.90	0.84	1.04	1.22	0.95	1.12	1.21	0.68	0.96	0.96	MW1170n		hypothetical protein	
1.23	0.82	0.72	0.50	0.91	0.78	1.24	1.08	0.82	0.90	1.44	MW1171		conserved hypothetical protein	
0.76	0.15	0.58	0.29	0.69	0.36	1.06	0.73	0.80	0.72	1.00	MW1172		hypothetical protein, similar to 2-oxoacid ferredoxin oxidoreductase, alpha subu	membrane bioenergetics
1.19	1.12	0.89	0.61	1.21	1.18	1.84	1.11	0.87	0.74	1.38	MW1173		hypothetical protein, similar to 2-oxoacid ferredoxin oxidoreductase, beta subu	membrane bioenergetics
1.44	1.02	0.86	0.69	1.58	1.09	1.32	1.34	0.65	0.79	1.29	MW1174		conserved hypothetical protein	
1.15	1.00	1.07	0.67	1.00	0.82	1.00	1.10	0.96	1.05	1.44	MW1175		conserved hypotehtical protein	
1.63	0.60	0.85	0.56	1.28	0.94	1.15	1.06	0.94	0.83	1.48	MW1176		conserved hypothetical protein	
1.37	1.08	0.96	0.84	1.23	1.14	1.16	1.23	0.95	0.90	1.45	MW1177		conserved hypothetical protein	
1.35	0.95	0.86	0.65	0.92	1.06	1.30	1.57	0.91	1.01	1.24	MW1178	mutS	DNA mismatch repair protein	DNA repair & modify
1.50	1.06	0.95	0.80	1.00	1.16	0.98	0.99	1.17	1.10	1.21	MW1179	mutL	DNA mismatch repair protein	DNA repair & modify
1.37	0.94	1.00	0.85	1.13	1.11	1.08	1.24	1.19	0.97	1.21	MW1180	glpP	glycerol uptake operon antiterminator regulatory protein	RNA synthesis
1.19	1.14	1.21	0.80	1.10	1.19	1.00	1.40	1.07	0.95	1.29	MW1181		hypothetical protein	
0.82	#NUM!	0.62	0.51	0.41	0.39	0.97	1.01	0.77	0.75	1.41	MW1181n		hypothetical protein	
1.27	1.46	1.68	0.76	1.26	1.54	1.00	1.66	0.84	1.79	1.32	MW1182	glpF	glycerol uptake facilitator	transport/binding
1.04	1.18	1.23	1.01	1.07	1.05	1.01	1.03	1.19	1.21	1.34	MW1183	glpK	glycerol kinase	carbohydrate metabolism
0.91	1.05	1.07	1.06	1.14	1.26	1.12	1.18	0.92	1.14	2.37	MW1184	glpD	aerobic glycerol-3-phosphate dehydrogenase	carbohydrate metabolism
0.89	1.02	0.91	0.85	0.91	1.25	0.77	1.00	0.81	0.90	1.06	MW1185		hypothetical protein, similar to lysophospholipase	lipid metabolism
1.01	0.91	1.00	0.97	1.13	1.16	0.97	1.07	0.77	1.05	1.21	MW1186	miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	RNA modification
1.10	0.78	0.84	1.01	0.70	0.99	0.87	1.00	0.90	1.08	1.51	MW1187		hypothetical protein, similar to host factor-1	phage-related
1.08	0.73	0.95	0.81	0.88	1.27	0.90	1.14	0.89	0.97	1.08	MW1188	bsaA	glutathione peroxidase	adaptation to atypical
0.83	0.97	0.79	0.93	0.91	0.71	0.86	0.65	1.15	0.64	0.88	MW1189		hypothetical protein, similar to GTP-binding protein proteinase modulator homolog	adaptation to atypical
0.88	1.17	1.05	1.05	1.09	1.05	0.98	1.24	0.87	1.05	0.87	MW1190		hypothetical protein, similar to aluminum resistance protein	transport/binding
0.81	0.51	0.69	0.74	0.60	0.69	0.70	0.92	0.46	0.95	0.15	MW1191	glnR	glutamine synthetase repressor	RNA synthesis
0.57	0.64	0.71	1.00	0.66	0.89	0.66	0.99	0.52	1.09	0.21	MW1192	glnA	glutamine-ammonia ligase	aminoacid metabolism
1.00	1.02	1.06	1.06	1.06	1.09	0.97	1.04	1.06	1.09	1.08	MW1193		hypothetical protein	
1.06	1.16	1.07	0.87	1.07	1.15	1.01	1.40	0.89	0.88	1.00	MW1194		hypothetical protein	
0.90	1.13	0.93	0.98	0.95	1.08	1.12	1.01	1.04	0.97	0.89	MW1195		hypothetical protein	
0.89	0.88	0.99	1.11	0.96	1.03	0.92	0.67	1.01	1.00	1.22	MW1195n		hypothetical protein	
0.83	1.39	1.12	0.96	1.04	1.21	1.02	1.29	0.95	1.06	1.06	MW1197		hypothetical protein	
0.95	1.27	0.95	0.79	0.94	0.97	0.83	1.31	0.84	1.02	1.16	MW1199		hypothetical protein	
1.27	1.17	0.97	1.03	0.90	1.22	0.96	0.92	1.77	0.86	1.18	MW1200		hypothetical protein	
0.75	1.12	0.86	1.02	0.91	1.10	0.76	0.87	1.12	0.91	0.98	MW1201		hypothetical protein	
0.96	0.97	0.84	1.03	0.81	1.05	0.97	0.93	1.05	0.93	0.94	MW1202		hypothetical protein	
0.80	1.22	1.06	1.27	1.07	1.18	0.78	0.93	0.72	1.03	0.90	MW1203		conserved hypothetical protein	
0.96	0.90	0.89	0.95	0.86	0.77	0.77	1.06	0.81	0.95	0.94	MW1204	dmpI	4-oxalocrotonate tautomerase	lipid metabolism
0.92	0.91	0.82	0.97	0.70	0.74	0.80	0.59	0.75	0.86	1.00	MW1205		cardiolipin synthetase homolog	lipid metabolism
0.83	0.99	1.03	1.17	1.04	1.00	0.83	0.75	1.16	0.99	0.96	MW1206		ABC transporter (ATP-binding protein) homolog category	transport/binding
1.05	1.10	0.95	0.75	0.98	1.14	0.83	1.37	0.68	0.97	1.22	MW1207		hypothetical protein, similar to ABC transporter integral membrane protein	transport/binding
1.27	0.94	0.94	0.83	0.91	1.07	1.04	0.90	1.07	1.13	1.27	MW1208		hypothetical protein, similar to two-component sensor histidine kinase	sensor
1.03	1.04	1.02	1.07	0.97	0.94	0.92	0.69	0.99	1.01	0.95	MW1209		hypothetical protein, similar to two-component response regulator	RNA synthesis

0.98	0.89	1.06	1.15	0.96	0.98	1.12	0.87	1.19	1.12	1.35	MW1210		hypothetical protein	
0.99	1.21	1.07	1.17	1.10	0.94	0.90	0.76	1.12	1.00	1.04	MW1211	nuc	thermonuclease	nucleic acid metabolism
1.32	0.98	1.21	1.11	1.05	0.74	1.27	0.76	1.30	1.01	1.42	MW1212		hypothetical protein	
1.33	0.84	0.79	0.41	0.73	0.43	0.84	0.51	0.85	1.00	1.04	MW1213		hypothetical protein	
0.95	0.45	0.40	0.30	0.52	0.20	0.47	0.20	0.65	0.79	0.84	MW1214		aspartate kinase homolog	amino acid metabolism
1.09	0.52	0.50	0.26	0.64	0.13	0.50	0.11	0.69	0.80	0.68	MW1215	dhoM	homoserine dehydrogenase	amino acid metabolism
1.07	0.44	0.45	0.19	0.58	0.11	0.59	0.17	0.66	0.88	0.77	MW1216	thrC	threonine synthase	amino acid metabolism
0.94	0.58	0.46	0.17	0.70	0.18	0.43	0.14	0.60	0.84	0.74	MW1217	thrB	homoserine kinase homolog	amino acid metabolism
1.08	0.57	0.40	0.24	0.57	0.13	0.60	0.17	0.66	0.89	1.22	MW1218		conserved hypothetical protein	
1.04	0.74	0.78	0.93	0.87	0.58	0.95	0.62	1.11	0.91	0.67	MW1219		hypothetical protein	
0.81	0.43	0.57	0.43	0.72	0.26	1.08	0.44	0.78	0.88	2.67	MW1220	gabP	gamma-aminobutyrate permease	transport/binding
1.17	1.07	0.87	0.54	0.85	1.22	1.87	1.07	0.90	0.85	0.75	MW1221	katA	catalase	detoxification
0.99	0.74	0.77	0.78	0.99	0.64	0.71	0.94	0.71	0.88	1.49	MW1222	rpmG	50S ribosomal protein L33	protein synthesis
1.01	0.82	1.06	1.32	1.10	0.91	1.08	0.69	1.29	1.04	0.84	MW1222n	rpmG	50S ribosomal protein L33	protein synthesis
1.32	0.97	0.97	1.09	1.29	0.94	1.17	1.05	0.90	1.04	0.19	MW1223	rpsN	30S ribosomal protein S14 homolog~ORFID:MW1223	protein synthesis
1.59	1.16	0.95	1.18	1.25	1.09	1.21	1.31	1.23	0.85	0.19	MW1223n	rpsN	rpsN	protein synthesis
1.45	1.05	1.05	0.79	1.16	1.21	1.29	1.67	0.77	0.89	0.64	MW1224		hypothetical protein, similar to GMP reductase	nucleic acid metabolism
1.42	1.39	0.99	0.75	1.08	1.00	1.40	1.30	1.03	1.03	0.83	MW1225		conserved hypothetical protein	
1.26	0.82	0.99	0.69	0.99	1.13	1.22	0.87	0.82	1.16	1.22	MW1226	lexA	SOS regulatory LexA protein	RNA synthesis
1.60	0.98	0.81	0.81	1.06	0.98	1.22	1.24	0.76	0.86	0.79	MW1227		hypothetical protein	
1.50	0.82	0.71	0.69	1.04	0.95	0.95	1.13	0.61	0.76	1.29	MW1228		conserved hypothetical protein	
0.85	1.16	0.77	1.16	0.91	0.80	0.92	2.00	1.21	0.83	1.09	MW1229	tkt	transketolase	carbohydrate metabolism
1.56	0.59	0.93	0.57	0.98	0.69	0.84	1.29	1.02	0.95	0.87	MW1230		conserved hypothetical protein	
1.37	1.39	1.06	0.95	1.18	0.99	1.04	1.48	1.06	0.97	1.03	MW1231		conserved hypothetical protein	
1.25	1.13	1.05	0.76	1.12	1.01	1.05	1.75	0.92	1.11	0.99	MW1232		hypothetical protein, similar to exonuclease SbcD	[illegible]
1.26	0.72	0.75	0.67	0.89	0.70	0.88	0.84	0.93	0.83	3.26	MW1233		hypothetical protein, similar to exonuclease SbcC	[illegible]
1.42	0.49	0.66	0.56	0.88	0.12	1.03	0.44	0.95	0.73	1.50	MW1234		hypothetical protein	
1.46	0.48	0.98	0.60	0.85	0.23	1.06	0.65	1.00	1.03	1.87	MW1235	mscL	large-conductance mechanosensitive channel	transport/binding
1.03	1.23	1.35	1.14	1.77	0.72	0.94	1.35	1.48	0.78	0.69	MW1236	opuD	glycine betaine transporter	transport/binding
1.29	0.82	1.01	0.64	0.89	0.90	0.91	1.24	0.65	1.06	0.44	MW1237	citB	aconitate hydratase	carbohydrate metabolism
1.22	0.91	1.00	1.24	0.81	0.89	0.95	0.75	1.14	1.06	1.22	MW1238		conserved hypothetical protein	
1.13	0.99	0.98	0.90	1.01	1.04	0.98	0.99	1.03	1.01	1.00	MW1239		conserved hypothetical protein	
1.13	0.85	1.04	0.98	1.00	0.74	0.94	0.63	0.92	1.20	1.46	MW1240		conserved hypothetical protein	
0.95	0.99	0.96	0.86	1.03	0.79	0.91	0.99	0.72	1.00	0.90	MW1241	parE	topoisomerase IV subunit B	DNA packaging
1.05	0.79	0.71	0.74	0.73	0.68	0.83	0.76	0.89	0.97	0.80	MW1242	parC	topoisomerase IV subunit A	
1.08	0.94	0.70	0.71	0.81	0.58	0.93	0.76	0.90	0.90	0.80	MW1242a	parC	topoisomerase IV subunit A	DNA packaging
0.91	1.27	1.47	1.36	1.24	1.49	1.06	1.11	1.29	1.29	1.11	MW1243	alsT	amino acid carrier protein	transport/binding
0.78	1.13	0.90	0.88	1.01	1.01	0.75	0.83	0.85	0.84	1.12	MW1244	glcT	transcription antiterminator	RNA synthesis
1.09	0.97	0.92	1.11	0.95	0.86	0.92	0.62	1.16	0.92	1.30	MW1245		hypothetical protein	
1.17	0.97	1.15	1.22	1.00	0.86	1.14	0.87	0.92	0.86	1.22	MW1245n		hypothetical protein	
1.22	0.56	0.74	0.78	0.85	0.64	0.93	0.70	0.95	0.82	1.72	MW1246		conserved hypothetical protein	
1.00	0.94	0.90	0.89	1.00	1.10	0.93	0.80	1.00	1.00	2.49	MW1247	fmtC	oxacillin resistance-related FmtC protein	miscellaneous
1.01	0.74	0.91	0.81	1.06	0.95	0.83	0.73	0.95	0.92	1.63	MW1248	msrA	peptide methionine sulfoxide reductase homolog	protein modification
1.14	0.90	0.98	0.83	0.89	0.89	0.96	0.94	0.91	1.04	1.49	MW1249	msrR	peptide methionine sulfoxide reductase regulator MsrR	RNA synthesis
1.32	0.60	0.78	1.04	0.94	0.74	0.94	0.64	0.97	1.07	0.86	MW1250	dmpI	4-oxalocrotonate tautomerase	
1.17	0.84	1.01	0.96	1.17	1.17	1.07	0.82	0.92	0.97	0.88	MW1251		hypothetical protein, similar to DNA-damage repair protein	DNA repair or modify
1.06	1.00	0.79	0.64	1.05	1.00	0.80	0.87	0.82	0.76	1.09	MW1252	tyrA	prephenate dehydrogenase	amino acid metabolism
1.20	1.06	0.96	0.94	1.06	1.06	1.04	0.89	0.87	1.01	0.71	MW1253		hypothetical protein, similar to glucanase	carbohydrate metabolism
0.90	1.06	1.03	1.00	0.95	1.11	0.95	0.87	0.92	1.10	1.11	MW1254		hypothetical protein, similar to anthranilate synthase component I	amino acid metabolism
0.88	1.04	1.10	1.11	1.09	1.39	1.12	1.09	1.19	1.17	1.04	MW1255	trpG	anthranilate synthase component II	amino acid metabolism
0.95	1.34	1.22	1.22	1.14	1.47	1.00	1.06	1.24	1.11	0.92	MW1256	trpD	anthranilate phosphoribosyltransferase	amino acid metabolism
0.86	1.30	1.26	1.14	0.98	1.44	1.16	1.25	1.24	1.29	1.05	MW1257	trpC	indole-3-glycerol phosphate synthase	amino acid metabolism
0.80	1.21	1.16	1.09	1.02	1.24	0.95	0.98	1.17	1.16	1.04	MW1258	trpF	phosphoribosylanthranilate isomerase	amino acid metabolism
0.86	1.21	1.31	1.07	1.15	1.46	1.08	1.21	1.01	1.11	0.87	MW1259	trpB	tryptophan synthase beta chain	amino acid metabolism
0.96	1.50	1.14	1.16	1.04	1.62	0.96	1.28	1.26	1.08	1.06	MW1260	trpA	tryptophan synthase alpha chain	amino acid metabolism
1.09	1.21	1.19	1.09	0.89	1.54	1.35	1.40	1.35	1.01	1.28	MW1261	femA	factor essential for expression of methicillin resistance	cell wall
1.19	0.45	0.77	0.62	0.63	1.04	1.30	1.44	1.09	0.96	1.28	MW1262	femB	FemB protein	cell wall
1.12	0.88	1.08	0.79	0.92	1.12	1.17	1.55	0.81	0.96	1.44	MW1265		conserved hypothetical protein	
1.12	0.94	1.01	1.00	0.90	1.00	1.35	1.25	1.16	1.01	1.07	MW1266		hypothetical protein	
0.97	0.94	0.86	0.63	1.03	1.08	1.12	1.19	1.03	0.98	1.13	MW1267	opp-2F	oligopeptide transporter putative ATPase domain	transport/binding
0.83	1.61	1.01	0.95	0.88	1.23	1.18	1.45	1.04	0.99	1.29	MW1268	opp-2D	oligopeptide transport ATPase	transport/binding
0.80	1.39	1.12	0.96	0.95	1.26	1.27	1.37	1.18	1.03	1.06	MW1270	opp-2B	oligopeptide transporter membrane permease domain	transport/binding
0.78	1.36	1.02	1.12	1.04	1.18	0.82	1.40	1.09	1.03	1.41	MW1271		hypothetical protein	
1.21	1.28	1.06	0.83	0.98	1.20	0.97	1.51	1.11	0.93	1.50	MW1271n		hypothetical protein	
0.94	1.36	1.22	0.95	1.10	1.68	1.06	1.74	1.14	0.98	1.40	MW1272		hypothetical protein, similar to oligoendopeptidase	amino acid metabolism
1.16	1.63	1.25	1.01	1.33	1.64	1.19	1.95	1.09	0.92	1.33	MW1273		hypothetical protein, similar to negative regulator PhoU	RNA synthesis
0.93	1.50	1.30	0.90	1.27	1.84	1.25	2.79	0.96	1.13	1.04	MW1274	pstB	phosphate ABC transporter, ATP-binding protein	transport/binding
0.85	1.24	1.29	0.84	1.05	1.55	1.12	2.07	1.07	1.16	0.96	MW1275		hypothetical protein, similar to phosphate ABC transporter	transport/binding
0.83	1.69	1.31	1.01	1.19	1.75	0.97	1.87	1.05	1.11	0.95	MW1276		hypothetical protein, similar to phosphate ABC transporter	transport/binding
0.83	1.44	1.34	1.07	1.27	1.82	1.04	2.02	1.01	1.03	0.97	MW1277		thioredoxine reductase	membrane bioenergetics
0.92	1.26	0.92	0.85	1.03	1.09	0.95	1.08	1.08	1.07	1.12	MW1278	uncated-S	truncated transposase	transposon and IS
0.92	1.12	1.03	0.78	0.95	1.02	0.84	0.74	1.00	1.26	1.20	MW1279		conserved hypothetical protein	
1.07	0.90	0.71	0.82	0.77	0.69	0.69	1.05	0.78	0.87	1.39	MW1280		ABC transporter (ATP-binding protein) homolog	transport/binding
0.79	0.93	0.76	0.69	0.76	0.65	0.65	0.76	0.54	0.88	0.85	MW1281	lysC	aspartokinase II	amino acid metabolism
0.91	0.82	0.73	0.60	0.71	0.58	0.66	0.64	0.57	0.89	0.85	MW1282	asd	aspartate semialdehyde dehydrogenase	amino acid metabolism
0.81	0.89	0.68	0.62	0.74	0.58	0.64	0.49	0.72	0.90	0.78	MW1283	dapA	dihydrodipicolinate synthase	amino acid metabolism
0.76	0.16	0.38	0.12	0.47	0.26	0.61	0.29	0.53	0.63	0.67	MW1284	dapB	dihydrodipicolinate reductase	amino acid metabolism
0.89	0.85	0.73	0.64	0.67	0.52	0.60	0.56	0.61	0.93	0.84	MW1285	dapD	tetrahydrodipicolinate acetyltransferase	amino acid metabolism
0.89	0.72	0.60	0.32	0.69	0.42	0.56	0.35	0.71	0.70	0.89	MW1286		hippurate hydrolase	nucleic acid metabolism
0.70	1.25	1.03	0.87	0.93	1.05	0.76	0.79	0.77	1.15	1.19	MW1287		hypothetical protein, similar to alanine racemase	amino acid metabolism
0.72	0.90	0.80	0.75	0.94	0.69	0.54	0.54	0.70	1.00	1.28	MW1288	lysA	diaminopimelate decarboxylase	amino acid metabolism
1.04	0.96	0.97	0.93	0.87	0.81	0.80	0.75	0.25	0.96	1.77	MW1289		hypothetical protein	
0.80	0.49	1.17	0.86	0.54	0.37	0.93	0.41	0.85	0.65	1.14	MW1290	cspA	major cold shock protein CspA	adaptation to atypical
0.88	0.52	0.72	1.17	0.67	0.25	0.68	0.27	0.85	0.81	1.34	MW1290n	cspA	major cold shock protein CspA	adaptation to atypical
0.85	1.03	0.92	0.93	0.86	0.93	0.83	0.78	0.87	1.03	1.69	MW1291		conserved hypothetical protein	
1.33	0.87	0.85	0.94	0.96	1.15	0.91	0.77	0.97	0.97	1.10	MW1292		conserved hypothetical protein	
1.24	1.22	0.92	0.89	0.92	1.18	0.82	0.92	0.81	0.94	1.14	MW1293		hypothetical protein, similar to 5-bromo-4-chloroindolyl phosphate hydrolysis prote	phosphate metabolism
1.19	0.96	0.89	0.81	0.86	1.12	1.02	1.06	0.88	1.16	1.27	MW1294		hypothetical protein, similar to tellurite resistance protein	detoxification
0.81	1.32	1.01	0.89	1.01	1.15	0.93	1.38	0.95	0.97	1.25	MW1295		truncated transposase	transposon and IS
1.10	0.49	0.70	0.65	0.98	0.72	1.38	0.92	1.05	0.69	0.98	MW1296		truncated transposase	transposon and IS
0.91	1.06	0.98	1.27	0.86	1.04	0.81	0.65	0.96	1.00	1.54	MW1297	braB	branched-chain amino acid carrier protein	transport/binding
1.04	1.17	1.05	1.07	1.03	1.64	0.95	0.91	1.10	1.03	1.34	MW1299		hypothetical protein, similar to nitric-oxide reductase	membrane bioenergetics
1.31	0.89	0.95	0.89	0.93	1.31	1.02	0.91	1.07	1.07	1.16	MW1300		conserved hypothetical protein	
1.03	0.82	0.98	0.90	0.90	1.82	1.12	0.78	1.14	1.14	1.00	MW1301		ABC transporter homolog	transport/binding
1.18	1.04	1.40	1.08	1.18	3.77	1.53	1.43	1.58	1.29	1.05	MW1302	odhB	dihydrolipoamide succinyltransferase	carbohydrate metabolism
1.21	1.81	1.80	1.27	1.15	5.01	1.50	1.40	1.58	1.33	0.99	MW1303	odhA	2-oxoglutarate dehydrogenase E1	carbohydrate metabolism
1.37	1.48	1.50	0.85	1.10	5.73	1.64	2.30	1.03	1.36	0.85	MW1303a	odhA	2-oxoglutarate dehydrogenase E1	carbohydrate metabolism

1.25	1.07	1.37	1.41	1.05	1.49	1.44	1.05	1.21	1.15	1.36	MW1304	arlS	putative protein histidine kinase ArlS	sensor
1.25	1.06	1.00	1.09	0.81	1.27	1.61	1.17	1.22	0.98	1.37	MW1305	ncated-a	truncated (putative response regulator ArlR	RNA synthesis
1.17	1.40	1.09	0.93	1.11	1.56	1.32	1.41	1.12	1.03	1.62	MW1305a	uncated-a	truncated (putative response regulator ArlR [S	RNA synthesis
1.35	0.95	1.08	0.90	0.89	1.15	1.45	1.13	1.12	1.05	1.22	MW1306		conserved hypothetcial protein	
1.19	0.99	0.86	0.67	0.82	0.91	0.92	1.12	0.87	0.93	1.26	MW1307	murG	undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase	cell wall
1.14	0.58	0.67	0.29	0.67	0.23	0.48	0.32	0.85	0.89	1.33	MW1308		conserved hypothetical protein	
1.10	1.14	1.00	0.94	0.95	1.07	0.97	1.23	0.86	1.01	1.20	MW1309		truncated transposase	transposon and IS
1.06	0.97	1.01	1.01	0.85	0.97	0.97	0.80	1.21	0.98	1.52	MW1310	ctpA	probable carboxy-terminal processing proteinase ctpA	aminoacid metabolism
1.41	0.67	0.81	0.96	0.67	0.89	1.47	1.32	0.82	0.97	1.06	MW1311		conserved hypothetical protein	
1.11	0.96	0.81	1.05	0.91	1.14	1.21	1.16	0.81	0.90	0.75	MW1312		PTS system, glucose-specific enzyme II, A component	transport/binding
1.24	0.56	0.62	0.83	0.58	0.91	1.34	0.97	0.81	0.77	0.87	MW1313		conserved hypothetical protein	
1.03	0.84	0.71	0.84	0.67	1.12	1.38	0.99	0.92	0.76	0.76	MW1314		peptide methionine sulfoxide reductase	protein modification
1.21	0.94	0.99	1.21	0.81	1.16	1.71	1.28	1.13	0.92	0.70	MW1315		conserved hypothetical protein	
1.29	0.61	0.81	0.54	0.79	0.93	1.35	1.17	0.90	0.84	0.84	MW1316	dfrA	dihydrofolate reductase	coenzyme metabolism
1.11	0.82	0.85	0.84	0.63	1.15	1.50	1.06	0.92	0.86	0.89	MW1317	thyA	thymidylate synthase	nucleic acid metabolism
1.24	0.63	0.72	0.83	0.73	0.82	1.23	1.07	0.99	0.80	0.72	MW1318		conserved hypothetical protein	
1.10	0.68	0.96	0.81	0.88	0.89	1.34	1.14	1.00	0.86	0.63	MW1319		conserved hypothetical protein	
1.24	0.91	0.96	1.07	0.95	1.06	1.11	0.90	1.15	0.86	0.66	MW1320		conserved hypothetical protein	
1.08	0.94	1.10	0.89	1.15	0.85	1.10	0.77	1.60	0.83	1.25	MW1321		conserved hypothetical protein	
1.06	0.93	0.94	1.06	0.92	0.92	1.03	0.92	1.11	1.07	1.03	MW1322		hypothetical protein	
0.87	1.00	1.00	1.00	1.00	1.00	2.34	0.00	1.00	1.00	1.00	MW1324	ebhA	hypothetical protein, similar to streptococcal adhesin emb	pathogenic factor
0.83	1.69	1.22	0.69	1.46	1.54	1.18	1.61	1.32	1.19	1.29	MW1324a	ebhA	hypothetical protein, similar to streptococcal adhesin emb	pathogenic factor
0.38	0.38	1.76	2.64	1.05	0.33	0.50	1.14	0.55	1.08	0.90	MW1325		Blt-like protein	transport/binding
0.54	0.31	1.79	1.59	1.20	0.33	0.50	1.51	0.45	0.96	1.00	MW1325n		Blt-like protein	transport/binding
0.39	0.27	2.07	2.07	1.05	0.39	0.63	3.29	0.38	1.09	0.75	MW1326		hypothetical protein, similar to amino acid pearmease	transport/binding
0.58	0.23	1.48	3.16	1.10	0.40	0.78	2.29	0.74	0.79	0.54	MW1327		threonine deaminase IlvA homolog	aminoacid metabolism
0.53	0.38	1.36	3.18	1.22	0.48	0.68	3.71	0.50	0.93	0.63	MW1328	ald	alanine dehydrogenase	aminoacid metabolism
1.04	0.72	0.88	0.86	0.91	0.70	0.69	1.12	0.65	0.92	0.81	MW1329		hypothetical protein, similar to 5'-3' exonuclease	DNA replication
0.98	1.02	0.98	0.73	0.96	1.05	0.86	1.02	1.02	1.02	0.81	MW1331		conserved hypothetical protein	
0.82	1.38	1.36	0.86	0.96	1.15	1.08	1.27	0.98	1.04	0.83	MW1332		hypothetical protein	
0.87	1.05	0.97	0.89	1.00	1.09	0.84	1.06	0.83	0.88	0.90	MW1333		conserved hypothetical protein	
1.41	0.86	1.21	1.21	1.14	2.25	1.40	1.24	1.24	1.51	0.61	MW1334		hypothetical protein	
1.56	0.82	1.04	1.02	1.46	2.11	1.51	1.45	1.19	1.52	0.56	MW1334n		hypothetical protein	
1.09	1.03	0.93	0.95	1.01	2.23	0.97	1.25	1.04	0.94	1.09	MW1335		conserved hypothetical protein	
1.06	1.13	0.96	1.10	1.10	3.94	0.97	1.30	1.19	0.86	1.02	MW1336		conserved hyothetical protein	
1.26	1.07	1.02	1.04	0.97	4.07	0.94	1.24	1.21	0.83	1.10	MW1337		conserved hypothetical protein	
0.79	0.77	1.21	1.41	1.13	1.01	0.91	0.88	0.96	1.03	1.16	MW1338		hypothetical protein	
1.01	1.07	1.09	0.93	1.17	1.05	1.12	1.02	1.09	0.94	0.70	MW1339	recU	recombination protein U homolog	DNA recombination
0.76	0.98	1.09	1.00	0.91	1.07	0.94	1.11	1.01	0.92	1.09	MW1340	pbp2	PBP2	cell wall
1.25	0.98	0.77	0.81	0.84	0.79	1.00	0.95	1.09	0.88	0.88	MW1341		hypothetical protein	
1.03	1.30	0.90	0.99	1.10	1.10	0.81	1.00	0.98	0.86	0.81	MW1342	nth	endonuclease-like protein	DNA repair or modify
1.14	1.07	0.95	0.89	0.86	0.95	1.10	1.11	0.86	1.04	0.97	MW1343		hypothetical protein, similar to chromosome replication initiation protein dnaD	DNA replication
0.96	0.94	0.95	1.09	0.92	0.81	1.01	0.89	1.09	0.94	1.69	MW1344	asnS	asparaginyl-tRNA synthetase	protein synthesis
1.33	1.10	0.84	0.71	0.99	1.08	0.95	1.80	0.89	0.92	1.19	MW1345	dinG	probable ATP-dependent DNA helicase dinG	DNA repair or modify
1.01	1.20	1.04	1.25	0.95	1.09	0.90	1.02	1.18	0.95	1.02	MW1346		hypothetical protein, similar to bifunctional biotin ligase/biotin operon represso	RNA synthesis
1.05	0.93	0.91	0.99	0.91	1.12	0.87	1.05	1.17	0.93	0.90	MW1347		hypothetical protein, similar to poly(A) polymerase	RNA synthesis
0.78	1.16	1.01	1.21	0.98	1.09	0.84	0.82	1.05	1.09	0.87	MW1348		hypothetical protein, similar to lipopolysaccharide biosynthesis-related pr homo	cell wall
0.99	0.90	0.89	0.89	0.89	0.87	0.92	0.76	0.94	0.98	0.99	MW1349		conserved hypothetical protein	
0.95	0.85	0.90	1.10	0.99	1.19	0.87	0.59	0.99	1.14	1.23	MW1350		conserved hypothetical protein	
0.94	0.60	0.83	0.51	0.80	0.50	0.89	0.57	0.73	1.07	1.33	MW1351		conserved hypothetical protein	
0.87	0.45	0.54	0.39	0.72	0.37	0.73	0.49	0.60	0.89	1.56	MW1352		conserved hypothetical protein	
0.77	0.75	0.71	0.71	0.92	0.58	0.61	0.52	0.90	0.77	1.39	MW1353		conserved hypothetical protein	
0.90	0.73	0.80	0.73	0.83	0.68	0.74	0.55	0.89	0.83	1.32	MW1354	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	aminoacid metabolism
1.02	0.71	0.84	0.75	0.80	0.63	0.87	0.70	0.79	0.86	1.36	MW1355	aroB	3-dehydroquinate synthase	aminoacid metabolism
0.84	0.74	0.74	0.63	0.79	0.61	0.67	0.54	0.83	0.81	1.34	MW1356	aroC	chorismate synthase	aminoacid metabolism
0.90	0.97	1.01	0.77	0.95	0.86	0.88	1.15	1.06	1.00	1.35	MW1357		hypothetical protein	
1.22	1.00	1.07	0.81	0.75	0.79	1.07	0.98	1.00	1.17	1.21	MW1358	ndk	nucleoside diphosphate kinase	nucleic acid metabolism
1.16	0.61	0.78	0.55	0.66	0.65	0.79	0.74	0.88	0.77	1.09	MW1359	gerCC	heptaprenyl diphosphate syntase component II	germination
1.10	0.83	0.63	0.71	0.54	0.91	0.92	0.78	0.97	0.78	1.07	MW1360	gerCB	menaquinone biosynthesis methyltransferase	germination
1.19	0.65	0.72	0.80	0.70	0.94	0.95	0.81	1.04	0.72	1.16	MW1361		hypothetical protein, similar to component A of hexaprenyl diphosphate synthase	
1.42	0.37	0.81	0.90	0.62	0.33	1.48	0.48	1.02	1.26	1.45	MW1362	hu	DNA-binding protein II	DNA packaging
0.81	0.76	0.69	0.55	0.70	0.49	0.78	0.86	0.84	0.82	0.79	MW1363	gpsA	glycerol-3-phosphate dehydrogenase	carbohydrate metabolism
0.78	0.76	0.49	0.84	0.58	0.56	1.04	0.99	0.90	0.81	0.94	MW1364		hypothetical protein, similar to GTP binding protein	
0.98	0.72	0.50	0.96	0.70	0.78	1.10	1.14	1.18	0.72	1.48	MW1365	rpsA	30S ribosomal protein S1	nucleic acid metabolism
1.15	0.52	0.63	0.55	0.95	0.69	0.89	0.69	0.88	0.65	0.86	MW1366	cmk	cytidylate kinase	nucleic acid metabolism
1.05	1.52	1.14	1.11	1.39	1.66	1.03	1.42	1.20	0.81	0.98	MW1367	ansA	probable L-asparaginase	aminoacid metabolism
1.26	1.31	1.16	1.01	1.36	1.70	1.06	1.90	1.20	0.87	0.79	MW1368		hypothetical protein, similar to thioredoxin reductase homolog	membrane bioenergetics
1.38	1.41	1.20	1.32	1.64	5.74	1.75	2.78	0.98	0.91	1.07	MW1369	ebpS	elastin binding protein	pathogenic factor
0.86	1.11	1.25	1.56	1.21	1.24	1.06	0.77	1.26	1.14	1.22	MW1370	recQ	probable ATP-dependent DNA helicase RecQ	DNA recombination
1.53	1.04	1.19	1.01	1.20	1.69	1.16	1.46	1.12	1.10	1.57	MW1370n	recQ	probable ATP-dependent DNA helicase RecQ	DNA recombination
1.18	1.66	1.28	1.05	1.39	1.73	1.42	1.37	1.19	0.94	1.21	MW1371		conserved hypothetical protein	
1.32	1.20	1.18	0.81	1.60	1.21	2.42	1.23	1.12	0.94	1.10	MW1372	fer	ferredoxin	membrane bioenergetics
1.37	2.03	1.46	1.31	1.64	1.74	1.26	1.88	1.19	1.11	1.08	MW1373		conserved hypothetical protein	
0.76	1.19	1.51	1.32	1.16	1.20	1.02	1.17	1.35	1.18	1.18	MW1374		conserved hypothetical protein	
1.01	1.26	1.43	1.19	1.20	1.10	1.24	1.41	0.92	1.15	1.09	MW1374n		hypothetical protein	
0.91	1.08	1.23	1.14	1.05	1.14	1.30	1.16	0.00	1.17	1.00	MW1375		conserved hypothetical protein	
0.91	1.01	1.20	0.91	1.13	1.21	1.04	1.56	1.10	0.95	0.92	MW1375n		hypothetical protein	
0.90	1.71	1.41	1.07	1.36	1.56	1.15	2.05	1.00	0.99	1.05	MW1376		hypothetical protein	
0.93	1.22	1.28	1.75	1.09	1.20	1.00	1.11	1.13	1.34	1.01	MW1377		truncated hypothetical protein	
0.92	0.96	1.22	1.59	1.09	1.21	1.00	1.45	1.05	1.18	1.09	MW1379	lukS-PV	on-Valentine leukocidin chain S precursor (Bacteriophage phi Sa 2	pathogenic factor
0.76	1.40	1.33	1.45	1.26	1.42	1.03	1.14	1.34	1.25	1.11	MW1380	runcated ly	truncated amidase (Bacteriophage phi Sa 2mw)	phage-related
0.81	1.28	1.29	1.31	1.06	1.38	0.94	1.38	1.13	1.23	1.21	MW1381		holin (Bacteriophage phi Sa 2mw)	phage-related
0.91	1.02	1.31	1.53	1.10	0.90	1.21	0.82	1.06	1.06	1.04	MW1383		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.75	0.81	1.09	1.56	1.15	1.10	1.01	0.87	0.92	1.17	1.27	MW1384		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.91	0.76	1.01	0.63	0.73	1.07	1.40	1.04	1.00	0.98	0.89	MW1385		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.84	0.29	0.94	0.39	0.69	0.97	1.09	1.35	0.65	0.85	0.82	MW1386		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.74	0.93	1.27	1.35	1.07	1.52	1.15	1.08	0.99	1.23	1.01	MW1387		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.81	1.04	1.25	1.12	1.05	1.75	1.19	1.42	0.91	1.21	1.23	MW1388		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.65	1.47	1.52	1.57	1.12	1.75	1.00	1.24	1.12	1.22	1.16	MW1389		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.71	1.21	1.50	1.50	1.22	1.49	1.12	1.17	1.05	1.28	0.98	MW1390		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.73	1.14	1.37	1.29	1.05	1.24	0.95	1.40	1.09	1.10	1.27	MW1391		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.86	0.98	1.37	1.51	1.06	1.32	1.11	1.23	1.00	1.22	1.46	MW1393		major tail protein	phage-related
0.81	1.13	1.29	0.84	0.89	1.13	1.14	1.24	1.04	1.24	1.36	MW1394		hypothetical protein	phage-related
0.73	0.54	0.80	0.53	0.83	0.49	0.74	1.17	0.49	1.12	1.57	MW1396		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.69	1.12	1.20	1.33	0.96	1.10	0.96	1.16	0.94	1.06	1.27	MW1397		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.76	1.02	1.43	1.50	1.03	1.26	0.98	1.28	0.96	1.15	1.63	MW1398		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.71	1.14	1.44	1.62	1.04	1.33	0.97	1.34	1.03	1.18	1.51	MW1399		protease	pathogenic factor

0.63	0.74	0.94	0.77	0.83	1.07	0.92	1.28	0.87	0.91	1.47	MW1400		portal protein	phage-related
0.67	0.79	0.83	0.94	0.79	1.07	1.23	1.32	0.85	0.97	1.15	MW1401		terminase large subunit	phage-related
0.79	0.91	1.01	0.90	1.19	1.13	1.27	1.29	1.02	0.84	1.15	MW1402		terminase small subunit	phage-related
0.82	0.85	0.92	0.65	1.19	0.99	1.16	0.92	0.94	0.89	0.84	MW1404		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.86	1.02	1.21	0.77	0.99	1.65	1.10	1.92	0.68	1.18	0.94	MW1405		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.89	0.90	0.87	0.69	0.69	1.12	0.92	1.12	0.86	0.80	0.99	MW1406		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.82	1.03	1.34	1.21	1.31	1.29	1.02	1.00	1.49	1.12	1.02	MW1407		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.88	0.97	1.37	1.00	0.97	1.35	1.09	1.31	0.85	1.29	1.04	MW1408		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.00	0.79	0.87	0.89	0.92	0.89	1.15	0.99	0.99	0.77	0.92	MW1409		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.92	0.90	1.03	0.82	0.94	1.08	1.42	1.56	1.09	0.84	1.02	MW1410		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.97	1.03	1.25	1.09	1.25	1.51	1.16	1.38	0.84	1.17	0.99	MW1411		hypothetical protein, similar to int gene activator RinB	phage-related
0.95	1.18	1.47	0.82	1.20	1.30	1.02	1.52	0.95	1.00	0.80	MW1412		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.21	0.96	1.19	0.90	1.15	1.35	1.16	1.70	0.78	1.04	0.90	MW1413		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.06	0.97	1.07	0.90	1.03	1.31	1.08	1.08	0.93	1.15	0.92	MW1413n		hypothetical protein(phiN315)	phage-related
1.02	1.52	1.24	1.16	1.15	1.40	1.16	2.10	0.90	0.93	1.02	MW1414n		hypothetical protein(phiN315)	phage-related
0.86	1.51	1.45	0.98	1.16	1.45	1.01	1.60	0.88	1.08	0.95	MW1415		hypothetical protein(phiN315)	phage-related
1.14	0.90	1.30	0.83	1.20	1.32	1.08	1.45	0.75	1.00	0.98	MW1416		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.85	1.32	1.28	1.14	1.12	1.35	1.24	1.51	0.83	1.12	0.99	MW1417		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.80	1.21	1.39	0.96	1.21	1.57	1.01	1.33	1.03	1.03	1.00	MW1418		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.11	1.00	1.25	0.99	1.17	1.07	1.30	1.80	0.83	1.20	0.83	MW1419		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.93	1.12	1.20	0.94	1.06	1.17	1.11	1.46	0.82	1.10	0.90	MW1419n		hypothetical protein(phiN315)	phage-related
0.99	1.03	1.37	0.97	1.24	1.20	1.31	1.73	0.67	1.17	0.88	MW1420n		hypothetical protein(phiN315)	phage-related
0.89	1.24	1.44	0.92	1.15	1.54	1.08	1.73	0.90	0.99	0.94	MW1421		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.98	1.09	1.51	1.19	1.24	1.50	1.15	1.99	0.91	1.12	0.87	MW1422		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.91	0.86	1.06	1.15	0.82	1.07	1.04	1.09	0.87	1.10	1.00	MW1422n		hypothetical protein	
0.71	1.45	1.47	1.36	1.25	1.43	0.92	1.28	1.02	1.23	0.82	MW1423		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.80	1.16	1.26	1.06	1.11	1.36	0.94	1.35	0.95	1.19	0.96	MW1424		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.85	1.06	1.37	0.90	1.12	1.32	1.16	1.73	0.84	1.24	0.86	MW1425		DNA polymerase	phage-related
0.91	1.11	1.35	1.39	1.32	1.27	1.01	1.24	0.92	1.13	0.86	MW1426		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.91	1.05	1.28	1.41	1.11	1.14	1.08	0.90	1.01	1.17	0.83	MW1427		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.87	1.15	1.36	1.13	1.11	1.10	0.87	1.31	0.97	1.13	0.90	MW1428		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.97	1.11	1.40	0.88	1.15	1.17	1.07	1.37	0.78	1.09	1.00	MW1429		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.11	0.98	1.22	0.86	1.08	1.06	1.01	1.23	0.82	1.15	1.01	MW1430		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.87	1.00	1.32	1.33	1.16	1.03	0.84	1.00	1.16	1.10	1.12	MW1431		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.23	1.24	1.29	1.02	1.07	1.41	0.84	0.77	1.38	1.01	1.34	MW1432		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.00	1.02	1.29	1.19	1.09	1.02	0.94	0.99	0.49	1.09	1.58	MW1433		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.89	0.96	1.45	1.53	1.20	1.02	1.07	0.97	1.02	1.29	1.13	MW1434		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
0.85	1.14	1.20	0.95	1.08	0.95	1.01	0.77	0.97	1.06	1.07	MW1435		hypothetical protein, similar to Cro-like protein	phage-related
1.05	0.91	1.20	1.30	1.16	1.04	1.12	0.98	1.14	0.94	0.88	MW1436		phage repressor (Bacteriophage phi Sa 2mw)	phage-related
1.20	0.77	1.21	1.27	1.23	1.09	1.19	0.96	1.25	1.00	0.88	MW1437		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.15	0.96	1.21	1.12	1.12	1.13	1.11	1.09	0.94	1.05	0.81	MW1438		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.36	0.84	1.22	0.87	1.07	0.92	1.25	1.13	0.73	1.02	0.92	MW1439		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.48	0.79	1.01	1.06	1.09	1.02	1.28	1.17	1.09	1.04	1.15	MW1440		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.00	0.00	0.19	0.77	0.07	#NUM!	1.00	1.00	2.80	0.59	0.30	MW1441		hypothetical protein (Bacteriophage phi Sa 2mw)	phage-related
1.11	1.24	1.34	1.33	1.26	1.28	1.16	1.24	1.24	1.16	0.92	MW1442	int	integrase (Bacteriophage phi Sa 2mw)	transposon and IS
1.07	1.43	1.31	0.88	1.26	1.40	1.19	3.24	0.73	1.17	0.76	MW1443		hypothetical protein	
0.87	1.16	1.03	1.26	0.98	1.00	1.13	0.80	1.00	1.09	1.11	MW1444		hypothetical protein	
0.99	1.26	0.88	0.96	1.00	1.06	0.86	0.92	0.97	1.80	1.08	MW1444n		hypothetical protein	
0.94	0.64	0.88	0.58	1.14	0.91	0.95	1.33	0.85	0.89	1.19	MW1445	srrB	staphylococcal respiratory response protein SrrB	sensor
0.87	0.90	0.80	0.86	1.29	1.01	0.96	1.78	0.65	0.82	0.97	MW1446	srrA	staphylococcal respiratory response protein SrrA	RNA synthesis
1.15	1.07	1.14	1.02	1.37	1.09	1.11	1.38	0.83	0.92	0.75	MW1447	rluB	ribosomal large subunit pseudouridine synthase B	nucleic acid metabolism
1.04	1.02	1.07	1.36	1.08	1.17	0.94	1.07	1.17	1.06	0.81	MW1448		conserved hypothetical protein	
1.29	1.12	0.88	0.87	1.11	1.12	1.06	1.07	0.97	1.04	0.78	MW1449		conserved hypothetical protein	
0.91	1.22	1.03	1.03	1.05	1.09	0.84	1.13	1.06	0.99	0.87	MW1450		conserved hypothetical protein	
0.95	1.00	0.51	0.72	1.10	0.73	1.04	0.92	1.02	0.72	0.67	MW1451	xerD	site-specific recombinase	phage-related
0.94	1.12	0.86	1.07	1.17	0.98	0.85	0.87	1.16	0.89	0.85	MW1452	fur	ferric uptake regulator homolog	RNA synthesis
1.01	1.02	0.98	1.02	1.11	1.14	0.93	1.00	1.01	0.96	0.98	MW1453		conserved hypothetical protein	
0.97	1.35	1.00	1.09	1.06	1.24	0.91	1.19	1.03	0.97	1.50	MW1454		conserved hypothetical protein	
0.96	0.82	0.96	0.84	0.93	1.17	1.01	1.16	0.83	0.93	1.37	MW1455		hypothetical protein	
0.82	0.99	0.96	1.37	1.03	1.07	0.80	0.89	1.12	1.00	1.11	MW1456		hypothetical protein, similar to oxidoreductase	lipid metabolism
0.92	0.54	0.66	0.75	0.70	0.51	0.92	0.53	0.99	0.76	0.71	MW1457		hypothetical protein, similar to pyrroline-5-carboxylate reductase	aminoacid metabolism
1.03	0.85	0.80	0.82	0.86	0.91	0.83	1.06	0.90	1.11	1.16	MW1458		conserved hypothetical protein	
0.75	1.07	1.04	1.15	1.05	1.55	0.91	1.02	1.00	1.16	1.75	MW1459	zwf	glucose-6-phosphate 1-dehydrogenase	carbohydrate metebolism
0.88	1.08	0.99	1.24	1.13	1.27	0.80	0.90	0.96	1.09	1.13	MW1460		transcription regulator AraC/XylS family homolog	RNA synthesis
0.91	1.27	1.17	1.22	1.21	1.37	1.05	1.19	1.11	1.34	0.94	MW1461	malA	alpha-D-1,4-glucosidase	carbohydrate metabolism
0.87	1.08	0.77	0.79	1.08	1.12	1.16	1.22	1.16	1.07	0.92	MW1462	malR	maltose operon transcriptional repressor	RNA synthesis
0.87	1.15	1.07	1.55	1.30	1.20	0.92	1.03	1.11	1.33	1.21	MW1463		conserved hypothetical protein	
0.81	1.16	0.97	1.39	1.11	1.27	0.86	1.34	1.21	0.99	1.26	MW1464	gnd	phosphogluconate dehydrogenase	carbohydrate metabolism
1.07	1.05	1.03	1.08	1.12	1.49	0.98	1.42	1.18	1.03	0.98	MW1465		hypothetical protein, similar to tripeptidase	aminoacid metabolism
1.10	1.37	1.15	1.60	1.08	1.26	1.13	1.46	1.35	0.98	0.82	MW1466		conserved hypothetical protein	
1.16	1.00	0.93	1.54	0.97	0.98	0.91	1.40	1.20	0.90	0.71	MW1467		conserved hypothetical protein	
0.91	1.15	1.10	1.12	1.05	1.37	0.90	1.07	1.38	1.06	1.27	MW1468	bmfBB	branched-chain alpha-keto acid dehydrogenase E2	aminoacid metabolism
1.00	1.30	1.02	1.21	0.93	1.43	0.95	1.77	1.43	0.97	0.99	MW1469	bfmBAB	branched-chain alpha-keto acid dehydrogenase E1	aminoacid metabolism
0.89	1.30	1.22	1.26	1.00	1.48	1.04	1.53	1.33	1.00	1.03	MW1470	bfmBAA	branched-chain alpha-keto acid dehydrogenase E1	aminoacid metabolism
0.88	0.94	0.78	0.70	0.84	1.27	0.93	1.71	1.16	0.94	1.13	MW1471		dihydrolipoamide dehydrogenase	carbohydrate metabolism
1.18	1.10	0.86	0.99	0.83	1.33	0.95	1.69	1.33	0.92	1.17	MW1472	recN	DNA repair protein	[illegible]
1.17	0.86	0.91	0.60	0.70	0.96	1.29	1.37	1.07	0.91	1.02	MW1473	ahrC	arginine repressor	RNA synthesis
1.09	1.14	0.92	0.95	0.87	0.73	0.99	1.09	1.32	0.98	0.90	MW1474	ispA	geranyltranstransferase homolog	lipid metabolism
0.97	0.68	0.78	0.75	0.78	0.66	0.75	0.81	1.09	0.86	0.91	MW1475		hypothetical protein, similar to exodeoxyribonuclease, small subunit	nucleic acid metabolism
0.95	1.09	0.88	0.99	0.92	0.86	0.81	1.01	1.27	0.90	0.98	MW1476		hypothetical protein, similar to exodeoxyribonuclease large subunit	nucleic acid metabolism
1.26	0.90	1.06	1.00	1.00	0.81	0.95	0.99	0.97	1.10	1.04	MW1477		hypothetical protein, similar to transcription termination factor	RNA synthesis
1.23	0.67	0.76	0.67	0.74	0.70	0.95	0.86	1.12	0.90	1.06	MW1478		conserved hypothetical protein	
0.97	0.82	0.81	0.71	0.77	0.67	0.87	1.11	1.00	0.87	1.18	MW1479	accC	acetyl-CoA carboxylase accC	lipid metabolism
1.33	1.11	0.86	0.67	1.17	1.14	0.78	1.12	0.96	0.73	1.15	MW1480	accB	acetyl-CoA carboxylase biotin carboxyl carrier subunit	lipid metabolism
1.34	1.26	0.84	1.01	1.16	0.79	0.78	0.85	0.96	0.89	1.85	MW1481		translation elongation factor EF-P	protein synthesis
1.32	1.31	0.90	0.92	1.28	1.23	0.81	1.39	0.78	0.79	1.39	MW1482		Xaa-Pro dipeptidase	protein modification
1.19	0.93	0.86	0.64	0.93	0.90	0.77	0.97	1.00	0.88	1.50	MW1484		hypothetical protein	
1.29	1.12	0.92	0.80	1.32	1.08	0.91	1.23	0.92	0.88	1.04	MW1485		conserved hypothetical protein	
1.10	0.65	0.65	0.93	0.86	0.51	0.71	0.61	1.11	0.99	1.37	MW1486		conserved hypothetical protein	
1.48	0.73	0.65	0.60	1.04	0.51	0.73	0.99	0.83	0.84	1.70	MW1486n		conserved hypothetical protein	
0.97	1.01	0.82	0.57	1.04	1.16	0.90	1.14	0.68	1.01	0.71	MW1487		glycine dehydrogenase (decarboxylating) subunit 2 homolog	aminoacid metabolism
1.09	0.88	0.98	0.56	0.98	1.36	0.94	1.45	0.90	0.95	0.68	MW1488		glycine dehydrogenase subunit 1	
1.03	1.17	0.95	0.74	1.07	1.77	0.83	1.20	0.86	0.90	0.73	MW1489	gcvT	aminomethyltransferase	aminoacid metabolism
1.14	0.81	0.90	0.82	1.02	0.97	0.88	0.81	0.71	0.86	1.20	MW1490		hypothetical protein, similar to shikimate kinase (SK)	aminoacid metabolism
0.94	1.22	0.94	0.84	1.13	1.20	0.78	1.02	0.84	1.05	1.00	MW1491	comYC	hypothetical protein, similar to ComYC protein	transformation/competence
0.67	1.29	1.07	1.07	1.06	1.32	0.91	1.09	1.04	1.00	1.01	MW1492		hypothetical protein	
0.95	1.22	1.04	1.02	1.03	1.23	0.91	1.33	0.95	0.87	1.07	MW1492n		hypothetical protein	

0.88	1.31	0.94	0.72	1.02	1.57	0.85	1.44	0.75	0.91	1.04	MW1493		hypothetical protein, similar to competence protein	transformation/competence
1.09	1.10	0.91	0.81	1.15	1.19	0.96	1.36	0.69	0.92	0.91	MW1494	comGC	exogenous DNA-binding protein comGC	transformation/competence
0.80	1.26	0.95	0.91	1.04	1.33	0.76	1.15	0.94	0.89	1.06	MW1495		hypothetical protein, similar to DNA transport machinery protein comGB	transformation/competence
0.91	0.92	0.95	0.77	0.88	1.24	0.95	1.26	0.84	0.97	1.26	MW1496		hypothetical protein, similar to late competence protein comGA	transformation/competence
1.00	1.29	1.01	0.99	1.01	1.18	0.96	1.15	0.98	0.92	1.21	MW1497		conserved hypothetical protein	
1.53	1.07	0.79	0.91	1.14	0.92	0.96	1.59	0.65	0.89	1.17	MW1498		conserved hypothetical protein	
1.00	1.29	1.08	1.05	1.10	1.17	0.93	1.25	1.04	0.94	1.11	MW1499	glcK	glucokinase	carbohydrate metabolism
1.47	0.82	0.86	0.86	0.85	0.86	1.19	1.08	1.19	0.82	1.11	MW1500		conserved hypothetical protein	
1.26	0.98	1.09	0.84	0.99	1.24	1.15	1.39	0.91	1.02	1.08	MW1501		conserved hypothetical protein	
1.10	1.07	1.07	1.31	1.12	1.09	1.05	1.12	0.91	0.99	1.03	MW1502		conserved hypothetical protein	
1.90	0.57	0.82	0.74	1.32	0.33	0.80	0.62	1.36	1.04	1.60	MW1503	rpmG	50S ribosomal protein L33	protein synthesis
1.57	0.60	1.04	0.71	0.99	0.56	0.73	0.73	1.23	1.17	1.79	MW1503n	rpmG	50S ribosomal protein L33	protein synthesis
1.34	1.22	1.22	1.16	1.24	1.55	1.06	1.16	1.39	1.02	1.07	MW1504	pbp3	penicillin-binding protein 3	cell wall
1.08	1.11	0.77	1.76	0.85	1.39	2.08	1.48	1.00	0.97	0.98	MW1505	sodA	superoxide dismutase SodA	detoxification
1.30	0.90	0.69	1.11	0.73	1.57	2.19	1.58	0.90	0.95	1.03	MW1505n	sodA	superoxide dismutase SodA	detoxification
0.89	1.09	1.02	1.22	1.19	1.08	1.04	1.01	1.11	1.01	0.83	MW1506		ferric uptake regulator homolog	RNA synthesis
0.84	1.00	0.92	1.41	1.08	1.11	0.89	0.79	1.19	0.91	0.64	MW1507		hypothetical protein, similar to ABC transporter	transport/binding
0.75	1.28	0.96	0.98	0.98	1.11	0.94	0.94	0.94	0.85	0.62	MW1508		hypothetical protein, similar to ABC transporter ATP-binding protein	transport/binding
1.00	0.73	1.05	0.95	0.98	0.84	0.92	0.76	1.00	1.01	0.72	MW1509		hypothetical protein, similar to endonuclease IV	DNA repair or modify
0.95	0.89	1.01	0.91	1.09	1.04	1.01	1.30	0.81	0.91	0.68	MW1510		hypothetical protein, similar to ATP-dependent RNA helicase	RNA modification
1.03	1.19	0.97	1.24	0.95	1.05	0.89	0.94	1.11	0.97	0.84	MW1511		conserved hypothetical protein	
1.02	1.26	1.10	1.32	1.09	1.23	1.09	1.02	1.41	1.02	0.87	MW1512		conserved hypothetical protein	
1.23	1.39	1.07	1.10	1.01	1.39	1.12	1.24	1.42	1.05	0.94	MW1513	sigA	RNA polymerase sigma factor	RNA Synthesis
1.32	1.34	1.40	1.09	1.04	1.31	1.29	1.52	1.34	1.22	0.85	MW1514	dnaG	DNA primase	DNA replication
1.06	1.13	1.05	1.38	1.01	1.29	0.83	1.17	1.11	0.95	0.74	MW1515		conserved hypothetical protein	
0.94	0.59	0.49	0.62	0.65	0.78	0.87	1.00	0.86	0.60	0.57	MW1516		conserved hypothetical protein	
1.08	1.34	0.87	1.15	1.00	1.13	0.81	1.13	1.36	0.98	1.49	MW1517	glyS	glycyl-tRNA synthetase	protein synthesis
1.07	1.01	1.03	0.89	1.09	1.30	1.03	1.32	1.05	1.03	1.02	MW1518		hypothetical protein, similar to DNA repair protein RecO	[illegible]
1.17	1.16	1.09	1.11	1.04	1.90	1.05	1.44	1.16	0.98	1.00	MW1519	bex	bex(GTP-binding protein)	miscellaneous
1.04	1.37	0.92	1.20	0.97	1.75	1.03	1.48	1.39	0.93	1.09	MW1520	cdd	cytidine deaminase	nucleic acid metabolism
1.11	1.30	1.00	1.15	0.91	1.98	1.07	1.35	1.31	0.97	1.05	MW1521		hypothetical protein, similar to diacylglycerol kinase	lipid metabolism
1.32	0.77	0.90	0.65	0.74	1.55	1.41	1.47	0.96	1.04	0.99	MW1522		conserved hypothetical protein	
0.87	1.19	0.95	1.13	0.91	1.90	0.96	1.09	1.15	0.89	0.91	MW1523	phoH	phosphate starvation-induced protein phoH homolog	phosphate metabolism
0.95	1.47	0.86	1.52	0.89	1.23	1.00	1.05	1.44	0.77	1.35	MW1524		conserved hypothetical protein	
0.90	1.32	1.08	1.73	0.95	1.62	1.08	1.38	1.65	0.86	1.39	MW1525		conserved hypothetical protein	
1.10	0.81	1.00	0.74	0.79	1.47	1.32	1.15	1.18	0.89	1.71	MW1526		conserved hypothetical protein	
1.56	0.53	0.69	0.76	0.97	0.12	0.87	0.21	1.17	1.30	1.29	MW1527	rpsU	30S ribosomal protein S21	protein synthesis
1.49	0.56	0.86	0.79	1.13	0.18	0.93	0.33	1.05	1.21	1.15	MW1527n	rpsU	30S ribosomal protein S21	protein synthesis
0.74	0.87	0.86	1.04	1.16	0.54	0.93	1.01	0.73	0.90	1.54	MW1528		conserved hypothetical protein	
1.04	0.92	0.81	0.79	1.12	1.05	0.76	1.02	0.87	0.69	1.26	MW1529		conserved hypothetical protein	
0.89	1.03	0.99	1.48	1.15	1.29	0.88	0.88	1.30	0.90	0.89	MW1530		conserved hypothetical protein	
0.95	0.89	0.97	0.73	1.08	1.28	1.10	1.24	0.91	0.89	0.79	MW1531	dnaJ	DnaJ protein (Hsp40)	adaptation to atypical
1.09	0.85	0.83	0.84	1.10	2.88	1.48	2.34	0.91	0.91	0.50	MW1532	dnaK	DnaK protein	protein folding
1.09	1.04	0.92	1.26	1.19	2.34	1.17	1.27	1.15	0.94	0.40	MW1533	grpE	GrpE protein (Hsp70 Cofactor Hsp20)	adaptation to atypical
1.22	0.91	0.83	1.12	1.28	3.06	1.32	2.14	0.87	0.90	0.41	MW1534	hrcA	Heat-inducible transcriptional repressor	RNA synthesis
0.93	1.03	1.00	1.35	1.06	1.38	1.02	0.83	1.08	1.03	0.82	MW1535	hemN	oxygen-independent coproporphyrinogen oxidase III	coenzyme metabolism
0.82	1.14	1.00	1.34	0.95	0.89	0.79	0.81	1.26	0.93	0.94	MW1536	lepA	GTP-binding protein	protein synthesis
1.01	1.06	1.00	0.97	1.03	1.06	0.79	1.13	0.90	0.92	0.92	MW1536n	lepA	GTP-binding protein	protein synthesis
1.29	0.74	1.10	0.83	0.83	0.28	0.63	0.42	0.95	0.99	1.24	MW1537	rpsT	30S ribosomal protein S20	protein synthesis
1.17	1.05	1.02	1.17	1.19	0.90	0.89	0.60	1.55	0.95	1.30	MW1538		conserved hypothetical protein	
1.06	1.18	1.75	0.81	0.93	1.49	1.01	1.50	1.02	1.00	1.55	MW1539		hypothetical protein, similar to ComEC late competence protein 3 (comE opero	transformation/competence
1.04	1.12	0.92	0.95	1.01	1.00	0.92	1.15	0.93	0.94	1.06	MW1540	comEB	late competence operon required for DNA binding and uptake comEB	transformation/competence
1.04	1.19	0.92	1.00	1.09	1.03	0.90	1.12	0.86	0.99	1.06	MW1541		ypothetical protein, similar to late competence operon required for DNA binding and up	transformation/competence
0.86	1.25	0.98	1.24	1.04	0.99	0.84	0.80	1.15	0.96	1.08	MW1542		conserved hypothetical protein	
1.13	0.75	0.92	0.83	1.06	0.95	0.92	0.91	1.02	0.94	1.11	MW1543		conserved hypothetical protein	
1.10	1.10	0.99	1.00	1.10	1.03	0.91	0.99	1.13	0.90	1.15	MW1544		conserved hypothetical protein	
1.17	1.03	1.14	1.04	1.06	0.91	0.97	1.05	1.14	0.89	1.09	MW1545		conserved hypothetical protein	
1.06	1.08	1.03	1.14	1.10	1.15	0.84	0.90	1.22	0.84	1.12	MW1546		conserved hypothetical protein	aminoacid metabolism
1.14	0.90	1.04	1.01	1.17	1.01	1.03	0.97	1.19	0.88	1.03	MW1547	aroE	shikimate dehydrogenease	aminoacid metabolism
1.15	0.98	1.11	1.05	1.06	0.96	0.91	0.95	1.17	0.79	0.99	MW1548		conserved hypothetical protein	
1.04	0.94	0.98	1.11	1.03	0.99	0.80	0.91	0.94	0.83	0.99	MW1549		conserved hypothetical protein	
0.98	0.94	0.95	1.21	1.06	0.96	0.77	0.75	1.17	0.84	0.89	MW1550	pfs	5'-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase	nucleic acid metabolism
1.18	1.05	1.03	1.05	1.15	0.97	0.92	0.87	1.43	0.93	1.13	MW1551		hypothetical protein	
0.67	1.47	1.06	1.21	1.07	1.19	0.80	0.93	1.29	0.94	0.96	MW1552		enterotoxin homolog	pathogenic factor
0.92	1.21	1.15	1.12	1.12	1.10	1.03	0.85	1.10	1.00	1.16	MW1552a		enterotoxin homolog	pathogenic factor
0.94	0.79	0.73	0.67	1.64	0.85	1.01	1.03	1.18	0.73	1.10	MW1552b	sea	hypothetical protein, similar to enterotoxin A precursor	pathogenic factor
1.00	0.93	1.09	1.23	0.97	1.04	1.02	0.76	0.90	1.02	1.17	MW1553		conserved hypothetical protein	
0.81	0.96	1.11	1.05	0.99	1.07	0.90	0.90	1.01	1.07	1.03	MW1554		conserved hypothetical protein	
0.86	1.15	0.99	0.83	1.15	1.26	0.91	1.12	0.92	0.96	0.94	MW1555		conserved hypothetical protein	
0.88	1.15	1.04	0.96	0.86	0.89	1.12	1.01	1.10	1.05	0.83	MW1556		acetyl-CoA carboxylase (biotin carboxylase subunit), accC homolog	lipid metabolism
0.86	1.00	1.00	0.74	0.95	0.98	0.79	1.01	1.07	1.00	1.07	MW1557		pothetical protein, similar to acetyl-CoA carboxylase (biotin carboxyl carrier subunit), a	lipid metabolism
0.85	1.00	1.04	0.97	0.97	1.07	0.93	1.04	1.15	1.02	1.12	MW1558		conserved hypothetical protein	
0.79	1.28	1.19	1.10	0.89	0.97	0.86	0.93	1.16	0.96	1.11	MW1559		conserved hypothetical protein	
1.02	0.80	0.96	0.97	0.90	0.79	0.82	0.62	1.01	0.89	1.11	MW1560	greA	transcription elongation factor	RNA synthesis
0.75	0.90	0.81	0.73	0.90	0.66	0.70	0.78	1.01	0.84	1.11	MW1561	udk	uridine kinase	nucleic acid metabolism
0.77	1.02	0.94	1.06	0.87	0.73	0.71	0.84	1.15	0.81	0.94	MW1562		hypothetical protein, similar to protease	aminoacid metabolism
0.83	1.40	0.99	1.04	1.09	0.92	0.77	0.84	1.07	0.92	0.93	MW1563		hypothetical protein, similar to protease	aminoacid metabolism
1.17	0.85	0.83	0.86	0.81	0.71	0.94	0.86	1.11	0.95	1.00	MW1564		hypothetical protein, similar to caffeoyl-CoA O-methyltransferase	coenzyme metabolism
1.23	0.65	0.55	0.58	0.75	0.46	0.81	0.48	1.05	0.78	1.03	MW1565		conserved hypothetical protein	
0.99	0.85	0.65	1.06	0.96	0.56	0.80	0.45	0.88	0.95	1.16	MW1566		conserved hypothetical protein	
1.26	0.60	0.40	0.72	0.70	0.40	1.11	0.52	0.82	0.80	1.13	MW1566n		conserved hypothetical protein	
1.12	0.67	0.68	0.77	0.87	0.44	0.90	0.45	0.75	0.90	1.16	MW1567		conserved hypothetical protein	
0.97	0.52	0.51	0.41	0.64	0.44	0.98	0.81	0.76	0.72	1.10	MW1568	alaS	alanyl-tRNA synthetase	protein synthesis
1.04	1.05	1.04	0.92	0.93	0.95	0.95	1.15	1.01	1.17	1.36	MW1569		hypothetical protein, similar to deoxyribonuclease	[illegible]
1.15	1.08	0.64	0.74	0.67	0.74	1.05	0.99	1.07	0.83	1.29	MW1570		conserved hypothetical protein	
1.14	1.05	0.89	0.97	0.94	0.91	1.21	0.99	1.26	0.87	1.15	MW1571	trmU	(5-methylaminomethyl-2-thiouridylate)-methyltran sferase	
1.06	0.60	0.84	0.51	0.78	0.86	1.14	0.89	0.85	0.93	1.05	MW1572		iron-sulfur cofactor synthesis protein homolog	miscellaneous
1.03	1.69	1.24	1.07	1.13	1.56	1.14	1.19	1.10	1.04	1.14	MW1573		conserved hypothetical protein	
2.01	0.97	0.93	1.03	0.75	2.04	5.06	1.40	1.36	1.72	0.99	MW1574		hypothetical protein	
2.14	1.31	0.95	0.79	0.88	4.44	4.81	1.30	1.40	1.55	0.94	MW1574n		hypothetical protein	
2.38	2.56	1.46	1.47	0.82	11.94	6.70	1.69	1.52	2.16	1.11	MW1575	csbD	sigmaB-controlled gene product	miscellaneous
1.11	0.69	0.90	1.06	1.30	0.89	1.03	0.91	0.83	0.98	1.15	MW1576		conserved hypothetical protein	
1.07	0.77	0.83	0.90	1.00	1.16	1.08	1.28	0.85	0.99	1.00	MW1577		conserved hypothetical protein	
1.09	1.37	0.97	0.97	1.15	1.16	0.86	1.29	1.05	0.88	0.83	MW1578		conserved hypothetical protein	
1.51	0.79	1.14	1.70	1.10	1.51	1.57	1.28	1.13	1.50	1.07	MW1579		hypothetical protein	
1.59	0.73	1.06	1.34	1.35	1.74	1.52	1.95	0.94	1.28	0.94	MW1579n		hypothetical protein	
0.85	1.21	0.94	0.76	1.29	1.06	0.95	1.98	0.92	0.94	0.95	MW1580	aspS	aspartyl-tRNA synthetase	protein synthesis

0.88	0.93	0.91	0.78	0.98	0.82	0.83	0.96	1.16	0.89	0.83	MW1581	hisS	histidyl-tRNA synthetase	protein synthesis
1.18	1.08	0.83	0.80	1.14	0.64	0.84	0.72	1.07	0.87	1.74	MW1582	lytH	N-acetylmuramoyl-L-alanine amidase	cell wall
1.25	0.94	0.77	0.67	1.29	0.52	0.92	0.61	0.87	0.86	1.55	MW1583		conserved hypothetical protein	
1.17	0.63	0.67	0.56	1.05	0.56	1.16	0.81	0.59	0.96	1.65	MW1584	relA	GTP pyrophosphokinase	[illegible]
1.15	0.92	0.85	0.85	1.28	0.69	0.96	0.66	1.29	0.83	1.00	MW1585	apt	adenine phosphoribosyl transferase	[illegible]
1.29	0.67	0.67	0.49	1.03	0.60	1.09	0.83	0.91	0.87	1.12	MW1586		hypothetical protein, similar to single-strand DNA-specific exonuclease	[illegible]
1.07	0.86	0.83	0.78	1.15	0.66	0.98	1.07	0.83	0.95	1.41	MW1587	secF	protein-export membrane protein SecDF	protein secretion
1.21	0.79	0.88	0.93	1.07	0.54	0.89	0.93	0.85	1.01	0.84	MW1588		conserved hypothetical protein	
0.91	1.09	1.02	1.15	1.10	0.75	0.83	0.82	1.12	0.91	0.76	MW1589	tgt	tRNA-guanine transglycosylase	RNA modification
0.93	1.02	1.00	1.01	1.14	0.88	0.80	0.76	1.07	0.83	0.85	MW1590	queA	S-adenosylmethionine tRNA ribosyltransferase	RNA modification
0.83	1.17	0.99	1.07	1.09	0.98	0.75	0.73	0.96	0.88	0.84	MW1591	ruvB	holliday junction DNA helicase	[illegible]
0.96	0.90	0.84	0.92	1.00	0.80	0.78	0.83	0.75	0.78	0.91	MW1592	ruvA	holliday junction DNA helicase	[illegible]
0.82	0.79	0.80	1.10	1.03	0.77	0.69	0.66	0.93	0.80	0.94	MW1593		hypothetical protein, similar to chorismate mutase	amino acid metabolism
0.83	0.79	0.86	0.89	1.05	0.96	0.83	0.76	0.79	0.94	0.81	MW1594	obg	Spo0B-associated GTP-binding protein	sporulation
0.70	0.66	0.90	0.87	0.93	0.23	0.57	0.39	0.75	0.99	0.58	MW1595	rpmA	50S ribosomal protei L27	protein synthesis
0.70	0.44	0.79	0.70	0.68	0.17	0.44	0.40	0.73	0.95	0.58	MW1596		conserved hypothetical protein	
0.61	0.57	0.77	0.62	0.79	0.17	0.46	0.30	0.75	0.90	0.51	MW1597	rplU	50S ribosomal protein L21	protein synthesis
0.64	0.68	0.87	0.76	0.82	0.20	0.45	0.29	0.77	0.94	0.50	MW1597n	rplU	50S ribosomal protein L21	protein synthesis
0.95	0.88	0.94	1.03	1.01	0.84	0.82	0.73	1.26	0.80	1.07	MW1598		hypothetical protein, similar to cell shape determinant mreD	cell wall
1.00	1.05	0.97	1.39	0.98	0.98	0.80	0.83	1.15	0.90	0.91	MW1599		hypothetical protein, similar to cell shape determinant mreC	cell wall
1.09	0.99	0.98	0.89	0.92	1.12	1.09	1.21	1.25	0.86	1.02	MW1600		hypothetical protein	
1.04	0.92	0.86	0.94	0.99	0.88	0.89	0.87	1.08	0.93	0.85	MW1601		hypothetical protein	
1.00	1.01	1.00	1.05	0.95	0.99	1.00	0.81	1.13	0.97	0.90	MW1602		hypothetical protein	
1.09	0.86	0.93	1.04	0.94	1.07	1.07	1.00	1.17	1.04	1.00	MW1603		hypothetical protein, similar to transporter PAB2175 from Pyrococcus abyss	transport/binding
1.02	1.28	1.00	0.98	1.08	1.09	1.26	1.00	1.42	1.02	1.03	MW1604	radC	DNA repair protein RadC homolog	DNA repair or modify
0.89	1.06	1.04	1.38	1.12	1.22	0.99	0.91	1.13	0.97	0.94	MW1604n	ncated#ra	truncated hypothetical protein, similar to DNA repair protein	DNA repair or modify
1.00	1.30	1.04	1.60	1.08	1.05	1.00	0.86	1.31	0.99	0.90	MW1605		hypothetical protein, similar to type IV prepilin peptidase	protein modification
0.82	0.94	0.88	0.70	0.90	0.94	0.81	1.03	1.32	1.01	1.07	MW1606	folC	folylpolyglutamate synthase	coenzyme metabolism
1.06	1.02	0.87	1.02	0.90	0.90	0.91	0.79	1.27	1.01	1.29	MW1608	tag	DNA-3-methyladenine glycosidase	DNA repair or modify
0.91	1.03	0.90	1.05	0.93	0.83	1.19	0.93	1.29	1.12	2.00	MW1609		conserved hypothetical protein	
1.18	0.76	0.70	0.60	0.67	0.66	1.21	0.81	1.16	1.00	1.71	MW1610		hypothetical protein	
0.98	0.86	0.77	0.73	0.90	0.73	0.90	0.91	1.25	0.98	2.25	MW1610n		hypothetical protein	
0.68	0.69	0.91	0.85	0.88	0.35	0.56	0.50	0.94	0.93	0.67	MW1611	hemL	glutamate-1-semialdehyde 2,1-aminomutase	coenzyme metabolism
1.03	1.13	0.84	0.77	1.10	0.94	1.09	1.10	1.39	0.98	1.24	MW1612	hemB	delta-aminolevulinic acid dehydratase	coenzyme metabolism
1.14	1.19	0.86	1.08	1.21	0.99	0.93	0.86	1.28	0.86	1.12	MW1613	hemD	uroporphyrinogen III synthase	coenzyme metabolism
1.22	1.17	0.75	0.53	0.96	0.63	0.98	0.78	1.27	0.73	1.04	MW1614	hemC	porphobilinogen deaminase	coenzyme metabolism
1.41	0.95	0.58	0.57	0.81	0.56	1.44	0.87	1.21	0.77	1.44	MW1615	hemX	hemA concentration negative effector hemX	coenzyme metabolism
1.07	1.07	0.87	1.15	0.91	1.33	1.47	0.85	1.16	0.82	1.29	MW1616	hemA	glutamyl-tRNA reductase	coenzyme metabolism
1.18	0.84	0.80	0.65	0.94	0.73	1.16	0.88	1.12	0.88	0.83	MW1617		conserved hypothetical protein	
1.11	1.03	0.71	0.73	0.97	0.69	0.85	0.89	1.12	0.68	0.70	MW1618	clpX	protease ClpX	adaptation to atypical
1.19	1.62	0.95	0.98	1.19	1.16	0.82	1.89	1.01	0.83	0.62	MW1619	tig	trigger factor	protein folding
1.14	0.86	0.71	0.86	0.77	0.71	0.99	0.88	1.15	0.80	0.86	MW1620		hypothetical protein	
1.04	0.57	0.74	0.35	0.81	0.60	1.11	0.73	0.90	0.88	0.82	MW1621		conserved hypothetical protein	
1.16	1.27	1.00	0.52	0.98	0.35	0.63	0.52	0.88	0.82	0.66	MW1622	rplT	50S ribosomal protein L20	protein synthesis
1.12	0.75	0.92	0.50	0.78	0.34	0.53	0.51	0.70	0.80	0.64	MW1623	rpmI	50S ribosomal protein L35	protein synthesis
1.10	0.86	1.03	0.47	0.88	0.52	0.52	0.54	0.80	0.85	0.67	MW1624	infC	translation initiation factor IF-3 infC	protein synthesis
0.97	1.30	1.32	1.18	1.44	0.89	1.63	0.96	0.82	1.22	0.49	MW1625	lysP	lysine-specific permease	transport/binding
1.10	0.62	0.82	0.91	1.04	0.36	1.49	0.33	0.86	0.92	0.23	MW1626	thrS	threonyl-tRNA synthetase 1	protein synthesis
1.21	0.74	0.89	0.79	0.97	1.16	0.98	1.00	0.67	0.96	0.88	MW1627	dnaI	primosomal protein	DNA replication
1.07	1.12	0.95	1.09	1.19	1.70	0.81	1.00	0.72	0.84	0.81	MW1628	dnaB	chromosome replication initiation/membrane attachment protein	DNA replication
1.15	0.94	0.81	1.05	1.16	1.41	0.82	0.86	0.61	0.78	0.75	MW1629		conserved hypothetical protein	
1.00	1.70	1.02	1.09	0.89	2.55	0.91	0.97	0.87	1.37	1.19	MW1630	gapB	glyceraldehyde 3-phosphate dehydrogenase 2	carbohydrate metabolism
1.01	1.04	0.99	1.00	1.04	1.32	0.91	1.05	0.86	0.95	0.88	MW1631		conserved hypothetical protein	
1.19	0.84	0.97	1.26	1.17	0.85	1.00	0.98	1.31	0.92	0.82	MW1632		hypothetical protein, similar to formamidopyrimidine-DNA glycosylase	DNA repair or modify
0.97	0.96	0.85	0.74	0.86	1.35	1.03	1.88	0.71	1.05	0.89	MW1633	polA	DNA polymerase I	DNA replication
1.02	0.82	1.10	0.81	0.90	1.29	0.96	1.60	1.07	1.09	1.91	MW1634-35		hypothetical protein	
1.13	1.46	1.12	0.99	1.07	1.95	1.00	2.32	0.97	0.95	1.23	MW1636	phoR	alkaline phosphatase synthesis sensor protein	sensor
0.96	1.18	1.04	1.27	1.09	2.14	0.93	1.44	1.16	1.04	0.98	MW1637	phoP	alkaline phosphatase synthesis transcriptional regulatory protein	RNA synthesis
0.97	1.45	1.02	1.05	1.10	2.65	1.02	1.91	0.90	0.91	1.02	MW1637n	phoP	alkaline phosphatase synthesis transcriptional regulatory protein	RNA synthesis
0.92	1.29	1.17	1.21	1.06	1.95	1.16	1.49	1.32	1.11	0.78	MW1638	citC	isocitrate dehyrogenase	carbohydrate metabolism
0.85	1.19	1.02	1.40	1.08	1.09	1.00	0.95	1.09	1.08	0.84	MW1639	citZ	citrate synthase II	carbohydrate metabolism
0.97	0.60	0.82	0.92	0.92	0.50	1.10	0.66	1.04	1.33	1.86	MW1640	aapA	D-serine/D-alanine/glycine TRANSPORTER	transport/binding
0.95	0.69	0.64	1.24	1.26	0.52	0.90	1.22	0.83	0.85	1.21	MW1641	pykA	pyruvate kinase	carbohydrate metabolism
0.84	0.42	0.55	0.98	0.90	0.33	0.79	1.29	0.74	0.65	0.77	MW1642	pfk	6-phosphofructokinase	carbohydrate metabolism
0.85	0.85	0.86	1.15	0.88	0.54	0.77	0.81	0.84	0.83	0.78	MW1643	accA	acetyl-CoA carboxylase carboxyl transferase subunit alpha	lipid metabolism
0.89	0.66	0.84	0.70	0.97	0.60	0.91	0.78	0.82	0.76	0.80	MW1644		acetyl-CoA carboxylase transferase beta subunit	carbohydrate metabolism
0.94	1.10	0.98	1.14	1.07	0.85	0.78	1.00	1.02	0.81	0.74	MW1645	mdh	malate dehydrogenase homolog	carbohydrate metabolism
0.87	1.00	0.76	0.78	0.85	0.90	0.91	1.10	0.95	0.98	0.95	MW1646	dnaE	DNA polymerase III, alpha chain	DNA replication
0.99	0.93	0.67	0.75	0.69	0.72	1.04	1.24	0.99	0.90	0.91	MW1646a	dnaE	DNA polymerase III, alpha chain	DNA replication
1.05	1.10	1.05	1.48	1.07	1.08	1.09	0.69	1.20	1.02	0.91	MW1647		conserved hypothetical protein	
0.95	1.09	1.11	1.34	1.00	1.36	0.90	0.97	1.09	1.12	0.86	MW1648		conserved hypothetical protein	
1.44	0.72	0.67	0.68	0.94	0.75	1.10	0.97	0.76	1.10	1.11	MW1649		conserved hypothetical protein	
1.23	0.65	1.03	1.39	1.05	1.36	1.48	1.64	1.04	1.02	0.82	MW1650		conserved hypothetical protein	
0.98	0.80	0.80	1.26	0.93	1.03	0.95	0.86	0.87	1.12	0.90	MW1651		Xaa-Pro dipeptidase homolog	protein modification
0.88	0.99	1.22	1.42	1.18	1.47	0.91	1.05	1.15	1.11	0.78	MW1652	ald	alanine dehydrogenase	amino acid metabolism
1.03	0.95	1.25	1.64	1.34	1.69	1.05	0.59	0.82	1.24	0.54	MW1653		conserved hypothetical protein	
0.87	1.23	0.99	1.50	1.20	1.03	1.02	1.34	1.11	1.02	1.49	MW1654	ackA	acetate kinase homolog	carbohydrate metabolism
1.03	1.12	1.01	1.06	0.91	1.22	0.95	1.41	1.26	1.02	0.94	MW1655		conserved hypothetical protein	
1.17	0.43	0.56	0.41	0.69	0.76	0.95	1.32	0.96	0.68	0.73	MW1656		hypothetical protein, similar to thioredoxin peroxidase	detoxification
0.96	1.00	0.92	0.95	0.99	0.95	0.85	1.10	1.07	1.01	1.24	MW1657		conserved hypothetical protein	
0.94	1.08	0.95	0.98	0.91	0.99	0.86	1.07	1.04	1.01	1.11	MW1658		hypothetical protein, similar to thiamine biosynthesis protein ThiI	coenzyme metabolism
0.87	1.18	1.03	1.01	0.95	0.92	0.88	0.88	1.17	1.00	1.03	MW1659		hypothetical protein, similar to iron-sulfur cofactor synthesis protein nifZ	coenzyme metabolism
0.89	0.82	0.79	1.19	0.96	0.84	0.80	0.83	1.07	0.95	1.18	MW1660		hypothetical protein, similar to septation ring formation regulator	RNA synthesis
0.94	1.12	0.77	1.06	0.87	0.78	0.74	0.75	1.10	0.91	1.23	MW1661		conserved hypothetical protein	
0.85	1.37	0.93	1.49	0.99	0.50	0.64	0.51	1.38	0.99	0.88	MW1662	rpsD	30S ribosomal protein S4	protein synthesis
0.91	0.62	0.60	0.30	0.54	0.52	0.80	0.79	0.56	0.88	1.17	MW1663		hypothetical protein, similar to glycerophosphoryl diester phosphodiesterase	lipid metabolism
0.97	0.92	0.71	0.75	0.71	0.60	0.74	0.65	0.88	0.87	1.33	MW1664		conserved hypothetical protein	
0.84	0.71	0.45	0.45	0.59	0.32	0.52	0.46	0.72	0.73	1.92	MW1665		hypothetical protein, similar to soluble hydrogenase 42 kD subunit	
0.89	0.75	0.46	0.46	0.58	0.32	0.62	0.62	0.67	0.88	2.02	MW1666	serA	D-3-phosphoglycerate dehydrogenase	amino acid metabolism
1.04	0.36	0.40	0.32	0.36	0.16	0.66	0.34	0.75	0.83	1.56	MW1667		hypothetical protein	
0.75	0.91	0.67	0.77	0.86	0.55	0.80	0.76	1.00	0.85	1.15	MW1668	ptaA	PTS system, N-acetylglucosamine-specific IIABC component	transport/binding
1.06	0.70	0.70	0.88	0.90	0.61	0.81	0.75	1.21	0.76	1.38	MW1669		hypothetical protein, similar to acylglycerol-3-phosphate O-acyltransfera homol	lipid metabolism
0.99	0.93	0.76	0.85	0.75	0.64	0.98	1.15	1.04	0.96	1.67	MW1670		hypothetical protein, similar to serine proteinase Do, heat-shock protein htrA	adaptation to atypical
1.11	1.52	0.97	1.07	0.97	0.93	0.99	1.60	1.04	0.89	1.28	MW1671	tyrS	tyrosyl-tRNA synthetase	protein synthesis
1.16	0.87	0.95	1.02	1.04	1.52	1.03	1.42	0.90	0.89	1.39	MW1672	sgtA	probable transglycosylase	cell wall
0.98	1.15	1.22	1.10	0.95	1.14	1.16	1.51	1.10	1.28	1.17	MW1674		hypothetical protein	
0.93	1.49	1.16	1.06	1.23	1.91	0.99	1.73	1.02	0.89	0.92	MW1674n		hypothetical protein	

1.14	1.24	0.99	0.74	0.98	2.10	1.04	2.22	0.79	0.85	0.79	MW1675	fhs	formyltetrahydrofolate synthetase	carbohydrate metabolism
1.02	0.86	1.15	1.07	1.00	1.60	1.16	0.98	0.99	1.27	0.93	MW1676	acsA	acetyl-CoA synthetase	carbohydrate metabolism
1.15	1.42	0.96	0.89	1.15	1.78	1.08	1.23	0.87	0.86	1.10	MW1677	acuA	acetoin dehydrogenase homolog	carbohydrate metabolism
1.15	1.41	1.13	0.86	1.19	1.91	1.17	1.47	1.01	0.91	1.03	MW1678	acuC	acetoin utilization protein	carbohydrate metabolism
0.78	1.32	0.82	0.69	0.90	0.98	0.85	0.66	1.19	0.93	1.50	MW1679	ccpA	catabolite control protein A	RNA synthesis
1.09	1.20	0.87	0.47	1.33	1.30	1.11	1.18	0.65	0.86	1.55	MW1679n	ccpA	catabolite control protein A	RNA synthesis
1.10	0.81	0.61	0.77	0.73	0.59	0.59	0.52	0.83	0.91	1.47	MW1680		chorismate mutase homolog	aminoacid metabolism
1.46	2.23	1.16	1.52	1.04	4.71	2.42	1.99	1.11	1.06	0.62	MW1681		hypothetical protein, similar to smooth muscle caldesmon	miscellaneous
1.66	1.55	1.06	1.25	0.72	3.14	3.36	2.51	1.04	1.46	0.79	MW1682		hypothetical protein, similar to general stress protein homolog	adaptation to atypical
1.25	1.66	1.20	1.31	1.03	1.93	1.43	2.51	1.04	1.10	0.66	MW1683	murC	UDP-N-Aacerylmuramate-alanine ligase	cell wall
1.12	1.15	1.12	1.55	0.98	1.77	1.48	1.98	1.44	1.10	0.63	MW1684	ftsK/spoIII	DNA translocase stage III sporulation prot homolog	sporulation
1.28	1.15	1.16	1.00	1.14	1.64	1.10	1.79	1.23	0.92	0.57	MW1685		phenylalanyl-tRNA synthetase (beta subunit) homolog	protein synthesis
1.31	1.67	1.24	1.26	1.13	1.77	1.24	2.00	1.41	0.98	0.52	MW1686		conserved hypothetical protein	
1.25	1.04	1.01	0.92	1.01	1.30	1.31	1.66	0.97	1.08	0.82	MW1687		thioredoxin homolog	membrane bioenergetics
0.96	1.12	1.02	1.21	1.00	1.29	0.95	1.01	1.26	1.10	0.70	MW1688		endo-1,4-beta-glucanase homolog	carbohydrate metabolism
1.13	0.86	0.81	0.85	0.95	1.01	1.00	0.90	0.96	0.91	0.90	MW1689		hypothetical protein	
0.91	1.16	0.99	1.08	1.03	1.10	0.88	0.97	1.04	0.95	0.92	MW1690		conserved hypothetical protein	
0.92	0.98	0.74	0.79	1.12	0.52	0.78	0.62	0.79	1.00	1.38	MW1691		conserved hypothetical protein	
0.85	0.95	0.76	0.90	1.03	0.51	0.77	0.57	0.89	0.94	1.62	MW1692		conserved hypothetical protein	
0.85	0.80	0.80	0.89	0.90	0.61	0.74	0.76	0.70	0.79	1.44	MW1693	dat	D-alanine aminotransferase	aminoacid metabolism
0.75	0.99	0.89	1.24	1.19	1.01	0.71	0.73	0.86	0.81	1.29	MW1694		Xaa-His dipeptidase homolog	protein modification
1.19	1.39	0.78	1.46	0.70	1.86	1.69	1.20	1.04	0.87	0.85	MW1695		hypothetical protein	
0.71	1.00	1.05	1.40	1.02	0.98	0.95	0.74	1.01	0.95	1.12	MW1697		spore cortex protein homolog	sporulation
0.90	1.10	1.24	1.41	1.17	1.29	0.98	0.92	1.22	1.04	0.96	MW1698		conserved hypothetical protein	
0.90	1.04	1.22	0.96	1.08	1.01	1.23	1.20	1.18	1.00	1.10	MW1699		hypothetical protein, similar to FmtB protein	pathogenic factor
0.79	0.90	1.02	1.31	1.14	0.92	0.97	0.73	1.14	1.10	1.23	MW1700		conserved hypothetical protein	
0.84	0.85	1.03	1.04	1.16	1.06	1.03	1.08	1.00	1.10	1.36	MW1701	leuS	leucyl-tRNA synthetase	protein synthesis
0.95	1.31	1.28	1.24	1.24	1.12	0.94	0.92	1.35	1.14	1.11	MW1702		multidrug resistance protein homolog	transport/binding
0.86	0.90	1.11	0.94	0.98	0.80	0.92	0.84	0.92	1.01	1.07	MW1703		conserved hypothetical protein	
1.01	0.85	0.79	1.05	1.01	0.64	0.89	0.53	0.93	0.92	1.18	MW1704		conserved hypothetical protein	
1.00	#NUM!	1.00	0.95	1.00	1.00	1.00	1.00	0.87	0.94	0.68	MW1705	rot	repressor of toxins Rot	RNA synthesis
1.28	0.46	0.73	0.79	1.21	0.59	1.55	1.29	0.86	0.77	2.95	MW1705a	rot	repressor of toxins Rot	RNA synthesis
1.03	0.93	0.95	0.91	0.93	1.12	0.88	0.78	1.11	1.03	1.21	MW1706		lysophospholipase homolog	lipid metabolism
0.88	1.11	0.90	0.54	0.86	3.11	1.02	0.97	0.91	1.38	1.32	MW1707		proline dehydrohenase homolog	aminoacid metabolism
1.05	1.03	1.03	0.94	0.95	1.27	0.99	0.84	0.91	1.15	1.31	MW1708	ribH	6,7-dimethyl-8-ribityllumazine synthase	coenzyme metabolism
0.95	1.20	1.12	1.37	1.03	1.37	1.02	0.87	1.39	1.11	1.32	MW1709	ribA	riboflavin biosynthesis protein	coenzyme metabolism
1.00	1.49	1.24	1.00	1.13	1.41	1.08	0.97	0.93	1.09	1.71	MW1710	ribB	riboflavin synthase alpha chain	coenzyme metabolism
1.04	1.38	1.27	1.15	1.04	1.22	1.09	0.92	1.22	0.92	1.43	MW1711	ribD	riboflavin specific deaminase	coenzyme metabolism
1.15	0.98	0.94	0.40	0.71	0.90	1.27	0.91	0.72	1.00	1.07	MW1712		hypothetical protein	
1.21	1.08	1.09	0.75	1.18	0.99	0.98	1.28	0.88	0.87	1.06	MW1713		arsenical resistance operon repressor homolog	RNA synthesis
0.98	1.15	1.24	1.24	1.22	1.00	0.95	1.01	1.21	1.04	1.07	MW1714		aesenical pump membrane protein homolog	transport/binding
1.08	0.71	0.59	0.66	0.97	0.40	1.01	0.42	1.18	0.73	1.89	MW1715		conserved hypothetical protein	
1.49	0.34	0.56	0.50	0.66	0.45	0.76	0.44	0.90	0.78	1.85	MW1716		hypothetical protein	
1.30	0.88	0.73	0.62	0.81	0.64	0.92	0.70	1.09	0.80	2.49	MW1717		hypothetical protein	
1.36	0.89	0.77	0.84	0.97	0.58	0.94	0.60	1.27	0.81	2.46	MW1718		hypothetical protein	
1.50	0.88	0.79	0.65	0.91	0.53	1.15	0.61	1.22	0.84	2.36	MW1719		hypothetical protein	
1.63	1.27	1.04	0.91	1.00	0.91	0.88	1.05	0.95	0.97	2.00	MW1720		hypothetical protein	
1.31	1.71	1.04	1.57	1.09	2.32	0.90	1.34	1.04	1.00	1.91	MW1721		hypothetical protein, similar to transaldolase	carbohydrate metabolism
1.34	1.22	1.03	0.73	1.06	1.03	0.94	1.09	1.02	0.98	1.40	MW1722		hypothetical protein	
1.44	1.04	1.02	0.77	1.14	1.08	1.09	1.43	0.78	1.04	1.28	MW1723		conserved hypothetical protein	
1.05	1.41	0.98	0.76	0.94	1.06	1.01	1.39	1.02	1.00	1.44	MW1724		hypothetical protein	
1.15	1.10	1.01	1.08	0.87	0.91	1.26	1.00	1.33	1.05	1.06	MW1725		hypothetical protein	
1.07	1.13	0.94	1.13	1.08	1.16	1.04	0.90	1.13	1.03	1.75	MW1726		plant metabolite dehydrogenase homolog	miscellaneous
0.85	1.09	0.76	0.86	0.97	0.91	0.70	0.84	0.87	0.83	1.56	MW1727		hypothetical protein	
0.77	1.03	0.91	0.86	1.32	1.04	0.70	0.72	0.75	0.99	1.27	MW1728	metK	S-adenosylmethionine synthetase	aminoacid metabolism
0.95	2.31	1.53	0.82	1.07	5.18	1.10	1.43	1.02	1.62	1.18	MW1729	pckA	phosphoenolpyruvate carboxykinase	carbohydrate metabolism
1.14	1.13	1.21	1.10	0.97	1.41	1.21	1.05	1.26	1.33	1.00	MW1730		hypothetical protein	
0.95	1.08	1.06	1.01	1.02	1.22	1.09	0.86	0.99	1.22	0.89	MW1730n		hypothetical protein	
0.98	1.05	1.12	1.01	1.10	1.36	1.08	1.05	1.07	1.20	1.08	MW1731		conserved hypothetical protein	
0.93	1.49	1.28	1.03	1.00	1.52	1.00	1.33	0.83	1.16	1.24	MW1732		conserved hypothetical protein	
1.17	0.92	1.10	0.99	1.06	1.22	1.05	1.16	0.84	1.17	0.99	MW1733		conserved hypothetical protein	
0.91	1.17	1.29	1.16	1.22	1.20	1.13	0.77	1.05	1.19	1.34	MW1734	menC	o-succinylbenzoic acid synthetase	coenzyme metabolism
0.85	1.16	1.30	1.20	1.09	1.48	1.06	1.11	0.96	1.25	1.38	MW1735	menE	O-succinylbenzoic acid-CoA ligase	coenzyme metabolism
1.15	0.39	1.14	0.19	1.00	1.21	1.63	1.22	0.69	1.08	1.45	MW1736		hypothetical protein	
1.21	1.48	2.38	1.61	1.14	6.92	1.70	1.33	1.31	1.26	1.36	MW1737	hypothetical protein, similar to latent nuclear antigen [Kaposi's sarcoma-associated he		miscellaneous
1.09	1.39	2.31	1.42	1.31	2.38	1.36	1.02	1.34	1.26	1.16	MW1738		conserved hypothetical protein	
0.93	1.02	1.48	1.36	1.20	1.88	1.06	1.27	1.16	1.23	0.96	MW1739		hypothetical protein	
0.86	1.59	1.35	1.18	1.09	1.49	1.14	1.32	0.13	1.18	1.06	MW1740		hypothetical protein	
0.89	1.41	1.18	0.97	0.92	1.60	1.19	1.25	1.16	1.00	1.02	MW1741		hypothetical protein	
0.77	1.38	1.17	0.91	0.97	1.56	1.04	1.23	1.63	0.84	1.04	MW1742		hypothetical protein	
0.85	1.32	1.12	1.19	0.97	1.44	0.97	1.37	1.17	1.17	1.11	MW1743		hypothetical protein	
1.02	1.14	0.80	0.80	0.85	1.27	1.21	1.04	1.25	0.81	0.85	MW1744		hypothetical protein	
1.00	0.91	0.96	1.57	1.09	0.94	0.92	0.77	0.99	1.01	0.90	MW1745a	incated-	truncated transposase	transposon and IS
0.98	0.95	1.12	1.12	1.00	1.11	0.98	1.08	1.11	1.01	0.97	MW1745b	incated-	truncated transposase	transposon and IS
1.07	0.57	0.77	0.75	0.76	0.89	1.26	1.51	1.08	0.75	0.99	MW1746		hypothetical protein (Genomic island nu Sa beta2)	
1.22	0.46	0.75	0.47	1.49	0.76	1.22	0.70	1.00	0.81	0.78	MW1747		truncated transposase (Genomic island nu Sa beta2)	transposon and IS
1.05	0.25	0.70	0.39	0.71	0.77	0.84	0.93	1.49	0.72	1.44	MW1748		hypothetical protein (Genomic island nu Sa beta2)	
0.99	0.87	0.54	0.37	0.54	0.80	1.13	1.17	0.78	0.77	1.29	MW1749		hypothetical protein (Genomic island nu Sa beta2)	
1.20	0.87	0.86	0.85	0.90	0.94	1.24	1.05	1.15	0.80	0.91	MW1750	hsdS	probable specificity determinant HsdS	DNA [illegible]
1.19	1.12	1.10	1.42	0.95	1.04	0.94	1.05	1.14	1.05	1.06	MW1750n		probable specificity determinant HsdS	DNA [illegible]
0.75	0.94	1.11	1.24	1.14	1.17	1.02	0.92	0.89	1.29	1.00	MW1751	type I restriction enzyme EcoR1 24II M PROTEIN homolog [Pathogenicity island SaI		DNA [illegible]
0.83	1.18	1.39	1.32	1.02	1.48	0.98	1.18	1.29	1.22	1.08	MW1752	splF	serine protease SplF	pathogenic factor
0.85	1.28	1.43	1.22	1.11	1.57	1.05	1.32	1.20	1.29	1.19	MW1753	splC	serine protease SplC	pathogenic factor
1.00	0.48	0.90	0.64	0.78	0.81	1.00	1.01	0.89	1.22	1.07	MW1754	splB	serine protease SplB	pathogenic factor
0.73	1.33	1.26	1.17	1.16	1.95	1.16	1.66	1.39	1.08	1.11	MW1755	splA	serine protease SplA	pathogenic factor
1.02	1.10	1.17	1.20	0.98	1.55	1.28	1.32	1.28	1.11	1.20	MW1756		hypothetical protein (Genomic island nu Sa beta2)	
0.87	1.40	1.03	1.00	1.41	2.15	1.53	2.01	1.36	0.86	0.98	MW1757		hypothetical protein, similar to Ear protein	detoxification
1.09	2.71	1.13	1.17	1.21	7.48	1.81	3.41	1.07	1.06	1.04	MW1758	bsaG	hypothetical protein, similar to EpiG	transport/binding
0.97	1.18	0.98	0.64	0.89	7.40	1.53	1.76	1.07	1.11	1.07	MW1758n	uncated-S	truncated hypothetical protein	transport/binding
0.95	2.76	1.31	1.30	1.30	11.97	1.90	2.82	1.13	0.92	1.02	MW1759	bsaE	hypothetical protein, similar tpo EpiE	transport/binding
1.00	2.45	1.29	1.10	1.24	17.86	1.51	3.35	1.03	0.92	0.89	MW1760	bsaF	hypothetical protein, similar to EpiF [Genomic island nu Sa beta2]	transport/binding
0.91	1.21	1.23	1.20	1.04	8.47	1.19	1.69	1.18	1.21	1.12	MW1761a	hypothetical protein, similar to epidermin leader peptide processing serine		pathogenic factor
0.94	0.91	0.99	0.85	1.09	4.75	1.20	1.51	1.01	1.15	1.08	MW1761b	hypothetical protein, similar to epidermin leader peptide processing serine		pathogenic factor
0.86	1.22	1.17	1.33	1.10	1.66	0.98	1.17	1.24	1.11	1.07	MW1762	bsaD	hetical protein, similar to lantibiotic epidermin biosynthesis protei	pathogenic factor
1.00	2.01	1.18	0.80	1.25	3.41	1.38	2.62	1.17	1.29	1.19	MW1763	bsaC	hetical protein, similar to lantibiotic epidermin biosynthesis protei	pathogenic factor
2.15	5.70	0.00	0.00	1.00	1.00	2.48	#NUM!	1.00	0.15	0.00	MW1764	bsaB	hetical protein, similar to lantibiotic epidermin biosynthesis protei	pathogenic factor
1.01	1.10	1.06	1.13	0.95	1.13	1.13	1.64	1.20	1.00	1.09	MW1766	bsaA1	hypothetical protein, similar to gallidermin precursor	pathogenic factor

0.97	1.18	0.83	0.84	0.79	1.05	0.98	0.94	0.96	1.09	0.88	MW1767	lukD	leukotoxin	pathogenic factor
1.01	1.31	1.26	1.18	0.99	1.09	1.14	1.23	1.09	1.17	1.09	MW1767n	lukD	leukotoxin, LukD	pathogenic factor
1.25	1.17	1.22	1.01	1.04	1.51	1.03	1.19	0.83	0.99	1.07	MW1768	lukE	leukotoxin LukE	pathogenic factor
1.25	0.88	0.72	0.45	0.60	0.84	1.04	1.22	1.06	0.92	0.85	MW1768n	lukE	leukotoxin LukE	pathogenic factor
1.18	1.50	1.06	1.15	1.32	1.42	0.98	1.41	0.99	0.86	1.17	MW1769		hypothetical protein (Genomic island nu Sa beta2)	
1.28	0.44	0.52	0.80	0.62	0.87	1.00	0.69	0.79	0.76	0.82	MW1770		hypothetical protein	
1.00	1.28	1.06	1.17	1.00	1.15	1.22	1.32	1.49	1.03	0.84	MW1771		conserved hypothetical protein	
1.31	0.95	1.12	0.92	1.18	1.10	1.07	1.36	0.97	0.93	1.00	MW1771n		conserved hypothetical protein	
1.25	1.19	1.16	1.17	1.18	0.95	1.28	1.26	1.26	0.87	0.76	MW1772	hemY	protoporphyrinogen oxidase	coenzyme metabolism
1.16	1.08	1.14	1.04	1.33	1.17	1.20	1.22	1.11	0.81	0.67	MW1773	hemH	ferrochelatase homolog	coenzyme metabolism
1.21	1.21	1.18	1.13	1.31	1.17	1.14	1.24	1.09	0.81	0.64	MW1774	hemE	uroporphyrinogen decarboxylase	coenzyme metabolism
1.17	0.33	0.58	0.63	1.00	0.52	0.73	0.62	0.53	0.99	0.64	MW1775	TRAP	signal transduction protein TRAP	sensor
0.90	0.99	1.02	1.33	1.00	0.57	0.99	0.65	1.44	0.76	1.20	MW1776		hypothetical protein, similar to ABC transporter ecsB	transport/binding
0.94	0.98	0.91	1.31	1.11	0.83	0.81	0.90	1.12	0.83	1.03	MW1777		ABC transporter ecsA homolog	transport/binding
0.92	0.72	0.65	1.24	1.00	0.92	0.72	0.71	0.60	0.70	0.68	MW1778	hit	Hit-like protein involved in cell-cycle regulation	miscellaneous
1.15	0.84	0.74	1.23	0.76	1.42	1.34	0.93	0.81	0.95	0.83	MW1779		conserved hypothetical protein	
1.29	1.25	0.99	1.00	1.25	1.59	1.13	1.26	0.69	0.93	0.93	MW1780		hypothetical protein	
1.08	0.95	0.85	0.95	0.99	0.98	0.90	0.77	0.99	0.86	1.28	MW1781		conserved hypothetical protein	
1.22	0.87	0.79	1.04	0.90	0.86	0.94	0.89	1.03	0.86	1.06	MW1782	prsA	peptidyl-prolyl cis/trans isomerase homolog	protein folding
1.04	0.97	0.89	1.05	1.01	0.77	0.92	0.79	0.77	0.94	1.06	MW1783	cbf1	cmp-binding-factor 1	pathogenic factor
1.15	0.98	1.02	0.99	1.01	0.91	0.89	1.29	0.81	0.94	1.02	MW1784		conserved hypothetical protein	
0.96	0.91	1.07	1.07	0.96	0.98	0.87	0.60	0.89	0.99	1.18	MW1785		conserved hypothetical protein	
1.36	0.77	0.85	0.97	1.02	0.86	0.86	0.85	1.12	1.03	0.91	MW1786		conserved hypothetical protein	
1.12	0.81	0.82	0.78	0.92	0.81	0.96	0.92	0.71	1.14	1.28	MW1787		conserved hypothetical protein	
1.00	0.84	0.89	0.98	0.83	0.87	0.87	0.76	0.90	1.04	1.75	MW1789		two-component response regulator homolog	RNA synthesis
0.98	1.01	0.91	0.93	1.06	1.01	0.84	0.82	1.04	1.10	1.38	MW1790		two-component sensor histidine kinase homolog	sensor
1.22	0.84	0.76	0.62	0.86	0.85	0.75	0.88	0.74	1.04	1.34	MW1791		conserved hypothetical protein	
0.90	1.10	0.98	1.09	0.97	1.16	0.88	0.95	0.85	1.16	0.90	MW1792	citG	fumarate hydratase, class-II	carbohydrate metabolism
0.91	0.77	0.91	1.29	0.96	1.25	0.78	0.74	0.85	1.00	1.11	MW1793		hypothetical protein	
1.07	1.03	0.86	1.07	0.87	1.41	1.41	1.08	0.97	1.15	1.04	MW1794		hypothetical protein	
1.12	1.02	0.90	1.03	0.85	1.91	1.59	0.92	1.04	1.20	1.02	MW1794n		hypothetical protein	
1.04	1.80	0.84	1.32	0.74	3.66	1.56	1.02	0.96	1.23	0.76	MW1795		hypothetical protein	
0.94	0.85	1.14	1.29	0.75	0.00	0.80	0.29	1.23	1.29	1.49	MW1796a		conserved hypothetical protein	
1.10	1.49	1.04	0.88	1.19	1.74	1.09	1.44	0.86	0.93	1.36	MW1796b		conserved hypothetical protein	
0.74	1.30	1.06	1.31	0.82	1.83	1.04	1.26	0.93	1.11	1.72	MW1797		conserved hypothetical protein	
0.77	1.12	1.15	1.40	1.11	2.15	0.91	0.95	1.14	1.08	1.09	MW1798		glutamate ABC transporter ATP-binding protein	transport/binding
1.03	0.95	0.99	0.74	0.81	1.74	1.36	0.90	1.20	1.23	1.09	MW1799		hypothetical protein, similar to glutamine-binding periplasmic protein	transport/binding
1.02	1.10	1.13	1.29	1.15	2.11	1.17	0.97	1.23	1.25	1.05	MW1799n		hypothetical protein, similar to glutamine-binding periplasmic protein	transport/binding
1.09	1.16	1.23	1.34	1.11	1.13	1.14	0.73	1.25	1.13	1.30	MW1800		hypothetical protein, similar to regulatory protein (pfoS/R)	RNA synthesis
1.09	0.60	0.60	0.77	0.69	0.45	1.10	0.45	0.76	0.92	0.94	MW1801		transcription regulator Fur family homolog	RNA synthesis
0.94	1.14	1.15	1.39	1.01	1.04	0.97	0.92	1.45	0.94	1.34	MW1802		hypothetical protein, similar to D-3-phosphoglycerate dehydrogenase	carbohydrate metabolism
1.02	0.95	1.05	1.07	1.02	1.28	0.95	0.98	1.10	0.87	1.06	MW1803		conserved hypothetical protein	
1.07	1.03	1.02	1.24	0.96	1.14	0.96	0.92	1.33	0.94	1.31	MW1803n		conserved hypothetical protein	
0.94	0.77	0.95	0.95	0.83	0.76	1.26	1.12	1.09	1.09	1.08	MW1804	gsaB	glutamate-1-semialdehyde aminotransferase	aminoacid metabolism
1.04	0.60	0.63	0.61	0.81	0.73	1.03	0.78	0.82	0.91	1.19	MW1805		conserved hypothetical protein	
0.97	0.94	0.94	0.79	0.92	0.91	0.86	0.95	1.00	0.92	1.06	MW1806		ABC transporter (ATP-binding protein) homolog	transport/binding
0.95	0.95	0.87	1.25	0.95	0.93	0.80	0.77	0.94	0.99	0.74	MW1807		conserved hypothetical protein	
1.11	0.99	0.95	0.96	0.91	1.00	1.11	0.90	1.14	1.03	1.19	MW1808		hypothetical protein, similar to A/G-specific adenine glycosylase	nucleic acid metabolism
1.13	0.86	0.71	0.64	0.72	0.81	1.06	0.92	0.92	0.85	0.85	MW1809		conserved hypothetical protein	
1.27	1.06	0.93	0.70	1.14	1.09	1.03	1.21	0.97	0.77	1.42	MW1810		hypothetical protein, similar to teichoic acid transport protein tagG	transport/binding
1.25	0.78	0.64	0.78	0.79	0.89	1.12	1.02	1.13	0.75	1.16	MW1811		hypothetical protein, similar to teichoic acid translocation ATP-binding protein ta	transport/binding
1.35	1.08	1.04	0.95	1.02	1.36	1.03	1.45	0.77	0.84	1.11	MW1812		conserved hypothetical protein	
1.06	0.84	0.85	0.74	0.75	1.01	1.26	0.94	1.02	0.79	0.93	MW1813		conserved hypothetical protein	
1.15	0.69	0.79	0.80	0.36	0.83	1.37	0.85	0.78	0.84	1.27	MW1814	sgtB	hypothetical protein, similar to penicillin-binding protein 1A/1B	cell wall
1.17	1.37	0.78	1.16	0.77	2.36	2.02	1.61	1.09	0.90	1.02	MW1815		conserved hypothetical protein	
1.19	1.03	0.83	0.78	0.91	1.16	1.08	1.33	0.88	0.97	1.25	MW1816		conserved hypothetical protein	
1.02	1.17	0.96	0.99	1.07	1.23	1.01	1.01	0.00	1.03	1.25	MW1816n		conserved hypothetical protein	
0.88	1.13	0.95	0.98	1.01	1.29	1.11	1.07	0.89	0.89	1.14	MW1817		conserved hypothetical protein	
1.19	1.07	0.85	0.83	1.08	1.28	1.01	1.27	0.84	0.78	1.39	MW1818		conserved hypothetical protein	lipid metabolism
1.04	0.84	0.87	0.69	1.16	1.21	1.06	1.62	0.62	0.87	1.47	MW1819	ampS	aminopeptidase ampS	protein modification
1.06	0.98	0.79	0.77	0.76	1.15	0.99	1.75	0.67	0.84	1.23	MW1820		conserved hypothetical protein	
1.26	0.92	0.73	0.68	1.02	1.24	1.06	1.36	0.74	0.99	1.36	MW1820n		conserved hypothetical protein	
1.49	1.29	0.81	0.96	0.97	2.04	2.14	1.45	0.73	0.87	0.87	MW1821		hypothetical protein, similar to protein-tyrosine phosphatase	protein modification
1.25	1.06	0.81	1.05	0.92	1.04	1.52	1.04	0.84	0.99	0.91	MW1822		hypothetical protein	
0.96	1.01	0.79	0.87	0.82	0.75	1.18	0.90	1.11	0.90	0.80	MW1823		hypothetical protein, similar to transporter	transport/binding
1.00	0.80	0.77	0.92	0.80	0.71	0.81	0.70	1.02	1.03	1.39	MW1824	vraR	two-component response regulator	RNA synthesis
1.00	1.19	1.00	1.15	0.99	1.17	0.93	1.10	1.02	0.95	1.22	MW1825	vraS	two-component sensor histidine kinase	sensor
1.17	0.91	0.86	0.71	0.84	0.93	1.03	0.91	1.05	0.95	1.20	MW1826		conserved hypothetical protein	
1.10	1.09	1.04	1.08	1.03	1.22	1.05	1.15	1.04	0.90	1.06	MW1827		hypothetical protein	
1.14	1.37	1.03	0.94	1.19	1.13	0.93	1.45	1.10	0.91	1.02	MW1828	map	methionyl aminopeptidase map	protein modification
1.04	1.69	1.14	0.77	1.06	1.07	1.10	1.53	1.17	1.08	1.22	MW1829		conserved hypothetical protein	
1.05	0.99	1.24	1.08	0.94	1.11	1.16	1.01	1.09	1.16	1.15	MW1830		hypothetical protein	
0.87	1.33	1.13	1.05	1.14	1.10	0.89	0.99	1.13	1.11	0.97	MW1831		hypothetical protein	
0.94	1.13	1.14	1.34	1.02	1.06	1.02	0.95	1.27	1.05	0.80	MW1832		hypothetical protein, similar to cobyric acid synthase CobQ	
1.12	1.56	1.10	1.12	1.23	1.41	0.88	1.45	1.00	0.86	0.68	MW1833		hypothetical protein, similar to UDP-N-acetylmuramyl tripeptide synthetase hom	cell wall
1.12	1.03	0.94	1.07	0.96	1.13	1.02	1.02	1.13	1.05	0.45	MW1834		hypothetical protein, similar to ferritin	miscellaneous
1.25	1.32	1.03	0.74	1.23	1.30	1.11	1.78	0.76	0.89	1.00	MW1835		hypothetical protein, similar to DNA polymerase III, alpha chain PolC type	DNA replication
1.14	1.08	1.10	1.37	1.09	1.25	1.10	1.04	1.44	1.03	0.98	MW1836		hypothetical protein, similar to DNA-damage inducible protein P	DNA repair or modify
1.06	1.29	1.04	1.09	1.10	1.03	1.06	1.07	1.09	1.05	0.90	MW1838		RNA methyltransferase homolog	RNA modification
0.92	1.24	1.01	1.32	1.05	1.00	0.83	0.98	1.20	0.86	0.89	MW1839		conserved hypothetical protein	
0.99	1.07	1.05	1.41	0.97	0.56	0.86	0.93	1.16	0.72	1.09	MW1840		glutamyl-tRNAGln amidotransferase subunit B	protein synthesis
0.97	1.10	1.00	1.29	1.11	1.48	1.10	1.25	1.11	1.03	1.18	MW1841a		glutamyl-tRNAGln amidotransferase subunit A	protein synthesis
1.15	1.04	0.87	0.93	0.88	1.69	1.49	1.26	1.00	1.07	1.14	MW1841b		glutamyl-tRNAGln amidotransferase subunit A	protein synthesis
1.24	0.95	0.98	1.00	1.03	0.76	0.85	0.92	0.95	0.81	0.91	MW1842		glutamyl-tRNAGln amidotransferase subunit C	protein synthesis
0.83	0.72	0.77	0.80	0.72	0.55	0.85	0.83	0.66	1.10	0.94	MW1843	putP	high affinity proline permease	transport/binding
1.15	0.99	1.12	1.15	1.02	0.88	0.99	0.89	0.89	1.02	1.10	MW1844		conserved hypothetical protein	
1.39	1.27	1.10	0.78	1.19	1.32	1.22	1.69	1.03	0.93	1.19	MW1845	lig	DNA ligase	DNA replication
1.16	1.19	1:11	0.87	1.16	1.21	1.09	1.39	1.11	0.90	1.12	MW1846	pcrA	ATP-dependend DNA helicase	DNA replication
1.33	1.27	1.03	1.11	1.16	1.31	0.99	1.54	0.90	0.89	1.14	MW1847	pcrB	conserved hypothetical protein	
1.22	0.82	0.98	0.77	1.17	0.82	0.78	1.61	0.66	0.94	0.87	MW1848		conserved hypothetical protein	
1.05	1.13	0.88	1.14	1.16	1.12	0.86	1.18	0.79	0.89	0.99	MW1849	purB	adenylosuccinate lyase	carbohydrate metabolism
1.02	0.84	0.48	0.66	0.93	0.70	0.93	0.81	0.96	0.70	1.49	MW1850		Staphopain, Cysteine Proteinase	protein modification
1.23	1.29	0.89	0.80	1.05	1.00	0.91	1.60	0.79	0.89	1.30	MW1851		hypothetical protein	
1.00	0.68	0.73	0.60	0.98	0.63	0.74	1.10	0.64	0.84	1.33	MW1852		conserved hypothetical protein	
1.10	1.18	0.87	1.03	1.02	1.00	0.93	0.98	0.92	0.86	0.86	MW1853	nadE	NAD synthetase, prefers NH3 over glutamine	miscellaneous
1.27	0.90	0.94	0.88	1.26	1.16	1.06	1.73	0.74	0.79	0.99	MW1854		nicotinate phosphoribosyltransferase homolog	coenzyme metabolism
0.94	1.30	0.97	1.15	1.00	1.11	1.02	1.15	0.89	0.84	0.65	MW1855		nitric-oxide synthase homolog	detoxification

0.99	0.81	0.95	0.83	1.01	0.68	1.18	1.28	0.81	0.88	0.84	MW1856		hypothetical protein, similar to chorismate mutase/prephenate dehydratase (ph	aminoacid metabolism
0.97	1.39	0.98	0.95	1.05	1.41	1.29	1.06	0.90	1.26	0.97	MW1857		hypothetical protein, similar to sodium-dependent transporter	transport/binding
0.79	1.00	1.12	0.80	0.89	1.11	1.28	1.21	0.81	1.04	1.04	MW1858		conserved hypothetical protein	
0.77	0.72	0.68	0.99	0.92	0.66	0.75	0.71	0.53	0.81	1.38	MW1859		pyrazinamidase/nicotinamidase homolog	coenzyme metabolism
0.90	0.50	0.65	0.71	0.99	0.42	0.87	0.79	0.54	1.00	1.39	MW1860		manganese-dependent inorganic pyrophosphatase	phosphate metabolism
0.95	1.19	0.89	1.15	0.91	1.12	0.97	0.79	1.03	0.99	1.38	MW1861	aldH	aldehyde dehydrogenase	carbohydrate metabolism
1.03	1.03	0.95	1.23	1.08	1.06	0.96	0.92	0.90	0.95	0.81	MW1862		conserved hypothetical protein	
1.22	1.10	0.99	1.09	1.02	1.07	1.01	0.95	0.64	1.01	1.24	MW1863		hypothetical protein	
1.30	1.18	0.85	0.84	1.09	0.91	1.06	0.86	0.86	1.04	1.18	MW1864	ncated-	truncated transposase	transposon and IS
0.81	1.27	1.35	0.96	1.17	1.36	0.95	1.72	0.91	1.08	0.98	MW1864n	ncated-	truncated transposase	transposon and IS
1.77	0.76	0.90	0.60	0.80	1.00	1.73	1.58	0.80	1.17	0.82	MW1865		hypothetical protein	
1.77	0.92	0.86	0.97	0.89	1.62	1.84	1.26	1.09	1.12	0.81	MW1865n		hypothetical protein	
1.02	0.92	0.95	1.09	1.11	1.00	1.09	0.89	0.94	1.02	1.21	MW1866		hypothetical protein	
1.06	1.06	0.99	1.14	1.02	0.89	0.91	0.93	0.83	1.07	1.30	MW1867		hypothetical protein	
0.93	0.90	0.94	1.14	1.06	0.78	1.00	0.92	0.97	0.96	1.49	MW1868		conserved hypothetical protein	
0.94	0.97	0.89	1.40	0.91	0.89	0.67	0.63	1.01	0.87	0.87	MW1869		hypothetical protein	
1.32	1.16	0.93	1.91	1.23	0.91	0.88	0.67	1.62	0.95	1.13	MW1871		conserved hypothetical protein	
1.05	1.16	1.11	1.25	1.12	0.89	0.94	0.73	1.44	0.95	1.07	MW1872		hypothetical protein, similar to ABC transporter, ATP-binding protein	transport/binding
1.43	1.44	0.90	0.84	1.24	1.08	1.07	1.09	1.18	0.82	1.16	MW1873		hypothetical protein	
1.34	0.95	0.91	1.02	1.23	0.91	0.98	0.72	1.75	0.88	1.15	MW1874		hypothetical protein, similar to ABC transporter, ATP-binding protein	transport/binding
1.37	1.14	0.98	1.14	1.22	0.99	0.94	0.83	1.61	0.93	1.15	MW1875		hypothetical protein, similar to transcription regulator, GntR family	RNA synthesis
1.13	1.14	1.07	0.87	1.14	1.15	1.02	1.16	1.08	0.94	1.09	MW1876		hypothetical protein	
1.06	1.02	1.07	1.14	1.00	0.74	1.12	0.79	1.05	1.03	1.17	MW1876n		hypothetical protein	
1.16	0.91	1.11	1.02	1.08	0.87	1.04	0.95	1.14	1.12	1.16	MW1877		hypothetical protein	
1.18	0.87	0.82	0.64	1.15	0.67	0.93	1.01	0.61	0.98	1.58	MW1878		hypothetical protein, similar to aspartate transaminase protein	aminoacid metabolism
1.33	0.56	0.55	0.76	0.78	0.48	0.59	0.42	0.99	0.74	2.51	MW1880a	cated#m	truncated map-w protein	pathogenic factor
1.30	0.46	0.47	0.56	0.78	0.43	0.65	0.59	0.98	0.79	3.01	MW1880b	ıcated#m	truncated map-w protein	pathogenic factor
1.50	0.97	0.71	0.74	1.03	0.72	0.79	0.58	0.94	0.86	1.16	MW1881	ncated#	truncated beta-hemolysin	pathogenic factor
1.24	0.68	0.72	0.59	0.99	0.70	0.73	0.85	1.00	0.79	2.77	MW1882		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
1.16	0.85	0.71	0.68	0.89	0.54	0.73	0.63	0.93	0.91	2.75	MW1882n		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
1.33	1.04	0.85	1.01	1.01	0.85	1.06	1.14	0.93	1.12	2.11	MW1883		hypothetical protein	
1.74	0.65	0.53	0.33	0.64	0.07	0.55	0.13	1.52	1.17	5.75	MW1884		hypothetical protein	
1.09	0.84	0.82	1.07	0.88	0.57	0.97	0.84	1.09	0.79	0.78	MW1885	sak	STAPHYLOKINASE PRECURSOR	pathogenic factor
0.93	0.74	0.95	0.86	0.94	0.70	1.31	1.10	1.15	0.96	0.82	MW1886		lytic enzyme	phage-related
0.89	0.76	0.83	0.61	0.79	0.82	1.11	0.99	0.86	0.82	0.87	MW1887		holin homolog	phage-related
1.50	0.20	0.64	0.50	0.88	0.22	1.00	0.41	1.12	0.93	0.51	MW1888		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
1.66	0.59	0.86	0.86	1.15	0.52	1.09	0.72	1.07	0.89	0.67	MW1888n		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
1.20	1.21	1.09	0.92	1.52	1.03	0.97	1.32	1.22	0.79	0.64	MW1889	sea	SEA	pathogenic factor
0.93	0.37	0.96	0.38	0.86	0.72	0.97	1.24	0.66	0.97	0.90	MW1890		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.75	1.12	1.15	0.93	1.09	1.19	0.91	1.64	0.89	1.11	0.87	MW1891		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
1.01	1.10	1.15	0.91	0.99	1.02	1.21	2.48	0.89	1.12	0.96	MW1892		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.98	1.29	1.16	0.96	1.11	1.01	1.18	1.79	0.76	1.10	0.83	MW1892n		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.77	1.29	1.34	1.09	1.28	1.44	1.04	1.95	0.95	1.09	0.95	MW1893		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.59	1.23	1.44	1.49	1.00	1.09	1.02	0.98	1.08	1.22	1.01	MW1894		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.79	1.22	1.26	1.07	1.30	1.44	1.03	1.63	0.83	1.10	1.02	MW1894n		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.80	0.94	1.27	1.27	1.10	1.43	1.11	1.52	0.87	1.17	0.99	MW1895		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.52	1.40	1.44	1.30	1.05	1.26	0.95	1.22	0.97	1.17	1.02	MW1897		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.75	0.89	1.09	0.99	0.90	1.03	1.07	1.08	0.92	1.07	0.89	MW1898		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.65	1.42	1.45	1.23	1.10	1.27	0.95	1.28	0.94	1.20	1.01	MW1899		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.64	1.52	1.37	1.15	1.08	1.18	0.94	1.29	0.81	1.24	1.08	MW1900		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.69	1.05	1.27	1.26	1.03	1.13	0.95	1.11	0.95	1.26	1.33	MW1901		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.55	1.32	1.31	1.30	1.09	1.31	1.08	1.19	1.03	1.15	1.17	MW1902		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.80	1.24	1.33	1.05	1.08	1.15	0.97	1.41	0.81	1.14	1.33	MW1903		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.64	1.35	1.38	1.32	1.11	1.37	1.12	1.38	0.97	1.27	1.12	MW1904		capsid protein	phage-related
0.68	1.14	1.35	1.72	1.17	1.41	0.86	0.90	1.07	1.22	1.01	MW1906		portal protein	phage-related
0.76	1.11	1.29	1.25	1.09	1.21	0.94	1.18	1.04	1.14	1.11	MW1907		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.70	1.27	1.52	1.19	1.16	1.58	1.07	1.31	1.06	1.34	1.03	MW1908		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.76	1.26	1.36	1.21	1.15	1.47	1.06	1.25	1.06	1.29	0.90	MW1909		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.80	0.98	1.07	1.35	1.13	1.33	1.09	0.82	0.94	1.26	1.12	MW1910		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.74	1.12	1.26	1.28	1.12	1.77	0.92	1.19	1.16	1.15	1.10	MW1911		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.80	1.24	1.30	1.26	1.11	1.21	0.88	1.17	1.17	1.24	1.01	MW1912		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.63	1.30	1.26	1.10	1.08	1.39	0.98	1.51	0.97	1.22	0.95	MW1914		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.89	1.44	1.18	1.21	0.83	1.26	1.53	1.06	0.94	1.42	1.29	MW1915		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.89	0.79	1.19	1.06	1.04	1.06	1.14	1.09	1.09	1.15	0.88	MW1916		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
1.01	0.72	1.13	0.81	1.14	1.05	1.15	1.17	1.05	1.13	0.87	MW1917		hypothetical protein(phiN315)	phage-related
0.81	1.09	1.23	1.05	1.17	1.38	0.87	1.53	1.08	1.15	0.79	MW1918		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.77	1.11	1.19	0.82	1.09	1.26	1.09	1.54	0.97	1.17	0.95	MW1919		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.76	1.22	1.34	0.99	1.19	1.35	1.11	1.55	0.70	1.27	0.81	MW1920		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.89	0.98	1.27	1.28	1.04	1.20	1.04	1.21	1.26	1.26	0.97	MW1921	ssb	single-strand DNA-binding protein	phage-related
1.00	0.96	1.25	0.86	1.25	1.16	0.88	1.87	0.71	1.23	0.85	MW1921n	ssb	single-strand DNA-binding protein	phage-related
0.69	0.96	1.16	1.03	1.16	1.08	1.03	0.90	0.94	1.27	0.80	MW1922		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.90	0.96	1.06	1.06	1.11	1.15	1.06	0.89	1.13	1.03	0.85	MW1923		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.84	1.29	1.12	0.82	1.08	1.35	0.95	1.45	0.85	1.19	0.82	MW1924		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.94	1.15	1.08	0.94	1.03	1.07	0.92	1.02	0.87	1.16	1.06	MW1925		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.95	0.90	1.10	1.01	0.93	1.02	0.87	1.09	1.03	1.17	1.24	MW1926		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
1.10	0.81	1.00	1.29	1.01	1.01	0.81	0.80	1.37	1.02	0.93	MW1926n		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.92	1.06	1.07	0.99	0.92	0.73	1.02	0.95	0.78	1.19	1.26	MW1927		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
1.02	1.08	1.10	0.90	1.02	0.94	0.84	1.10	0.69	1.10	1.14	MW1927n		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
1.12	0.76	0.87	0.94	0.99	0.69	0.92	0.76	0.98	1.06	1.54	MW1930		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.98	0.73	0.98	1.02	0.95	0.90	0.88	0.68	0.94	1.15	1.04	MW1932		anti repressor	phage-related
0.94	0.90	0.87	1.13	0.85	0.74	0.81	0.92	0.95	1.02	1.02	MW1935		hypothetical protein (Bacteriophage phi Sa 3mw)	phage-related
0.98	0.90	1.11	1.27	1.01	0.91	0.93	0.74	1.12	1.01	0.91	MW1936		phage repressor (Bacteriophage phi Sa 3mw)	RNA synthesis
1.01	0.86	1.00	1.16	1.13	1.04	0.92	0.76	1.10	0.96	0.91	MW1936n		repressor homolog (Bacteriophage phi Sa 3mw)	RNA synthesis
1.45	0.63	0.62	0.56	0.81	0.46	0.88	0.81	0.70	0.82	0.88	MW1937	seg2	staphylococcal enterotoxin SeG	pathogenic factor
1.11	0.67	0.61	0.70	0.80	0.49	0.85	0.54	0.92	0.80	1.03	MW1938	sek2	staphylococcal enterotoxin Sek	pathogenic factor
1.02	1.02	0.81	1.30	1.03	0.70	0.71	0.48	1.06	0.96	1.05	MW1938a	sek	SEK	pathogenic factor
0.92	1.03	1.11	1.08	1.10	1.09	0.90	0.97	1.19	1.07	1.26	MW1939	int	integrase (Bacteriophage phi Sa 3mw)	phage-related
0.95	1.23	1.20	1.17	1.11	0.95	0.91	1.03	1.03	1.07	1.04	MW1940	uncated#l	truncated beta-hemolysin	pathogenic factor
1.13	0.77	0.71	0.98	0.88	0.71	0.67	0.64	1.20	0.89	2.40	MW1941	luk	al protein, similar to synergohymenotropic toxin precursor - Staphylococcus i	pathogenic factor
1.20	0.94	0.82	1.01	0.86	0.82	0.73	0.81	1.08	0.91	2.38	MW1942	lukM	hypothetical protein, similar to leukocidin chain lukM precursor	pathogenic factor
1.15	1.07	1.04	1.16	0.94	1.90	1.50	1.19	1.08	1.03	1.11	MW1943		hypothetical protein, similar to succinyl-diaminopimelate desuccinylase	aminoacid metabolism
0.93	1.24	0.87	1.08	0.83	1.18	1.04	1.14	1.16	0.87	1.15	MW1947		hypothetical protein, similar to acetyltransferase (Genomic island nu Sa 4mw)	
1.03	1.03	0.84	0.80	0.73	1.05	1.33	1.26	1.01	0.92	1.02	MW1948		hypothetical perotein (Genomic island nu Sa 4mw)	
0.97	0.85	0.86	0.62	0.83	1.04	0.97	0.96	0.83	0.94	0.85	MW1949		hypothetical protein, similar to bacteriophage terminase small subur	phage-related
1.03	1.11	1.06	1.36	1.11	1.37	1.02	0.93	1.12	1.03	0.76	MW1949n		hypothetical protein, similar to bacteriophage terminase small subunit	phage-related
0.93	1.26	0.85	0.98	0.75	1.05	1.16	1.22	1.00	0.95	1.09	MW1950		truncated hypothetical protein (Genomic island nu Sa 4mw)	
0.93	1.14	1.20	1.35	1.06	1.52	1.09	1.05	1.02	0.99	1.01	MW1950n		hypothetical protein	

0.94	1.11	0.88	0.99	0.95	1.16	1.14	1.23	1.08	0.88	0.94	MW1951	truncate	ed hypothetical protein, similar to integrase (Genomic island nu S	phage-related
0.99	1.02	0.90	0.85	0.82	0.78	1.23	1.11	0.99	0.90	0.81	MW1952	truncate	ed hypothetical protein, similar to integrase (Genomic island nu S	phage-related
0.92	0.79	0.91	0.84	1.10	1.35	1.15	1.82	1.02	0.87	0.54	MW1953	groEL	GroEL protein	protein folding
0.92	0.72	0.85	1.05	0.92	1.26	0.86	0.96	0.90	0.84	0.49	MW1954	groES	GroES protein	protein folding
1.16	0.86	0.95	0.85	1.30	0.85	1.29	1.53	0.82	0.93	1.15	MW1955		conserved hypothetical protein	
1.30	0.97	0.79	0.74	1.26	0.97	1.23	0.84	0.86	0.84	0.86	MW1956		hypothetical protein, similar to SdrH	
1.41	1.40	1.09	1.30	1.08	1.11	0.90	1.04	1.20	1.06	1.09	MW1957		conserved hypothetical protein	
1.55	1.41	1.16	0.81	1.01	1.34	0.89	1.32	1.22	1.00	0.75	MW1958		hypothetical protein	
22.49	11.59	4.62	0.20	0.48	1.93	0.39	0.55	36.90	1.86	0.40	MW1959	hld	delta-hemolysin	pathogenic factor
19.72	13.15	4.63	0.42	0.44	2.15	0.38	0.85	21.68	1.70	0.29	MW1959n	hld	delta-hemolysin	pathogenic factor
5.75	5.08	4.34	0.30	0.54	2.41	0.79	1.79	6.56	1.57	0.59	MW1960	agrB	accessory gene regulator B	protein modification
3.89	3.49	4.12	0.73	0.63	2.01	0.66	0.91	7.67	1.12	0.41	MW1960n	agrB	accessory gene regulator B	protein modification
5.64	3.76	4.94	0.42	0.76	3.94	0.67	1.71	6.58	1.42	0.51	MW1961	agrD	AgrD	RNA synthesis
7.03	5.12	5.06	0.49	0.71	3.38	0.80	2.62	7.29	1.67	0.59	MW1962	agrC	AgrC	sensor
4.52	7.28	4.41	0.70	0.75	3.10	0.60	1.14	7.73	1.42	0.74	MW1962n	agrC	accessory gene regulator C	sensor
3.86	5.51	4.23	0.80	0.85	3.05	0.78	1.31	7.55	1.49	0.95	MW1963	agrA	accessory gene regulator A	RNA synthesis
1.13	1.55	1.38	1.03	0.92	1.54	0.95	1.22	1.47	1.26	1.24	MW1964		hypothetical protein, similar to fructokinase	carbohydrate metabolism
1.00	1.40	1.26	1.03	0.94	1.58	0.98	1.26	1.11	1.30	1.31	MW1965	scrB	sucrose-6-phosphate hydrolase	carbohydrate metabolism
0.96	1.77	1.35	1.14	1.01	1.69	0.91	1.14	1.11	1.26	0.98	MW1966	scrR	sucrose operon repressor	RNA synthesis
0.98	1.48	1.36	1.15	1.07	1.27	1.05	1.22	0.92	1.35	1.24	MW1967	nrgA	probabale ammonium transporter	transport/binding
0.84	0.98	1.09	1.21	1.12	1.10	0.86	0.80	1.04	1.17	1.66	MW1968		conserved hypothetical protein	
0.92	1.17	1.31	1.27	1.13	1.42	1.03	0.94	1.24	1.14	1.67	MW1969		conserved hypothetical protein	
0.91	0.85	0.99	0.92	1.10	0.72	0.79	0.67	0.92	0.98	1.49	MW1970		conserved hypothetical protein	
0.96	1.31	1.15	1.39	1.15	1.18	0.88	0.89	1.19	1.05	1.15	MW1971	vga	hypothetical ABC transporter ATP-binding protein	transport/binding
0.92	0.97	1.06	1.11	1.05	1.13	0.84	0.77	1.07	1.02	1.06	MW1972		hypothetical protein, similar to DNA mismatch repair protein MutS	DNA repair or modify
1.18	1.07	1.16	1.16	1.15	1.09	1.02	0.88	1.17	1.01	1.24	MW1973		hypothetical protein, similar to O-sialoglycoprotein endopeptidase	protein modification
1.22	1.27	1.02	1.04	1.08	0.97	1.07	0.87	1.05	1.01	1.35	MW1974		hypothetical protein, similar to ribosomal-protein-alanine N-acetyltransfer	protein modification
1.10	1.15	1.05	1.07	1.09	1.01	0.86	0.88	1.19	0.99	1.27	MW1975		hypothetical protein, similar to glycoprotein endopeptidase	protein modification
1.16	0.99	0.85	0.92	0.91	0.73	0.73	0.76	0.85	0.87	1.26	MW1976		conserved hypothetical protein	
0.98	1.30	1.05	1.35	0.99	0.95	0.73	0.75	1.01	1.10	0.88	MW1977	ilvD	dihydroxy-acid dehydratase	aminoacid metabolism
1.00	1.09	0.74	0.91	0.75	0.73	0.73	0.64	0.73	0.97	0.93	MW1978	ilvB	acetolactate synthase large subunit	aminoacid metabolism
1.27	1.16	0.73	0.65	0.70	0.65	0.78	0.74	0.82	0.96	1.10	MW1979		hypothetical protein, similar to acetolactate synthase small subunit	aminoacid metabolism
1.05	0.99	0.78	0.82	0.71	0.68	0.61	0.58	0.79	0.97	0.83	MW1980	ilvC	alpha-keto-beta-hydroxylacil reductoisomerase	aminoacid metabolism
1.09	1.19	0.93	0.91	0.76	0.89	0.71	0.72	0.95	1.00	0.97	MW1981	leuA	2-isopropylmalate synthase	aminoacid metabolism
1.16	1.14	1.00	0.83	0.77	0.81	0.83	0.72	0.97	1.07	1.14	MW1982	leuB	3-isopropylmalate dehydrogenase	aminoacid metabolism
1.05	1.10	1.12	0.93	0.85	0.78	1.08	0.79	1.19	1.15	1.07	MW1983	leuC	3-isopropylmalate dehydratase large subunit	aminoacid metabolism
1.29	1.03	1.05	1.25	0.92	0.90	1.03	0.72	1.36	1.07	1.20	MW1984	leuD	3-isopropylmalate dehydratase small subunit	aminoacid metabolism
1.37	1.57	1.27	1.26	1.15	1.12	1.21	0.93	1.27	1.11	1.18	MW1985	ilvA	thereonine dehydratase	aminoacid metabolism
1.20	1.10	0.83	0.80	1.09	0.75	1.04	0.63	1.20	0.87	1.16	MW1986		conserved hypothetical protein	
1.12	0.75	0.90	0.59	0.91	0.61	1.35	0.80	0.94	1.07	1.11	MW1987		conserved hypothetical protein	
1.38	0.76	0.70	0.81	1.47	0.88	1.32	0.72	0.91	1.03	1.15	MW1988	sigB	sigma factor B	RNA synthesis
1.22	0.81	0.74	0.95	1.22	0.68	1.21	0.68	1.05	0.91	1.02	MW1989	rsbW	anti-sigmaB factor	RNA synthesis
1.43	0.57	0.72	0.81	1.17	0.58	1.29	0.69	1.04	0.85	0.96	MW1990	rsbV	anti-sigmaB factor antagonist	RNA synthesis
1.31	0.39	0.69	0.48	0.92	0.67	1.33	0.74	0.76	0.86	0.94	MW1991	rsbU	sigmaB regulation protein RsbU	RNA synthesis
1.25	0.61	0.68	0.81	0.97	0.45	0.94	0.64	0.67	0.85	0.85	MW1992		conserved hypothetical protein	
1.35	0.45	0.54	0.60	0.75	0.42	1.03	0.44	0.89	0.84	0.98	MW1993		hypothetical protein	
1.34	0.65	0.71	0.75	1.10	0.51	0.89	0.51	0.66	0.72	0.83	MW1993n		hypothetical protein	
0.87	1.05	0.98	1.12	1.12	0.97	0.85	0.71	0.95	0.89	0.96	MW1994	alr	alanine racemase	aminoacid metabolism
1.45	0.79	0.89	0.73	1.17	0.88	0.83	1.01	0.78	0.84	1.01	MW1995	dpj	holo-ACP synthase	protein modification
1.06	1.21	1.07	0.89	1.05	0.96	0.78	0.85	1.00	0.87	1.08	MW1996		conserved hypothetical protein	
0.98	1.11	1.07	0.80	1.21	1.15	0.86	0.99	0.90	0.85	1.06	MW1997		conserved hypothetical protein	
0.73	1.15	1.19	1.34	1.20	1.00	0.83	0.83	1.06	1.05	1.05	MW1998		hypothetical protein	
1.01	1.10	1.13	0.78	1.35	1.00	0.98	1.27	0.77	0.93	1.05	MW1999	kdpC	probable potassium-transporting ATPase C chain	transport/binding
1.07	1.23	1.07	0.71	1.37	1.36	1.11	1.85	0.68	0.97	1.02	MW2000	kdpB	probable potassium-transporting ATPase B chain	transport/binding
0.82	1.24	1.02	0.90	1.08	1.17	0.91	0.93	0.93	1.01	0.90	MW2000n	kdpB	probable potassium-transporting ATPase B chain	transport/binding
0.71	0.64	0.71	0.51	0.91	0.77	1.08	0.96	0.83	0.76	0.81	MW2001	kdpA	probable potassium-transporting ATPase A chain	transport/binding
0.70	1.05	0.75	0.73	0.70	0.95	1.10	0.96	0.81	1.02	1.05	MW2002	kdpD	sensor protein KdpD	sensor
0.86	1.29	1.05	0.89	1.07	1.19	0.92	1.20	0.82	1.07	1.01	MW2002n	kdpD	sensor protein KdpD	sensor
0.96	1.49	0.94	0.88	0.96	1.04	1.07	1.26	0.94	1.08	1.20	MW2003	kdpE	KDP operon transcriptional regulatory protein KdpE	RNA synthesis
0.93	1.22	1.11	0.85	1.05	1.10	0.80	1.17	0.81	1.14	0.92	MW2003n	kdpE	KDP operon transcriptional regulatory protein KdpE	RNA synthesis
0.82	1.95	0.97	1.13	1.06	0.87	0.68	0.83	0.96	1.32	0.75	MW2004		hypothetical protein, similar to ATP-dependent RNA helicase	RNA modification
0.80	1.00	0.90	0.90	1.14	0.91	0.79	1.01	0.83	0.97	1.17	MW2005	murF	N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl	cell wall
0.89	1.06	0.87	0.95	0.99	0.90	0.75	0.94	0.73	0.93	1.18	MW2006	ddlA	D-alanine-D-alanine ligase	cell wall
1.03	1.00	1.02	0.99	0.99	0.85	1.04	1.14	0.84	1.22	1.49	MW2007		hypothetical protein, similar to rod shape determining protein RodA	cell division
1.92	1.03	1.00	1.41	1.25	4.62	1.55	1.39	1.15	0.98	0.50	MW2008		hypothetical protein	
1.36	0.82	0.97	1.08	0.76	3.40	1.42	1.07	1.11	1.10	0.72	MW2008n		hypothetical protein	
0.92	0.93	1.05	0.99	1.09	1.18	0.94	1.05	0.95	1.03	1.02	MW2009		hypothetical protein	
1.00	1.05	0.99	1.03	1.03	1.18	0.92	1.00	0.52	1.00	0.96	MW2010		conserved hypothetical protein	
1.01	0.98	0.93	1.09	1.05	0.91	0.90	0.87	1.05	1.00	1.19	MW2011		hypothetical protein, similar to cardiolipin synthetase	lipid metabolism
0.91	1.08	1.18	1.11	1.07	0.97	0.91	0.84	0.93	1.05	1.25	MW2012		conserved hypothetical protein	
0.93	1.69	1.17	1.21	1.22	0.68	0.93	0.82	1.33	1.01	0.80	MW2013		lipoprotein precursor	transport/binding
1.03	0.98	0.71	1.00	1.20	0.86	0.78	1.48	1.11	0.68	1.04	MW2014	thiE	Chain B, thiamin phosphate synthase	coenzyme metabolism
0.78	1.10	1.77	1.11	1.18	0.97	0.99	1.11	0.88	1.20	0.86	MW2015	thiM	hydroxyethyl thiazole kinase	coenzyme metabolism
0.73	1.02	1.04	1.43	1.13	1.14	0.90	0.82	1.09	1.08	0.78	MW2016	thiD	phosphomethylpyrimidine kinase	coenzyme metabolism
0.67	1.23	1.11	1.23	1.05	1.20	1.05	1.03	1.09	1.09	0.87	MW2017		hypothetical protein, similar to trasncriptional activator TenA	RNA synthesis
0.97	0.97	0.91	1.10	0.89	0.90	1.04	1.23	1.06	1.01	1.16	MW2018		hypothetical protein	
0.98	1.08	1.32	1.04	0.95	1.12	0.95	1.04	1.06	1.06	1.03	MW2019		hypothetical protein	
0.91	1.15	1.17	1.29	1.00	1.20	1.06	1.04	1.21	1.13	0.97	MW2020		hypothetical protein, similar to SceD precursor	pathogenic factor
1.10	1.08	1.04	1.13	1.13	1.06	1.05	0.90	1.07	1.08	1.10	MW2021		hypothetical protein, similar to single strand DNA binding protein	DNA replication
0.91	0.93	0.89	1.29	0.93	0.94	1.04	0.81	0.96	1.00	0.84	MW2022		conserved hypothetical protein	
0.95	0.96	0.81	0.96	0.92	0.95	1.04	0.93	0.99	0.93	1.25	MW2023	fabZ	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	lipid metabolism
1.01	1.47	0.92	0.95	1.01	1.57	1.23	1.49	0.78	0.72	1.05	MW2024	murA	UDP-N-acetylglucosamine 1-carboxyvinyl transferase 1	cell wall
0.88	0.99	0.91	1.02	0.80	0.88	1.45	0.95	0.81	0.95	1.24	MW2024n	murA	UDP-N-acetylglucosamine 1-carboxyvinyl transferase 1	cell wall
0.97	1.00	0.98	1.12	0.84	1.30	1.28	1.06	0.94	1.01	1.02	MW2025		conserved hypothetical protein	
0.80	0.97	1.11	1.02	1.14	0.66	1.08	0.96	1.24	0.95	0.81	MW2026	atpC	FoF1-ATP synthase epsilon subunit	membrane bioenergetics
0.89	1.26	1.33	1.26	1.17	0.77	1.12	1.27	1.40	0.82	0.95	MW2027	atpD	ATP synthase beta chain	membrane bioenergetics
0.78	1.16	1.45	1.26	1.18	1.05	1.14	1.25	1.60	0.76	0.75	MW2028	atpG	ATP synthase gamma chain	membrane bioenergetics
0.93	1.30	1.45	1.45	1.33	1.13	1.12	1.54	1.39	0.83	0.77	MW2029	atpA	ATP synthase alpha chain	membrane bioenergetics
1.25	1.19	1.34	1.04	1.30	1.00	1.23	1.30	1.45	0.73	0.79	MW2030	atpH	ATP synthase delta chain	membrane bioenergetics
1.06	1.35	1.71	1.37	1.33	1.18	1.25	1.45	1.72	0.78	0.84	MW2031	atpF	ATP synthase B chain	membrane bioenergetics
1.09	1.07	1.67	1.55	1.14	1.32	1.35	1.05	1.68	0.76	0.83	MW2032	atpE	ATP synthase C chain	membrane bioenergetics
1.06	0.88	1.81	0.99	0.94	1.69	1.45	1.49	1.30	0.84	0.87	MW2033	atpB	ATP synthase A chain	membrane bioenergetics
1.02	1.00	1.28	0.71	0.90	1.31	1.51	1.25	1.05	0.69	0.71	MW2034		hypothetical protein	
0.92	0.88	0.61	1.02	0.67	1.36	1.11	1.12	0.92	0.74	1.22	MW2035	mnaA	UDP-GlcNAc 2-epimerase	carbohydrate metabolism
0.85	1.04	1.09	1.07	0.95	1.56	1.00	0.96	1.07	0.94	1.37	MW2036	upp	uracil phosphoribosyl transferase	nucleic acid metabolism
0.97	0.51	0.89	0.73	0.66	1.68	1.29	1.15	0.86	0.84	1.32	MW2037	glyA	serine hydroxymethyl transferase	aminoacid metabolism
0.85	0.88	0.67	0.75	0.71	1.68	0.86	0.90	0.83	0.78	1.16	MW2038		conserved hypothetical protein	

0.97	0.76	0.64	0.77	0.67	0.91	1.09	0.79	0.88	0.74	1.06	MW2039		hypothetical protein, similar to phosphatase	protein modification
0.95	0.90	0.80	0.85	0.76	0.94	0.99	0.95	0.99	0.74	0.86	MW2040		conserved hypothetical protein	
1.07	0.54	0.86	0.59	0.71	0.59	1.26	1.10	1.01	0.82	0.67	MW2041		hypothetical protein, similar to protoporphyrinogen oxidase (hemK)	coenzyme metabolism
1.29	0.94	1.09	0.67	1.07	0.94	0.86	1.17	1.10	0.86	0.68	MW2042	prfA	peptide chain release factor 1	protein synthesis
1.23	1.14	1.07	0.89	1.17	1.21	0.96	1.22	1.09	0.82	0.69	MW2043	tdk	thymidine kinase	nucleic acid metabolism
1.68	0.84	0.88	0.73	1.11	0.69	1.01	0.99	0.78	0.81	1.00	MW2044	rpmE	ribosomal protein L31	protein synthesis
1.00	1.41	0.98	0.67	1.26	1.26	0.93	1.65	0.84	0.87	1.16	MW2045	rho	transcription termination factor Rho	RNA synthesis
0.93	1.54	0.91	1.46	0.82	2.42	1.91	1.29	1.11	1.03	0.76	MW2046		hypothetical protein, similar to aldehyde dehydrogenase	carbohydrate metabolism
1.37	0.87	1.10	0.87	0.98	1.35	1.24	1.29	1.02	1.26	0.79	MW2047		conserved hypothetical protein	
1.04	1.21	0.94	0.88	1.16	1.24	0.84	1.52	0.66	0.83	0.68	MW2048	murZ	UDP-N-acetylglucosamine 1-carboxylvinyl transferase 2	cell wall
1.07	1.10	0.91	1.00	1.12	1.09	0.91	1.24	0.73	0.79	0.75	MW2048n	murZ	UDP-N-acetylglucosamine 1-carboxylvinyl transferase 2	cell wall
1.05	0.86	0.51	1.21	1.30	0.94	0.80	2.61	1.04	0.79	1.42	MW2049	fbaA	fructose-bisphosphate aldolase	carbohydrate metabolism
0.96	1.09	0.83	0.89	0.94	0.96	0.68	0.91	0.91	0.90	0.92	MW2050		hypothetical protein	
0.68	0.99	0.84	0.98	0.93	0.89	0.63	1.19	0.75	0.84	0.50	MW2051	ctrA	CTP synthase	nucleic acid metabolism
1.00	0.75	0.76	0.69	0.91	0.55	0.65	0.87	0.66	0.86	0.96	MW2052	rpoE	probable DNA-directed RNA polymerase delta subunit	RNA synthesis
0.76	0.98	0.85	0.88	0.95	0.85	0.85	1.19	0.76	0.94	0.70	MW2053		hypothetical protein, similar to spermine/spermidine acetyltransferase blt	aminoacid metabolism
0.89	1.16	1.11	1.12	0.99	0.75	0.92	0.91	1.18	1.06	0.80	MW2054		hypothetical protein, similar to hypothetical protein T13D8.31 - Arabidopsis thaliana	
1.00	0.89	0.69	0.86	1.16	0.61	0.82	0.81	0.91	0.91	1.21	MW2055		hypothetical protein	
0.81	0.76	0.77	0.70	0.86	0.76	0.77	0.90	0.61	0.94	1.45	MW2056		hypothetical protein	
0.77	0.97	0.85	0.91	0.92	0.94	0.73	1.15	0.62	1.01	1.25	MW2057	hmrA	similar to amidase (HmrA)	cell wall
1.10	0.79	0.96	1.02	0.85	0.92	0.89	0.87	0.92	0.96	1.48	MW2058	luxS	autoinducer-2 production protein LuxS	RNA synthesis
0.97	1.09	1.22	1.98	1.00	2.62	1.20	1.52	0.99	1.02	0.76	MW2059		conserved hypothetical protein	
0.88	1.48	1.33	2.28	1.07	3.37	1.09	1.53	1.02	1.06	0.65	MW2060	pdp	pyrimidine nucleoside phosphorylase	nucleic acid metabolism
0.76	1.11	1.29	1.45	0.96	2.14	1.14	1.57	0.87	1.23	0.75	MW2061		deoxyribose-phosphate aldolase	nucleic acid metabolism
1.17	0.78	0.77	1.22	0.86	1.07	1.05	1.04	1.01	0.93	1.46	MW2062	deoD	purine nucleoside phosphorylase	nucleic acid metabolism
0.89	0.96	0.82	1.09	0.91	1.06	0.83	0.97	0.83	0.90	1.57	MW2062n	deoD	purine nucleoside phosphorylase	nucleic acid metabolism
0.70	0.73	0.66	1.52	0.73	0.84	0.77	0.79	0.75	0.59	0.96	MW2063	dps	general stress protein 20U	adaptation to atypical
1.03	0.97	0.97	1.06	0.98	1.32	1.03	1.11	0.52	0.87	1.74	MW2064		conserved hypothetical protein	
1.00	0.71	0.77	0.70	0.88	0.90	0.90	0.73	0.92	0.90	1.20	MW2065		hypothetical protein	
1.07	0.84	0.83	0.87	0.90	0.58	0.89	0.53	0.94	0.98	0.97	MW2066		hypothetical protein	
0.84	1.00	0.90	1.08	1.00	0.72	0.83	0.54	0.96	0.94	1.08	MW2067		hypothetical protein, similar to mannnose-6 phospate isomelase pmi	carbohydrate metabolism
1.09	1.27	1.07	1.38	1.00	3.00	1.82	1.70	1.18	1.10	0.78	MW2068		conserved hypothetical protein	
0.93	0.73	1.15	1.29	0.94	0.79	0.93	0.67	0.79	0.95	1.12	MW2069	czrA	repressor protein	RNA synthesis
0.77	0.45	1.22	1.16	0.92	0.34	0.73	0.36	0.68	1.13	1.15	MW2070	czrB	cation-efflux system membrane protein homolog	transport/binding
1.18	1.21	0.76	0.79	0.79	0.54	0.93	0.62	1.26	0.92	0.77	MW2071	ncated-	lytic regulatory protein truncated with Tn554	RNA synthesis
1.14	1.46	0.86	1.00	0.90	0.53	0.81	0.64	1.26	0.99	0.79	MW2071a	ncated-	lytic regulatory protein truncated with Tn554	RNA synthesis
1.92	0.57	1.00	1.03	1.25	0.56	1.48	0.52	1.20	1.29	0.78	MW2072		hypothetical protein	
1.15	0.97	1.02	0.85	0.94	1.12	1.15	1.53	0.89	1.10	1.14	MW2073		hypothetical protein, similar to transposase for IS232	transposon and IS
1.05	0.94	0.86	1.14	0.85	0.87	1.11	0.86	0.88	1.07	1.04	MW2073n		hypothetical protein, similar to transposase for IS232	transposon and IS
1.11	0.96	1.03	1.07	1.12	1.53	1.30	1.17	0.85	1.13	0.98	MW2074		hypothetical protein, similar to transposase for IS232	transposon and IS
1.24	0.97	0.89	0.92	0.78	0.76	1.22	1.03	0.96	1.00	1.01	MW2075		hypothetical protein, similar to transposase for IS232	transposon and IS
1.20	1.01	1.05	1.09	0.95	1.07	1.19	1.00	1.09	1.17	1.20	MW2075n		hypothetical protein	
0.92	1.04	1.04	1.12	0.91	0.97	1.01	1.00	0.94	1.09	1.16	MW2076		hypothetical protein, similar to transposase for IS232	transposon and IS
1.10	0.77	0.94	0.67	1.21	0.99	0.94	0.86	0.90	0.97	1.01	MW2077		hypothetical protein	
1.05	0.93	1.02	0.83	0.76	1.17	1.36	1.22	0.97	1.18	0.99	MW2078		conserved hypothetical protein	
0.94	1.00	0.97	0.82	0.80	1.36	1.05	1.10	0.76	1.11	0.87	MW2079		hypothetical protein, similar to transposase for IS232	transport/binding
0.99	0.96	1.15	0.87	0.54	5.28	1.64	2.25	0.71	1.27	0.68	MW2080	glmS	glucosamine-fructose-6-phosphate aminotransferase	aminoacid metabolism
0.94	1.20	1.16	0.84	0.89	1.63	2.42	2.40	0.73	1.47	0.92	MW2081		hypothetical protein	
0.95	1.28	1.16	1.08	0.97	1.36	1.69	1.82	1.27	1.16	1.03	MW2081n		hypothetical protein	
0.87	1.05	0.95	0.94	0.68	1.54	5.92	1.64	1.00	3.10	0.93	MW2082	mtlF	PTS system, mannitol specific IIBC component	transport/binding
0.93	1.04	0.94	0.72	0.76	2.15	3.94	1.50	0.90	1.68	0.60	MW2083		hypothetical protein, similar to transcription antiterminator BglG family	RNA synthesis
1.04	1.14	0.83	0.99	0.58	2.22	4.37	1.73	0.87	1.33	0.82	MW2084	mtlA	PTS system, mannitol specific IIA component	transport/binding
0.81	1.40	1.15	1.24	1.00	2.93	4.93	1.77	1.19	1.34	0.73	MW2085	mtlD	mannitol-1-phosphate 5-dehydrogenase	carbohydrate metabolism
0.87	0.70	1.04	0.72	0.83	1.60	2.72	1.59	1.07	1.32	0.86	MW2086-87	fmtB#mr	FmtB protein	pathogenic factor
0.73	1.30	1.31	0.94	1.29	1.64	1.48	1.39	1.00	1.33	1.01	MW2087		truncated FmtB	pathogenic factor
1.00	0.85	0.97	1.01	1.18	0.91	1.06	0.95	1.13	1.07	1.19	MW2088	lmM#fem	phosphoglucosamine-mutase	carbohydrate metabolism
1.32	1.02	0.80	1.03	1.01	0.98	1.49	1.00	1.30	0.80	1.04	MW2089		conserved hypothetical protein	
0.95	0.53	0.85	1.36	0.82	0.65	1.16	0.86	1.16	0.74	0.87	MW2090		conserved hypothetoical protein	
1.24	0.79	1.33	0.89	0.99	1.14	1.99	1.06	1.33	1.07	0.94	MW2091	arg	arginase	aminoacid metabolism
1.21	0.94	1.15	0.91	1.23	1.06	1.10	1.21	1.10	1.02	0.89	MW2092		hypothetical protein, similar to ATP-binding Mrp-like protein	pathogenic factor
0.92	1.12	1.10	1.12	1.10	0.94	1.08	0.86	1.32	1.17	1.21	MW2093		hypothetical protein, similar to multidrug resistance protein	transport/binding
0.90	0.84	1.01	0.76	0.97	0.86	1.06	0.85	1.09	1.21	1.39	MW2093a		hypothetical protein, similar to multidrug resistance protein	transport/binding
1.15	1.07	1.22	0.88	1.08	0.88	1.15	0.97	1.02	1.20	1.19	MW2094		hypothetical protein	
1.02	1.13	1.12	0.73	1.21	1.06	1.16	1.31	0.68	1.08	1.14	MW2095		hypothetical protein, similar to multidrug transporter	transport/binding
1.39	0.86	1.03	0.85	1.16	0.85	1.22	1.12	0.96	1.27	0.85	MW2096		hypothetical protein, similar to hemolysin III	pathogenic factor
1.05	1.17	1.30	1.27	1.21	1.52	1.09	1.27	0.96	1.15	0.94	MW2097		hypothetical protein, similar to UDP-N-acetylglucosamine pyrophosphorylase	cell wall
0.97	1.26	1.12	1.20	0.92	1.12	1.05	0.70	1.15	1.18	1.02	MW2098		conserved hypotehtical protein	
1.01	2.07	1.70	0.86	1.18	3.72	1.00	1.33	0.68	1.48	1.33	MW2099		conserved hypothetical protein	
0.86	1.20	0.85	0.86	1.14	1.19	0.86	1.14	0.78	1.24	0.59	MW2100		conserved hypotehtical protein	
0.74	0.63	0.92	0.81	1.09	0.88	0.70	1.14	0.88	0.98	0.84	MW2101		hypothetical protein, similar to ferrichrome ABC transporter (permease)	transport/binding
0.78	0.71	0.91	0.70	1.19	0.94	0.76	1.24	0.75	0.97	0.92	MW2102		hypothetical protein, similar to ferrichrome ABC transporter (permease)	transport/binding
0.65	0.66	0.76	1.57	1.04	0.60	0.52	1.07	0.74	0.73	1.01	MW2103		hypothetical protein, similar toferrichrome ABC transporter (binding p	transport/binding
0.69	0.46	0.69	1.34	0.92	0.43	0.58	0.72	1.02	0.73	1.19	MW2103n		hypothetical protein, similar toferrichrome ABC transporter (binding prote)	transport/binding
0.88	0.87	0.97	1.13	0.85	0.92	1.27	1.12	1.18	0.96	1.01	MW2104		conserved hypothetical protein	
0.82	0.94	0.78	0.84	0.87	1.56	1.08	1.57	1.08	0.99	1.08	MW2105		conserved hypothetical protein	
0.85	1.60	1.10	0.96	1.09	1.91	0.98	1.53	1.06	0.92	1.00	MW2106		hypothetical protein, similar to transporter	transport/binding
1.00	1.17	1.00	0.83	0.92	1.79	1.41	2.14	0.81	1.09	0.92	MW2107		hypothetical protein	
1.40	3.16	0.87	1.17	0.66	19.95	5.37	3.21	0.88	1.46	0.66	MW2108	asp23	alkaline shock protein 23, ASP23	adaptation to atypical
1.64	3.05	0.81	1.21	0.62	33.96	6.53	3.60	0.92	1.43	0.78	MW2109		hypothetical protein	
1.20	4.68	1.13	1.39	0.73	31.70	5.53	3.18	0.95	1.58	0.67	MW2110		hypothetical protein	
1.23	1.77	0.97	1.17	0.77	3.35	2.51	1.41	1.15	1.16	0.84	MW2111		glycine betaine transporter opuD homolog	transport/binding
1.12	1.12	1.10	1.08	0.87	1.12	1.20	0.89	0.94	1.20	0.81	MW2112		hypothetical protein, similar to alginate lyase	carbohydrate metabolism
0.79	1.30	1.80	0.95	1.01	1.35	1.20	1.38	0.91	1.26	0.87	MW2113		hypothetical protein, similar to quinone oxidoreductase	membrane bioenergetics
0.82	2.39	2.56	1.23	1.10	1.73	1.04	1.26	0.92	1.14	0.96	MW2114		conserved hypothetical protein	
0.68	11.40	25.53	1.06	1.09	1.73	1.13	1.38	0.94	1.37	0.91	MW2115	lacG	6-phospho-beta-galactosidase	carbohydrate metabolism
0.79	14.22	34.67	1.19	1.06	1.73	1.26	1.33	1.10	1.45	0.92	MW2116	lacE	PTS system, lactose-specific IIBC component	transport/binding
0.83	5.08	20.37	1.16	1.12	1.28	1.20	1.19	1.05	1.21	1.04	MW2117	lacF	PTS system, lactose-specific IIA component	transport/binding
0.70	10.67	16.83	1.22	1.16	1.61	1.09	1.20	1.07	1.50	0.89	MW2118	lacD	tagatose 1,6-diphosphate aldolase	carbohydrate metabolism
0.83	7.93	24.60	1.33	1.07	1.48	1.05	1.28	0.96	1.54	0.83	MW2119	lacC	tagatose-6-phosphate kinase	carbohydrate metabolism
0.74	1.45	16.33	1.17	1.10	0.95	1.11	0.70	1.00	1.48	0.94	MW2120	lacB	galactose-6-phosphate isomerase LacB subunit	carbohydrate metabolism
0.79	3.86	23.77	1.06	1.04	1.32	1.12	0.92	1.05	1.59	0.89	MW2121	lacA	galactose-6-phosphate isomerase LacA subunit	carbohydrate metabolism
0.84	1.71	2.05	1.42	1.14	1.48	0.98	0.96	1.14	1.20	1.16	MW2122	lacR	lactose phosphotransferase system repressor	RNA synthesis
0.85	1.50	1.74	1.06	1.09	1.21	1.00	1.09	0.94	1.24	0.96	MW2123		hypothetical protein, similar to regulatory protein, SIR2 family	RNA synthesis
0.98	1.16	1.36	0.85	1.07	1.23	1.05	1.34	0.82	1.14	1.02	MW2124		hypothetical protein	
0.95	1.19	0.95	1.00	0.82	0.90	1.11	1.02	1.10	1.10	1.35	MW2124n		hypothetical protein	
0.83	1.42	1.73	0.83	1.13	1.08	1.06	1.54	0.62	1.19	1.15	MW2125		hypothetical protein, similar to YnaE	
0.77	1.28	1.73	1.64	1.04	1.34	1.24	1.14	0.98	1.34	1.76	MW2126		hypothetical protein	

0.98	1.34	1.33	1.15	0.98	1.30	1.03	0.96	1.04	1.22	0.93	MW2127		hypothetical protein, similar to oxidoreductase, aldo/keto reductase family	carbohydrate metabolism
0.86	1.48	1.56	1.14	0.90	1.05	0.98	0.98	0.94	1.22	1.08	MW2128		hypothetical protein, similar to transcription regulator MerR family	RNA synthesis
0.76	1.01	0.82	0.74	0.82	0.89	0.93	0.85	0.87	1.05	0.67	MW2129	hysA	hyaluronate lyase precursor	pathogenic factor
0.75	1.17	0.87	0.90	0.73	0.84	1.13	1.04	0.96	0.93	0.79	MW2130		hypothetical protein, similar to MHC class II analog	pathogenic factor
0.73	0.50	0.45	0.53	0.65	0.39	0.66	0.49	0.76	0.97	0.34	MW2131		hypothetical protein, similar to alpha-acetolactate decarboxylase	carbohydrate metabolism
0.92	0.74	0.82	0.78	1.12	0.71	0.87	0.64	1.10	0.98	0.86	MW2131n		hypothetical protein, similar to alpha-acetolactate decarboxylase	carbohydrate metabolism
0.57	0.68	0.44	0.71	0.81	0.37	0.69	0.46	0.92	1.07	0.28	MW2132	alsS	alpha-acetolactate synthase	carbohydrate metabolism
0.61	0.83	0.86	0.89	0.88	0.81	0.81	0.81	0.95	1.03	0.96	MW2133		hypothetical protein	
0.81	1.20	0.87	1.00	0.98	0.76	0.95	0.98	0.77	1.07	1.17	MW2134		hypothetical protein	
0.96	1.11	0.99	0.98	1.01	0.78	0.82	0.86	0.92	1.10	0.91	MW2135		hypothetical protein	
1.00	0.73	0.80	0.61	1.02	0.30	0.58	1.26	0.68	0.93	0.57	MW2136	rpsI	30S ribosomal protein S9	protein synthesis
1.21	0.53	0.81	0.70	1.03	0.30	0.68	1.01	0.89	0.90	0.52	MW2137	rplM	50S ribosomal protein L13	protein synthesis
1.23	0.98	0.94	0.72	1.05	0.84	0.89	1.03	0.91	0.80	1.32	MW2138	truA	tRNA pseudouridine synthase A	RNA modification
1.10	0.95	0.86	0.73	1.07	0.83	0.80	1.00	0.77	0.79	1.46	MW2139		conserved hypothetical protein	
1.07	1.02	0.87	0.72	1.22	0.79	0.79	1.11	0.72	0.80	1.33	MW2140		hypothetical protein, similar to ABC transporter (ATP-binding protein)	transport/binding
0.92	1.15	0.72	0.86	1.02	0.81	0.77	0.75	0.74	0.89	1.10	MW2141		hypothetical protein, similar to ABC transporter (ATP-binding protein)	transport/binding
1.11	1.30	0.88	1.24	1.16	0.56	1.12	0.93	1.20	0.80	0.52	MW2142	rplQ	50S ribosomal protein L17	protein synthesis
0.98	1.26	1.01	1.23	1.30	0.66	1.09	1.00	1.31	0.77	0.48	MW2143	rpoA	DNA-directed RNA polymerase alpha chain	RNA synthesis
1.27	1.07	0.87	0.80	1.37	0.47	1.36	1.33	0.95	0.99	0.53	MW2144	rpsK	30S ribosomal protein S11	protein synthesis
1.27	1.01	1.00	1.01	0.91	0.52	0.84	1.09	1.24	0.86	0.51	MW2145	rpsM	30S ribosomal protein S13	protein synthesis
0.96	1.29	0.96	1.03	1.05	0.63	1.05	0.77	1.43	0.79	0.45	MW2146	rpmJ	50S ribosomal protein L36	protein synthesis
1.19	1.01	0.82	0.68	1.11	0.64	1.15	0.70	1.39	0.81	0.45	MW2146n	rpmJ	50S ribosomal protein L36	protein synthesis
1.09	1.10	0.96	1.04	1.29	0.87	1.14	0.97	1.22	0.79	0.45	MW2147	infA	translation initiation factor IF-1	protein synthesis
0.82	1.70	1.05	1.38	1.15	0.78	0.96	0.73	1.67	0.86	0.51	MW2148	adk	adenylate kinase	nucleic acid metabolism
0.79	1.45	1.06	0.97	0.99	0.66	0.95	0.82	1.35	0.81	0.45	MW2149	secY	preprotein translocase SecY subunit	protein secretion
0.86	1.37	1.01	1.29	0.92	0.50	1.14	0.67	1.63	0.89	0.50	MW2150	rplO	50S ribosomal protein L15	protein synthesis
0.67	1.17	0.83	1.10	0.86	0.45	0.93	0.59	1.22	0.78	0.40	MW2151	rpmD	50S ribosomal protein L30	protein synthesis
0.76	1.46	0.86	0.86	0.98	0.46	0.92	0.78	1.13	0.83	0.44	MW2151n	rpmD	50S ribosomal protein L30	protein synthesis
0.83	1.69	1.05	1.07	1.01	0.48	1.16	0.63	1.69	0.79	0.36	MW2152	rpsE	30S ribosomal protein S5	protein synthesis
0.75	0.99	0.87	1.12	0.66	0.39	0.89	0.62	1.30	0.84	0.40	MW2153	rplR	50S ribosomal protein L18	protein synthesis
0.82	1.70	1.13	1.44	1.07	0.56	0.90	0.69	1.49	0.88	0.41	MW2154	rplF	50S ribosomal protein L6	protein synthesis
0.87	1.43	1.07	1.06	1.07	0.56	0.86	0.73	1.48	0.77	0.38	MW2155	rpsH	30S ribosomal protein S8	protein synthesis
0.90	1.19	1.06	1.11	1.01	0.48	0.95	0.79	1.34	0.85	0.44	MW2156	rpsN	30S ribosomal protein S14	protein synthesis
0.84	1.93	1.10	1.71	1.06	0.59	0.80	0.59	1.67	0.85	0.38	MW2157	rplE	50S ribosomal protein L5	protein synthesis
0.94	1.31	1.30	1.21	1.06	0.60	0.94	0.65	1.63	0.82	0.42	MW2158	rplX	50S ribosomal protein L24	protein synthesis
0.93	2.01	1.39	1.23	0.99	0.52	1.00	0.75	1.47	0.81	0.40	MW2159	rplN	50S ribosomal protein L14	protein synthesis
1.12	1.69	1.20	1.11	1.14	0.55	0.98	1.16	1.24	0.75	0.39	MW2160	rpsQ	30S ribosomal protein S17	protein synthesis
1.17	1.27	1.15	1.32	0.99	0.39	0.90	0.50	1.47	0.85	0.39	MW2161	rpmC	50S ribosomal protein L29	protein synthesis
0.72	1.31	1.42	1.12	1.04	0.59	0.90	0.67	1.54	0.81	0.42	MW2162	rplP	50S ribosomal protein L16	protein synthesis
0.80	1.76	1.29	1.42	1.08	0.59	0.70	0.64	1.60	0.77	0.43	MW2163	rpsC	30S ribosomal protein S3	protein synthesis
0.81	1.38	1.34	1.09	0.96	0.55	0.79	0.64	1.34	0.77	0.46	MW2164	rplV	50S ribosomal protein L22	protein synthesis
0.83	1.31	0.97	1.04	0.87	0.38	0.72	0.57	1.22	0.68	0.47	MW2165	rpsS	30S ribosomal protein S19	protein synthesis
0.70	1.51	1.10	1.16	0.97	0.47	0.61	0.57	1.39	0.73	0.44	MW2166	rplB	50S ribosomal protein L2	protein synthesis
0.73	0.96	0.95	0.96	0.88	0.33	0.67	0.56	1.18	0.74	0.53	MW2167	rplW	50S ribosomal protein L23	protein synthesis
0.77	1.11	1.09	0.92	0.84	0.35	0.73	0.64	1.11	0.82	0.53	MW2168	rplD	50S ribosomal protein L4	protein synthesis
0.87	1.29	1.08	0.76	0.90	0.41	0.68	0.58	0.96	0.73	0.49	MW2169	rplC	50S ribosomal protein L3	protein synthesis
0.79	1.00	0.97	0.86	0.95	0.42	0.61	0.60	1.16	0.71	0.51	MW2170	rpsJ	30S ribosomal protein S10	protein synthesis
1.26	0.97	1.00	1.15	0.94	0.70	0.83	0.79	1.26	0.91	0.90	MW2171		hypothetical protein	
0.94	0.95	0.95	0.92	0.98	0.59	0.92	0.67	1.03	1.06	2.06	MW2172		conserved hypothetical protein	
0.77	1.12	0.80	0.73	0.74	0.62	0.89	0.94	0.85	0.97	0.97	MW2173	topB	DNA topoisomerase III topB	DNA packaging
0.87	0.80	0.62	0.83	0.84	0.59	0.78	0.76	0.94	0.79	0.99	MW2174		conserved hypothetical protein	
0.92	1.21	0.96	1.17	0.87	0.65	0.90	0.77	1.20	0.92	1.44	MW2175	glcU	glucose uptake protein homolog	transport/binding
0.95	0.74	0.71	0.43	0.64	0.57	0.86	0.74	0.51	0.91	1.42	MW2176		conserved hypothetical protein	
1.20	0.68	0.83	0.81	1.02	0.56	0.92	0.67	1.00	0.95	1.40	MW2177		conserved hypothetical protein	
1.27	0.75	0.86	0.90	1.03	0.56	0.98	0.59	1.15	0.88	1.32	MW2177n		conserved hypothetical protein	
1.11	0.82	0.80	0.84	0.81	0.54	1.01	0.60	1.29	0.86	1.42	MW2178		hypothetical protein	
1.02	0.91	0.91	1.06	1.10	1.07	1.12	1.08	0.83	0.84	1.21	MW2180	fmhB	FmhB protein	cell wall
1.33	1.04	0.99	0.84	1.02	1.17	1.00	1.25	0.85	0.86	1.09	MW2181		hypothetical protein	
1.04	0.91	1.02	0.82	0.85	1.09	0.89	0.78	0.90	1.05	1.22	MW2182		hypothetical protein	
1.15	1.17	0.93	0.83	1.41	1.15	1.04	1.44	0.67	0.85	0.98	MW2183		hypothetical protein, similar to transcription regulator MarR family	RNA synthesis
1.24	1.07	1.07	0.83	0.99	1.02	1.12	1.22	0.85	0.89	1.04	MW2184		hypothetical protein	transport/binding
1.27	1.18	0.87	0.76	1.12	1.06	0.98	1.01	0.79	0.86	1.27	MW2185	sarV	staphylococcal accessory regulator A homolog	RNA synthesis
1.15	1.20	1.06	0.86	1.18	0.96	1.00	1.51	0.86	0.84	1.15	MW2186	moaA	molybdenum cofactor biosynthesis protein A	coenzyme metabolism
1.23	1.05	1.03	0.87	1.36	1.09	0.90	1.36	0.92	0.85	1.11	MW2187	mobA	molybdopterin-guanine dinucleotide biosynthesis mobA	coenzyme metabolism
1.15	1.10	0.88	0.91	1.10	0.90	0.92	0.83	1.02	0.81	0.94	MW2188	moaD	probable molybdopterin synthase small subunit	coenzyme metabolism
1.06	0.93	0.81	0.87	0.99	0.82	0.92	1.17	0.84	0.87	0.93	MW2189	moaE	molybdopterin converting factor moa	coenzyme metabolism
1.34	0.89	0.95	0.82	1.07	0.90	0.84	1.19	0.72	0.83	0.90	MW2190	mobB	probable molybdopterin-guanine dinucleotide biosynthesis mobB	coenzyme metabolism
1.28	0.85	1.17	0.83	1.28	0.96	1.08	1.35	0.73	1.01	0.89	MW2191	moeA	molybdopterin biosynthesis protein moeA	coenzyme metabolism
1.10	0.96	0.92	0.86	1.03	0.89	0.94	0.82	0.85	0.95	1.01	MW2192	moaC	molybdenum cofactor biosynthesis protein C	coenzyme metabolism
1.14	0.80	1.10	0.89	1.29	0.95	0.93	1.30	0.79	0.89	0.86	MW2193	moaB	molybdopterin precursor biosynthesis moaB	coenzyme metabolism
0.97	0.70	1.04	0.85	0.95	0.86	0.88	1.16	0.72	0.85	0.75	MW2194	moeB	molybdopterin biosynthesis protein moeB	coenzyme metabolism
1.15	0.57	0.80	0.75	1.02	0.63	0.91	0.92	0.72	0.91	0.91	MW2195	modC	molybdenum transport ATP-binding protein ModC	transport/binding
1.18	0.40	0.40	0.59	0.70	0.40	0.90	0.63	0.79	0.59	0.70	MW2196	modB	probable molybdenum transport permease	transport/binding
1.01	0.67	0.97	0.84	1.06	0.79	0.77	0.86	0.74	0.83	0.61	MW2197	modA	probable molybdate-binding protein	transport/binding
1.02	1.16	1.11	1.04	1.13	1.08	0.91	0.98	0.66	1.04	0.81	MW2198	narQ	FdhD protein homolog	carbohydrate metabolism
1.05	0.90	1.09	1.00	1.01	0.84	0.97	0.90	0.71	1.07	1.03	MW2199		hypothetical protein	
1.03	0.90	0.90	1.25	1.08	0.83	0.84	0.65	0.77	0.99	1.10	MW2200		hypothetical protein, similar to biotin biosynthesis protein	coenzyme metabolism
0.85	0.70	0.91	1.09	1.11	0.92	0.79	0.85	0.77	1.01	1.01	MW2201		hypothetical protein, similar to inosine-adenosine-guanosine-nucleoside hydrola	nucleic acid metabolism
0.81	0.49	0.89	0.93	1.00	0.53	0.74	0.58	0.57	1.04	1.49	MW2202		hypothetical protein, similar to ferrichrome ABC transporter fhuD precursor	transport/binding
0.83	0.76	0.85	0.88	0.98	0.85	0.91	0.92	0.72	1.05	1.38	MW2203		hypothetical protein, similar to butyryl-CoA dehydrogenase	lipid metabolism
0.90	1.22	1.05	1.12	0.97	1.07	0.93	0.98	0.86	1.03	1.04	MW2204		hypothetical protein	
0.96	0.90	1.08	1.15	0.98	0.95	0.87	1.05	0.97	0.96	0.96	MW2204n		hypothetical protein	
0.76	1.00	1.07	1.04	1.01	1.10	0.90	0.86	0.97	1.00	1.06	MW2205		hypothetical protein, similar to urea transporter	transport/binding
0.99	1.00	1.10	1.31	1.17	1.36	1.00	1.14	1.15	1.19	0.96	MW2206	ureA	urease gamma subunit	amino acid metabolism
0.95	1.01	1.12	1.37	1.09	1.09	1.15	0.89	0.97	1.11	0.84	MW2207	ureB	urease beta subunit	amino acid metabolism
0.82	0.98	1.07	1.22	1.11	1.21	1.06	0.76	0.98	1.21	0.92	MW2208	ureC	urease alpha subunit	amino acid metabolism
0.80	1.00	1.06	1.17	1.04	1.25	0.83	0.92	0.94	1.13	1.06	MW2209	ureE	urease accessory protein UreE	amino acid metabolism
0.77	1.32	1.11	1.21	1.16	1.26	0.96	1.03	1.04	1.11	0.98	MW2210	ureF	urease accessory protein UreF	amino acid metabolism
0.67	1.15	1.08	1.51	1.25	1.22	0.86	0.69	1.16	1.12	0.92	MW2211	ureG	urease accessory protein UreG	amino acid metabolism
0.87	1.42	1.16	1.02	1.36	1.36	0.95	1.17	1.04	0.97	1.02	MW2211n	ureG	urease accessory protein UreG	amino acid metabolism
0.90	1.12	1.03	0.80	1.30	1.08	1.00	1.08	0.80	0.97	1.23	MW2212	ureD	urease accessory protein UreD	amino acid metabolism
1.71	0.72	1.02	0.78	1.38	0.37	1.15	0.41	2.13	1.12	2.99	MW2213	sarR	staphylococcal accessory regulator A homolog	RNA synthesis
1.12	1.12	1.09	1.00	0.94	0.77	1.01	0.84	1.30	1.14	1.38	MW2214		conserved hypothetical protein	
0.97	1.42	1.11	0.94	1.20	1.16	0.94	1.24	0.85	0.96	3.37	MW2215		hypothetical protein	
0.93	0.45	0.67	0.27	0.71	0.49	1.00	0.84	0.62	1.04	3.38	MW2216		hypothetical protein, similar to transcription regulator	RNA synthesis
1.36	0.79	0.95	0.69	1.72	0.68	0.71	0.52	1.30	0.68	1.00	MW2217		secretory antigen precursor SsaA homolog	pathogenic factor
1.89	0.84	0.85	0.60	1.75	0.55	0.83	0.85	0.93	0.63	0.90	MW2217n	ssaA	secretory antigen precursor SsaA homolog	pathogenic factor

0.99	1.00	0.80	0.69	0.82	0.94	1.53	1.14	0.95	0.85	1.21	MW2218		hypothetical protein	
1.00	1.03	1.08	1.17	0.99	1.10	1.01	0.61	1.11	0.98	1.05	MW2218n		hypothetical protein	
0.96	1.05	0.98	0.92	0.87	0.78	1.47	0.82	1.08	1.00	1.26	MW2219		hypothetical protein, similar to Na+/H+ antiporter	transport/binding
0.95	1.28	0.88	0.95	1.09	0.98	1.38	0.99	0.84	0.76	1.10	MW2220		hypothetical protein, similar to D-octopine dehydrogenase	aminoacid metabolism
0.94	1.05	0.89	0.75	0.68	0.64	1.30	0.74	0.85	0.74	1.20	MW2221		conserved hypothetical protein	
1.11	0.74	0.72	0.49	1.41	0.20	0.79	0.29	1.06	0.74	0.97	MW2222	ssaA	hypothetical protein, similar to secretory antigen precursor SsaA	pathogenic factor
1.56	0.44	0.58	0.23	1.06	0.12	1.18	0.14	1.09	0.48	0.94	MW2222n	ssaA	hypothetical protein, similar to secretory antigen precursor SsaA	pathogenic factor
1.18	0.54	0.70	0.67	1.32	0.69	1.36	0.89	1.05	0.73	0.83	MW2223		hypothetical protein	
1.11	0.46	0.77	0.42	0.74	0.96	1.44	0.70	0.71	0.93	0.80	MW2224		hypothetical protein, similar to glycerate dehydrogenase	aminoacid metabolism
1.20	0.42	0.57	0.37	0.76	0.57	0.95	0.92	0.72	0.75	0.79	MW2225		hypothetical protein, similar to monooxygenase	aminoacid metabolism
0.99	0.58	0.58	0.59	0.82	0.74	0.96	0.73	0.84	0.72	1.12	MW2226		hypothetical protein, similar to autolysin E	cell wall
1.02	1.06	1.00	1.24	1.00	1.02	0.84	0.67	1.04	1.07	1.16	MW2227		hypothetical protein	
1.58	0.80	0.60	0.53	1.01	1.51	1.57	0.78	0.97	0.71	0.65	MW2228		conserved hypothetical protein	
1.18	0.59	0.49	0.48	0.79	1.95	2.09	0.93	0.89	0.72	0.51	MW2229		formate dehydrogenase homolog	carbohydrate metabolism
1.15	1.03	0.97	1.00	1.09	1.79	1.25	1.22	0.68	0.98	0.70	MW2230		hypothetical protein, similar to lyt divergon expression attenuator LytR	RNA synthesis
1.18	1.34	1.00	0.83	1.08	1.69	1.28	1.42	0.79	0.92	0.86	MW2231		hypothetical protein, similar to suppressor protein suhB	carbohydrate metabolism
1.05	0.66	0.74	0.75	0.91	0.89	0.99	1.06	0.60	0.92	0.83	MW2232		conserved hypothetical protein	RNA synthesis
1.01	0.75	0.97	1.16	0.94	0.83	0.72	0.67	0.93	1.15	1.09	MW2233		truncated transposase	transposon and IS
1.31	1.10	0.90	0.64	1.13	1.14	0.89	1.28	0.74	1.02	1.26	MW2234		hypothetical protein, similar to protein of pXO2-46	
1.14	1.19	0.92	0.84	0.91	1.16	1.09	1.13	0.97	1.07	1.19	MW2235		hypothetical protein	
1.58	1.32	0.83	0.85	0.87	1.72	0.95	0.87	1.03	1.01	1.12	MW2236		hypothetical protein, similar to transcription regulator, RpiR family	RNA synthesis
0.94	0.67	0.89	0.51	0.90	0.75	1.00	1.12	0.66	1.10	1.51	MW2237		hypothetical protein, similar to transport protein	transport/binding
1.30	0.70	0.99	0.70	1.02	0.81	0.99	1.03	0.73	1.11	1.05	MW2238		hypothetical protein	
0.96	1.06	0.99	1.00	1.08	1.08	0.95	1.13	0.88	1.00	0.93	MW2239		hypothetical protein	
1.15	0.74	0.79	0.74	0.93	0.69	0.74	0.82	0.82	1.08	0.91	MW2239n		hypothetical protein	
1.09	0.82	0.74	0.69	0.86	0.72	0.69	0.81	0.69	1.01	1.17	MW2240		hypothetical protein	
1.02	0.82	0.68	0.65	0.94	0.70	0.58	0.80	0.54	1.04	1.34	MW2241		hypothetical protein, similar to phosphoglycolate phosphatase	carbohydrate metabolism
0.84	0.71	0.74	0.69	1.08	0.78	0.75	0.76	0.50	1.26	1.15	MW2242		hypothetical protein, similar to sodium-dependent transporter	transport/binding
0.97	0.88	0.78	0.79	1.07	0.97	0.85	0.96	0.71	1.28	1.04	MW2243		hypothetical protein	
0.77	1.06	0.85	0.79	2.44	1.02	0.86	1.00	0.80	4.02	0.99	MW2244	glvC	PTS system, arbutin-like IIBC component	transport/binding
0.83	0.96	0.82	0.78	1.13	1.02	0.81	1.02	0.61	1.25	1.19	MW2245		hypothetical protein, similar to transcriptional regulator	RNA synthesis
1.20	0.79	0.85	0.50	0.97	1.07	0.82	0.91	0.68	1.07	1.11	MW2246		hypothetical protein	
0.66	0.85	0.84	1.03	1.13	1.06	0.74	0.76	0.70	1.21	1.75	MW2247		hypothetical protein, similar to Na+/H+ antiporter, putative	transport/binding
0.82	1.03	0.85	0.84	1.00	1.13	0.90	0.83	0.70	1.07	1.48	MW2248		hypothetical protein	
0.88	1.33	0.98	1.06	1.02	2.49	1.31	1.01	0.70	1.26	0.95	MW2249		hypothetical protein, similar to dehydrogenase	carbohydrate metabolism
0.72	0.84	1.09	1.14	0.85	1.09	1.00	0.89	0.79	1.27	0.89	MW2250		hypothetical protein, similar to amino acid amidohydrolase	aminoacid metabolism
0.80	0.92	1.04	0.93	1.05	1.51	1.03	0.78	0.75	1.21	0.96	MW2251	hutI	imidazolonepropionase	aminoacid metabolism
0.79	1.02	1.00	1.07	1.16	1.95	1.10	1.01	0.91	1.28	0.89	MW2252	hutU	urocanate hydratase	aminoacid metabolism
0.89	1.37	1.07	0.89	1.12	1.62	1.13	1.23	0.78	1.06	0.89	MW2253		hypothetical protein, similar to transcription regulator LysR family	RNA synthesis
1.32	1.49	0.96	1.20	1.10	2.68	1.90	1.42	0.93	1.09	0.74	MW2254		hypothetical protein, similar to formiminoglutamase	aminoacid metabolism
0.89	0.66	0.70	0.87	1.08	0.67	0.99	0.52	0.78	0.81	1.36	MW2255		hypothetical protein	
1.04	0.96	0.87	1.15	1.22	0.95	1.00	1.02	1.09	0.99	1.13	MW2256		hypothetical protein, similar to ribose 5-phosphate isomerase (rpi)	nucleic acid metabolism
0.87	0.86	1.04	1.41	1.12	0.87	0.96	0.86	0.94	1.00	1.10	MW2257		conserved hypothetical protein	
0.80	0.83	0.72	1.20	0.96	0.70	0.86	0.58	0.70	0.95	1.50	MW2258		hypothetical protein, similar to aldose 1-epimerase	carbohydrate metabolism
0.95	0.73	0.76	0.83	1.03	0.89	0.86	0.98	0.61	0.80	1.40	MW2259		conserved hypothetical protein	
0.93	0.85	0.92	0.86	1.07	1.13	0.98	1.64	0.72	0.93	1.15	MW2260		conserved hypothetical protein	
0.97	1.02	1.06	1.27	1.09	1.03	0.91	0.99	0.96	1.02	0.98	MW2261		hypothetical protein, similar to ABC transporter (ATP-binding protein)	transport/binding
1.03	0.91	0.96	0.99	1.00	0.99	0.91	1.20	1.02	0.94	0.86	MW2263		conserved hypothetical protein	
1.00	0.85	1.04	1.03	0.96	0.95	0.93	0.94	0.91	1.03	1.14	MW2264		hypothetical protein	
0.89	1.09	1.08	1.08	1.05	0.98	0.98	1.09	1.12	1.01	0.92	MW2265		hypothetical protein, similar to DNA-3-methyladenine glycosidase	DNA repair or modify
1.00	0.55	0.69	0.47	0.68	0.66	0.86	0.73	0.66	0.96	1.15	MW2267	fni	isopentenyl diphosphate isomerase	lipid metabolism
0.90	0.83	0.84	0.74	0.92	0.97	0.84	0.87	0.92	0.87	1.31	MW2268		hypothetical protein, similar to divalent cation transport	transport/binding
0.91	1.01	0.90	1.19	0.93	1.22	0.87	0.84	1.06	0.91	1.09	MW2269		conserved hypothetical protein	
0.99	0.92	0.92	1.03	0.86	1.02	0.91	0.91	1.05	1.06	1.12	MW2270		hypothetical protein	
0.99	0.73	0.69	0.72	0.82	0.75	0.89	0.77	0.85	0.76	1.57	MW2271		hypothetical protein, similar to esterase	carbohydrate metabolism
1.10	0.58	0.71	0.81	0.68	0.59	1.01	0.77	0.85	0.81	1.44	MW2272		hypothetical protein	
0.84	0.69	0.68	0.80	0.70	0.84	1.02	1.10	0.86	0.80	1.13	MW2273		hypothetical protein, similar to multidrug resistance protein	transport/binding
0.93	0.57	0.80	0.47	0.79	0.84	1.12	0.78	0.95	0.89	0.84	MW2274		conserved hypothetical protein	
0.94	0.67	0.64	0.74	0.67	0.77	0.91	0.87	0.76	0.74	1.04	MW2276	tcaB	TcaB protein	transport/binding
1.12	0.87	0.78	0.70	0.87	0.80	0.94	0.99	0.92	0.97	1.33	MW2277	tcaA	TcaA protein	
1.27	0.64	0.61	0.61	0.80	0.58	1.00	0.70	1.14	0.83	1.07	MW2278	tcaR	TcaR transcription regulator	RNA synthesis
0.78	1.08	0.90	0.88	1.02	0.79	0.97	0.93	0.97	1.14	1.25	MW2279		hypothetical protein, similar to membrane protein	transport/binding
0.84	1.10	1.08	1.11	1.14	1.09	0.90	1.16	0.86	1.06	1.02	MW2280		hypothetical protein, similar to ABC transporter, ATP-binding protein	transport/binding
0.69	1.10	1.06	1.14	0.98	1.27	0.86	1.00	0.89	1.07	1.00	MW2281		conserved hypothetical protein	
0.91	1.32	1.18	1.15	1.41	1.46	0.94	1.48	0.72	0.98	0.86	MW2282		hypothetical protein, similar to two component response regulator	RNA synthesis
0.80	1.15	1.04	0.89	1.06	1.36	0.90	1.19	0.85	1.02	0.83	MW2283		hypothetical protein, similar to two component histidine kinase sensor	sensor
0.80	1.34	0.96	0.91	1.11	1.28	0.94	1.28	0.95	1.01	0.94	MW2284		conserved hypothetical protein	
0.78	1.22	0.99	1.00	0.90	1.12	0.90	1.06	1.10	1.00	0.98	MW2285		hypothetical protein	
0.78	1.55	1.15	1.00	1.07	1.32	0.83	1.10	1.05	1.11	0.90	MW2286		hypothetical protein, simialr to malate:quinone oxidoreductase	carbohydrate metabolism
0.86	0.39	0.90	1.00	1.12	0.69	1.43	0.43	0.76	0.91	2.18	MW2287		L-lactate permease lctP homolog	transport/binding
0.82	0.39	0.63	0.34	0.54	0.77	1.01	0.93	0.60	1.02	1.42	MW2288		hypothetical protein	
1.11	0.61	0.62	0.88	0.87	1.74	1.29	0.83	0.82	0.80	0.59	MW2289		hypothetical protein, similar to TpgX protein	
0.94	1.08	1.00	0.95	0.96	1.15	1.04	0.94	1.25	0.89	1.07	MW2290		/pothetical protein, similar to transcription repressor of sporulation, septation and degr	RNA synthesis
0.80	0.88	1.03	1.08	1.13	1.17	0.96	1.01	1.05	0.97	0.95	MW2291		conserved hypothetical protein	
1.30	0.44	0.74	0.47	0.87	0.71	1.27	0.76	0.84	0.80	0.79	MW2292		hypothetical protein, similar to export protein	transport/binding
1.05	1.31	1.11	0.91	1.26	1.48	1.06	1.49	0.97	1.06	0.92	MW2293		hypothetical protein, similar to attachment to host cells and virulence	
0.89	1.14	1.16	1.10	1.14	1.36	0.95	1.10	1.20	1.25	1.00	MW2294		hypothetical protein, similar to thioredoxin reductase	membrane bioenergetics
0.97	1.25	1.03	1.06	1.04	1.29	1.06	1.22	0.84	1.19	0.93	MW2294n		hypothetical protein, similar to thioredoxin reductase	membrane bioenergetics
1.22	0.59	1.04	0.87	1.04	0.31	0.91	0.49	1.05	1.08	0.98	MW2295		hypothetical protein	
0.82	1.21	0.86	1.03	1.25	1.27	0.95	1.14	0.85	1.32	0.96	MW2296		hypothetical protein, similar to phage infection protein precursor	phage-related
0.88	1.12	1.03	1.29	1.15	1.06	0.86	0.90	1.07	1.14	0.93	MW2297		hypothetical protein, similar to transcriptional regulator tetR-family	RNA synthesis
1.12	1.27	1.01	1.20	1.18	1.20	0.90	1.32	0.88	1.05	1.21	MW2298		hypothetical protein, similar to cationic transporter	transport/binding
0.84	1.29	1.04	2.12	1.06	1.45	0.87	0.88	1.08	4.24	1.64	MW2299	scrA	PTS system, sucrose-specific IIBC component	transport/binding
0.84	1.38	1.00	1.19	1.19	1.82	0.90	1.17	0.99	1.46	1.34	MW2300		hypothetical protein	
1.24	0.90	0.83	0.72	0.87	1.00	1.07	1.24	0.72	1.26	1.78	MW2301		hypothetical protein, similar to transcription regulatory protein	RNA synthesis
1.32	0.98	0.77	0.68	0.85	1.00	1.30	0.81	0.84	1.01	1.02	MW2302		hypothetical protein, similar to general stress protein 26	adaptation to atypical
1.13	0.46	0.65	0.79	0.77	0.30	0.78	0.57	1.01	0.86	0.97	MW2303		hypothetical protein	
0.87	0.56	0.75	0.65	0.96	0.25	0.81	0.69	0.72	1.06	0.90	MW2304	gltT	proton/sodium-glutamate symport protein	transport/binding
0.98	0.73	0.50	0.64	1.19	0.32	0.83	0.50	0.89	0.74	1.03	MW2305		hypothetical protein	
1.27	0.61	0.68	0.64	1.01	0.60	0.76	0.51	0.61	0.92	1.75	MW2306		hypothetical protein, similar to transcriptional regulator	RNA synthesis
1.10	0.80	0.81	0.85	1.07	0.62	1.09	0.92	1.04	0.96	1.13	MW2307		hypothetical protein, similar to small heat shock protein	adaptation to atypical
1.41	0.81	0.87	1.29	1.62	0.75	3.41	0.86	2.00	1.08	0.97	MW2308	narK	nitrite extrusion protein	transport/binding
1.51	0.90	1.06	0.89	1.08	0.94	2.14	1.09	1.48	1.03	1.02	MW2309		hypothetical protein	
1.16	1.50	0.92	1.06	1.27	1.17	1.44	0.97	1.26	0.98	1.15	MW2312		hypothetical protein, similar to transcriptional regulator	RNA synthesis
1.52	0.95	0.73	0.70	1.04	1.17	2.22	1.33	1.39	0.97	0.89	MW2313		hypothetical protein, similar to response regulators of two-component regulat	RNA synthesis
1.28	1.13	0.88	1.36	1.45	1.43	1.77	0.87	1.60	0.96	0.86	MW2314		hypothetical protein, similar to two component sensor histidine kinase	sensor
1.68	1.12	0.92	1.07	1.20	1.44	1.90	0.99	1.54	0.93	0.97	MW2315		hypothetical protein	

1.76	1.07	0.91	0.97	1.26	1.10	2.58	1.09	1.46	1.02	0.98	MW2316	narI	nitrate reductase gamma chain	membrane bioenergetics
1.76	0.94	1.03	1.17	1.38	1.22	2.82	0.95	1.54	1.01	1.01	MW2317		hypothetical protein, similar to nitrate reductase delta chain	membrane bioenergetics
1.31	0.98	0.94	1.28	1.46	1.36	2.02	0.96	1.64	1.02	0.76	MW2318	narH	nitrate reductase beta chain narH	membrane bioenergetics
1.43	0.92	0.90	0.93	1.26	1.25	2.44	1.06	1.42	1.02	0.90	MW2319	narG	respiratory nitrate reductase alpha chain	membrane bioenergetics
1.34	1.05	0.97	1.09	1.36	1.13	2.22	0.80	1.59	0.93	0.77	MW2320	nasF	uroporphyrin-III C-methyl transferase	coenzyme metabolism
1.68	0.96	0.96	1.47	1.38	1.16	2.17	0.67	1.43	0.91	0.88	MW2321	nasE	assimilatory nitrite reductase	amino acid metabolism
1.43	0.71	0.59	0.56	0.97	0.97	2.20	1.27	1.07	0.90	0.87	MW2322	nasD	nitrite reductase	amino acid metabolism
1.04	0.95	0.86	1.21	1.03	1.03	1.28	0.78	1.29	0.78	0.84	MW2323		hypothetical protein, similar to NirR	amino acid metabolism
1.12	0.91	0.98	0.97	1.07	0.98	1.31	0.92	1.17	0.95	0.97	MW2324		conserved hypothetcial protein	
1.12	0.64	1.46	1.21	1.01	0.48	1.25	1.04	1.24	0.97	1.35	MW2325		hypothetical protein, similar to NirC	transport/binding
1.59	0.76	1.18	1.14	1.31	0.38	1.00	0.94	1.35	0.72	1.27	MW2326		hypothetical protein	
1.26	1.09	1.06	1.58	1.28	0.52	0.86	1.23	1.11	0.75	1.29	MW2326n		hypothetical protein	
1.05	0.98	0.94	1.28	1.02	0.72	1.04	0.87	1.10	0.92	0.91	MW2327		conserved hypothetical protein	
1.04	0.98	0.97	1.00	1.01	0.89	1.08	0.97	1.02	0.98	0.12	MW2328		hypothetical protein, similar to Zn-binding lipoprotein adcA	transport/binding
1.18	0.91	1.01	1.11	0.95	0.74	1.22	0.94	0.95	1.00	0.87	MW2329		conserved hypothetical protein	
1.29	0.69	0.71	0.71	0.99	0.70	1.00	0.61	0.81	0.87	0.83	MW2330		conserved hypothetical protein	
0.98	0.74	0.70	1.03	0.82	0.68	0.87	0.62	0.86	0.74	1.17	MW2332		hypothetical protein	
0.96	0.73	0.78	0.63	0.65	0.64	1.07	0.91	0.74	0.95	0.84	MW2333	fmhA	fmhA protein	cell wall
0.80	0.81	0.53	0.71	0.63	0.68	0.74	0.88	0.68	0.82	3.38	MW2334		hypothetical protein, similar to ABC transporter, ATP binding subunit	transport/binding
0.67	1.00	0.58	0.75	0.65	0.74	0.69	0.90	0.77	0.85	3.35	MW2335		hypothetical protein, similar to ABC transporter, permease protein	transport/binding
0.67	0.92	0.66	0.91	0.65	0.77	0.82	0.88	0.86	0.82	3.01	MW2336		hypothetical protein, similar to ABC transporter, periplasmic amino acid-binding pr	transport/binding
0.81	0.87	0.69	0.60	0.66	0.65	0.95	0.84	0.98	0.91	1.32	MW2337		hypothetical protein, similar to multidrug resistance protein	transport/binding
0.99	0.88	0.85	0.94	0.72	0.73	1.00	1.04	0.97	1.01	0.11	MW2338		hypothetical protein	
0.65	1.16	0.72	0.96	0.77	0.87	0.82	1.19	0.66	1.01	2.50	MW2339		phosphoglycerate mutase, pgm homolog	carbohydrate metabolism
0.76	1.15	0.84	0.90	0.95	0.83	0.77	1.15	0.80	0.99	1.47	MW2340		conserved hypothetical protein	
1.25	0.55	0.64	0.52	1.02	0.24	0.65	0.67	0.67	0.93	4.23	MW2341	sbi	IgG-binding protein SBI	pathogenic factor
0.80	0.94	1.21	1.06	1.15	0.78	1.07	1.07	1.12	1.14	0.96	MW2342	hlgA	gamma-hemolysin chain II precursor	pathogenic factor
1.14	0.74	0.80	0.79	1.10	0.90	0.85	0.86	0.73	1.02	0.98	MW2342n	hlgA	gamma-hemolysin chain II precursor	pathogenic factor
0.93	1.05	1.06	1.27	1.06	1.07	0.93	1.56	1.03	1.02	1.09	MW2343	hlgC	gamma-hemolysin component C	pathogenic factor
0.85	1.14	1.17	0.97	1.03	0.89	0.91	1.14	1.08	1.12	0.89	MW2343n	hlgC	gamma-hemolysin component C	pathogenic factor
0.97	1.05	1.22	1.31	0.96	1.03	1.13	1.28	1.00	1.25	1.23	MW2344	hlgB	gamma-hemolysin component B	pathogenic factor
0.76	1.39	1.97	0.95	1.02	1.26	1.20	2.10	0.87	1.29	1.10	MW2344n	hlgB	gamma-hemolysin component B	pathogenic factor
0.78	1.78	1.21	1.06	1.19	1.02	1.01	1.47	0.82	1.18	1.06	MW2345		hypothetical protein, similar to BioX protein	
0.71	1.77	1.43	1.24	1.48	1.53	1.12	1.77	1.01	1.10	1.10	MW2346		hypothetical protein, similar to 6-carboxyhexanoate—CoA ligase	coenzyme metabolism
0.73	1.28	1.32	1.12	1.17	1.22	1.28	1.44	0.70	1.24	0.88	MW2348	bioB	biotin synthase	coenzyme metabolism
0.73	1.37	1.33	1.21	1.16	1.36	1.13	1.24	0.78	1.30	0.93	MW2349	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	coenzyme metabolism
0.77	1.08	1.55	1.29	1.17	1.20	1.11	1.21	0.90	1.37	0.98	MW2350	bioD	dethiobiotin synthetase	coenzyme metabolism
0.77	1.08	1.17	1.39	1.06	1.14	1.04	0.90	1.04	1.19	1.17	MW2351		hypothetical protein, similar to ABC transporter, ATP-binding protein	transport/binding
0.72	1.11	1.24	1.24	1.13	1.31	1.06	1.15	1.02	1.11	1.11	MW2352		hypothetical protein, similar to lipoprotein inner membrane ABC-transporter	transport/binding
1.12	1.07	1.21	1.16	1.11	1.39	1.19	0.96	0.32	1.18	1.36	MW2354		hypothetical protein	
0.76	1.51	1.16	1.21	1.04	1.28	0.93	1.17	1.09	1.16	0.90	MW2355		conserved hypothetical protein	
0.75	1.04	1.07	1.38	1.02	1.30	0.85	0.84	0.87	1.09	0.71	MW2356		conserved hypothetical protein	
0.76	1.05	0.96	1.25	0.93	1.27	0.82	0.69	0.92	1.05	0.84	MW2357		hypothetical protein	
0.76	1.26	1.34	1.52	1.11	0.92	1.00	0.66	1.19	1.26	1.83	MW2358		hypothetical protein, similar to bicyclomycin resistance protein TcaB	transport/binding
1.01	0.95	1.29	1.48	0.99	1.07	1.14	0.75	1.01	1.24	0.99	MW2359		hypothetical protein, similar to transcriptional activator	RNA synthesis
0.85	1.00	1.01	1.20	0.90	1.28	0.81	0.80	0.91	1.18	1.42	MW2360		hypothetical protein	
0.77	1.15	1.21	1.33	1.13	1.29	0.89	0.92	1.06	1.15	1.25	MW2361		conserved hypothetical protein	
0.83	1.37	1.22	1.29	1.21	1.29	0.96	0.92	1.03	1.28	1.14	MW2362a	uncated-S	uncated hypothetical protein, similar to D-serine/D-alanine/glycine transport	transport/binding
0.86	1.18	1.25	1.37	1.04	0.97	0.99	0.77	1.00	1.06	1.08	MW2362b	uncated-	truncated-SA	transport/binding
0.81	1.06	0.77	1.01	0.93	0.79	0.74	0.67	1.00	0.95	2.49	MW2364		conserved hypothetical protein	
0.82	1.11	0.98	1.03	0.90	0.87	0.91	0.87	1.12	1.06	1.60	MW2365		hypothetical protein, similar to beta-lactamase	cell wall
0.93	0.87	1.00	0.90	0.90	0.80	1.12	0.80	0.96	1.09	1.05	MW2366		hypothetical protein, similar to glucose epimerase	carbohydrate metabolism
0.72	0.81	0.78	0.84	0.90	0.75	0.73	0.77	0.82	0.96	1.64	MW2367		hypothetical protein, similar to 2-dehydropantoate 2-reductase	coenzyme metabolism
0.96	0.86	1.13	1.48	1.23	0.53	1.15	0.77	1.46	0.93	1.00	MW2369	opuCD	probable glycine betaine/carnitine/choline ABC transporter opuCD	transport/binding
0.89	0.81	1.01	1.09	0.92	0.53	1.07	0.68	1.36	0.88	0.86	MW2370	opuCC	glycine betaine/carnitine/choline ABC transporter opuCC	transport/binding
0.88	0.64	1.10	1.32	1.18	0.79	0.94	0.74	0.99	0.87	0.89	MW2371	opuCB	probable glycine betaine/carnitine/choline ABC transporter opuCB	transport/binding
0.95	0.97	1.09	1.50	1.19	0.86	0.86	0.81	0.95	0.87	0.82	MW2372	opuCA	glycine betaine/carnitine/choline ABC transporter opuCA	transport/binding
0.97	0.56	0.73	0.88	0.81	0.68	1.13	0.78	0.93	0.72	0.84	MW2373		conserved hypothetical protein	
0.94	0.62	0.87	0.54	0.94	0.76	1.46	0.86	0.95	0.90	0.89	MW2374		hypothetical protein, similar to amino acid transporter	transport/binding
1.08	0.65	0.66	0.75	0.89	1.72	1.17	1.03	0.95	0.82	0.67	MW2375		hypothetical protein, similar to para-nitrobenzyl esterase chain A	lipid metabolism
0.98	1.16	1.26	1.10	1.29	1.32	1.32	1.02	0.99	1.23	1.55	MW2376		hypothetical protein, similar to chloramphenicol resistance protein	transport/binding
1.16	0.60	0.72	0.58	0.69	1.15	1.85	1.42	0.86	0.81	1.03	MW2377		conserved hypotehtical protein	transport/binding
1.13	0.54	0.86	0.59	1.02	1.03	1.92	1.12	0.99	0.78	0.78	MW2378		hypothetical protein, similar to ABC transporter (ATP-binding protein	transport/binding
0.80	1.04	0.97	1.42	1.14	1.21	0.93	0.82	0.94	1.07	1.13	MW2379		hypothetical protein, similar to endo-1,4-beta-glucanase	carbohydrate metabolism
1.67	0.55	0.70	0.64	1.28	0.79	0.83	0.74	0.83	0.85	0.68	MW2380		conserved hypothetical protein	
1.99	0.53	0.70	0.62	1.33	0.64	0.85	0.66	0.76	0.83	0.69	MW2381		hypothetical protein	
0.95	0.62	0.79	0.94	1.11	0.94	0.85	0.89	0.69	0.93	0.47	MW2382		conserved hypothetical protein	
0.98	1.37	1.00	0.78	1.07	0.94	1.06	1.30	0.95	0.97	0.97	MW2383		hypothetical protein, similar to glutamate synthase (ferredoxin)	amino acid metabolism
1.16	0.92	0.91	1.09	0.89	0.93	1.09	0.91	1.03	1.11	0.95	MW2385		hypothetical protein	
1.51	0.94	1.03	0.84	1.16	1.18	1.19	1.32	0.92	0.89	0.96	MW2385n		hypothetical protein	
1.00	1.51	1.50	1.15	1.64	1.25	0.92	2.02	1.23	0.93	0.65	MW2386		hypothetical protein, similar to antibiotic resistance protein	transport/binding
0.90	1.33	1.39	1.32	1.21	1.05	1.05	1.29	1.15	1.06	0.55	MW2387	opp-1F	oligopeptide transporter putative ATPase domain	transport/binding
0.91	1.36	1.63	1.50	1.29	1.18	1.09	1.41	1.34	1.12	0.54	MW2388	opp-1D	oligopeptide transporter putative ATPase domain	transport/binding
1.01	1.10	1.60	1.35	1.13	1.03	1.05	1.20	1.56	1.18	0.67	MW2389	opp-1C	oligopeptide transporter putative membrane permease domain	transport/binding
0.99	1.03	0.88	0.82	1.01	1.13	0.96	1.42	0.64	0.93	1.21	MW2390	opp-1B	oligopeptide transporter putative membrane permease domain	transport/binding
0.85	1.27	1.76	2.00	1.20	1.17	1.01	1.26	1.77	1.11	0.45	MW2391	opp-1A	oligopeptide transporter putative substrate binding domain	transport/binding
0.80	1.32	1.67	1.82	1.25	1.23	1.07	1.21	1.47	1.09	0.40	MW2391n	opp-1A	oligopeptide transporter putative substrate binding domain	transport/binding
0.81	1.38	1.44	1.33	1.29	1.42	1.07	1.44	1.47	1.09	0.51	MW2392		conserved hypothetical protein	
0.86	1.53	1.42	1.19	1.11	1.31	1.17	1.53	1.13	1.11	0.57	MW2393		conserved hypothetical protein	
0.95	1.28	1.44	1.21	1.17	1.18	1.25	1.19	0.95	1.24	0.86	MW2394		hypothetical protein, similar to diaminopimelate epimerase	amino acid metabolism
0.83	1.34	1.11	1.14	0.92	1.13	1.21	1.29	1.04	1.09	1.12	MW2395		hypothetical protein	
1.02	1.14	1.09	1.23	1.27	1.78	1.25	1.01	1.15	1.02	0.70	MW2396		hypothetical protein, similar to glucose 1-dehydrogenase	carbohydrate metabolism
0.94	0.78	0.74	0.59	0.80	0.70	1.03	0.82	0.65	1.15	1.59	MW2397		hypothetical protein, similar to efflux pump	transport/binding
1.11	1.18	0.89	0.96	1.02	1.30	1.49	0.99	0.97	1.08	1.08	MW2398		conserved hypothetical protein	
1.20	1.20	1.17	1.12	0.98	1.06	1.16	0.97	1.17	1.14	1.04	MW2399		hypothetical protein	
2.32	1.18	1.12	1.51	0.00	1.16	0.87	0.74	1.61	1.13	0.78	MW2399n		hypothetical protein	
1.17	0.36	0.77	0.28	0.52	0.70	1.21	1.13	0.70	0.75	0.80	MW2400		hypothetical protein	
1.09	0.92	0.89	1.05	0.90	0.73	1.00	0.86	0.99	0.92	1.06	MW2401		hypothetical protein	
1.28	0.49	0.84	0.46	0.76	0.82	1.09	0.93	0.67	1.00	1.01	MW2402		hypothetical protein	
1.08	1.08	1.04	0.99	1.06	0.94	0.96	1.15	0.91	0.96	1.09	MW2402n		hypothetical protein	
1.19	1.17	0.94	0.86	0.79	0.94	1.21	1.14	0.97	1.11	1.17	MW2403		hypothetical protein, similar to oxidoreductase	carbohydrate metabolism
1.25	1.07	1.15	1.43	1.21	1.12	1.06	0.74	1.45	1.18	1.02	MW2404		hypothetical protein	
1.44	0.91	1.64	1.54	1.85	2.12	1.70	0.67	1.26	1.26	1.44	MW2405		hypothetical protein	
1.34	0.81	1.01	0.78	0.87	0.67	1.34	0.90	0.98	0.94	1.01	MW2406		hypothetical protein	
0.87	0.97	1.05	1.06	1.09	0.77	1.00	0.92	1.00	0.98	1.03	MW2406n		hypothetical protein	
1.15	1.07	0.96	1.17	0.90	0.88	1.04	1.07	1.24	0.98	1.01	MW2407		hypothetical protein	
1.17	0.86	1.00	0.97	0.95	0.92	0.97	1.23	1.27	0.98	1.07	MW2407n		hypothetical protein	

1.08	0.92	0.97	0.96	0.86	0.93	1.14	1.21	1.27	1.04	1.12	MW2408		hypothetical protein	
0.75	1.83	0.96	0.76	1.00	3.52	1.28	2.21	1.01	1.08	1.22	MW2409		conserved hypothetical protein	
1.05	0.81	0.86	1.14	0.98	0.80	1.05	1.10	0.99	1.07	0.87	MW2409n		conserved hypothetical protein	
1.11	0.97	1.05	1.08	0.90	0.96	1.02	1.17	0.93	1.11	0.85	MW2410		hypothetical protein, similar to mutator protein mutT	[illegible]
0.96	0.95	1.08	1.08	1.00	1.06	0.91	1.06	1.02	1.15	1.25	MW2411		hypothetical protein, similar to phosphomannomutase	carbohydrate metabolism
1.21	1.21	1.48	1.56	1.15	1.18	1.04	1.09	1.82	0.99	1.11	MW2412		hypothetical protein	
1.08	1.10	1.18	0.98	0.91	0.97	1.40	1.36	1.20	1.21	1.33	MW2413		hypothetical protein	
1.09	1.22	1.24	1.24	0.95	1.25	1.13	1.33	1.08	1.11	1.39	MW2414		hypothetical protein	
1.04	0.89	1.31	0.68	0.99	0.80	1.12	1.03	1.01	1.07	1.72	MW2415		conserved hypothetical protein	
1.09	0.85	0.89	0.65	0.87	0.70	1.04	1.21	0.87	1.07	1.27	MW2415n		conserved hypothetical protein	
0.81	0.58	0.73	0.66	1.75	0.79	1.17	0.84	0.77	0.82	3.96	MW2416		hypothetical protein, similar to surface protein precursor	pathogenic factor
0.88	0.87	0.98	0.87	0.98	0.93	1.09	0.94	1.16	1.07	4.15	MW2416n		hypothetical protein, similar to accumulation-associated protein	
0.91	1.10	0.87	0.85	1.09	0.82	1.05	1.04	0.99	1.00	1.64	MW2417	sarT	staphylococcal accessory regulator A homolog	RNA synthesis
0.82	0.93	1.13	0.74	1.14	0.87	0.94	1.08	0.32	1.10	2.62	MW2418	arH2(sarU	staphylococcal accessory regulator A homolog	RNA synthesis
0.87	0.68	0.79	0.51	0.88	0.60	0.71	0.64	0.62	0.92	1.39	MW2419	gtaB	UTP-glucose-1-phosphate uridyltransferase	cell wall
0.69	0.58	0.63	0.60	1.04	0.50	0.67	0.49	0.67	0.66	1.23	MW2420	fnbB	fibronectin-binding protein homolog(fmbB)	pathogenic factor
0.70	0.73	0.88	0.76	1.40	0.62	1.02	0.65	0.85	0.84	1.47	MW2421	fnb	fibronectin-binding protein homolog(fnbA)	pathogenic factor
0.82	1.14	1.21	1.16	0.94	1.32	1.06	1.17	1.06	1.25	1.07	MW2422		hypothetical protein	
0.88	1.40	1.08	0.50	1.06	0.96	1.19	1.23	0.84	1.26	1.06	MW2423	gntP	gluconate permease	transport/binding
0.84	1.51	1.22	0.80	1.42	1.46	1.06	1.32	0.81	1.29	0.88	MW2424	gntK	gluconokinase	carbohydrate metabolism
0.84	1.76	1.33	0.97	1.36	1.46	0.97	1.43	0.89	1.26	0.95	MW2425	gntR	gluconate operon transcriptional repressor	RNA synthesis
0.87	1.81	1.22	0.84	1.51	1.56	0.96	1.66	0.76	1.09	0.96	MW2426		hypothetical protein, similar to transcriptional regulator, MerR family	RNA synthesis
0.96	1.95	1.24	0.82	1.12	1.24	1.26	1.47	1.03	1.16	1.04	MW2427		hypothetical protein, similar to GTP-pyrophosphokinase	nucleic acid metabolism
1.71	3.13	1.04	1.05	0.91	2.12	3.86	0.79	0.93	1.15	1.08	MW2428		conserved hypothetical protein	
0.98	1.52	1.34	0.87	1.31	1.36	1.09	1.54	1.00	1.10	1.06	MW2429		conserved hypothetical protein	
0.86	1.44	1.21	1.12	0.93	1.05	1.07	1.63	0.89	1.26	1.15	MW2430		hypothetical protein	
1.02	1.67	1.65	0.94	1.30	1.33	1.11	1.63	0.79	1.34	1.21	MW2431		hypothetical protein, similar to glucarate transporter	transport/binding
1.07	1.08	1.20	1.53	1.21	1.09	1.03	0.95	1.17	1.26	1.35	MW2432		hypothetical protein, similar to alkaline phosphatase	phosphate metabolism
0.86	0.64	0.61	1.01	1.00	0.37	0.56	0.83	0.63	0.81	2.54	MW2433		hypothetical protein, similar to ABC transporter	transport/binding
0.89	0.66	0.68	1.11	0.95	0.43	0.63	1.14	0.65	0.93	3.21	MW2434		hypothetical protein, similar to membrane spanning protein	transport/binding
0.84	1.10	1.14	0.74	1.00	1.16	1.14	1.75	0.74	1.36	0.90	MW2435	fbp	fructose-bisphosphatase	carbohydrate metabolism
1.09	0.97	1.09	1.03	1.09	0.99	0.94	0.88	0.96	1.18	1.19	MW2437		conserved hypothetical protein	
0.77	1.18	1.22	1.12	1.22	1.35	0.92	1.22	0.90	1.06	0.86	MW2438		conserved hypothetical protein	
0.78	1.34	1.21	1.06	1.25	1.42	0.99	1.47	1.02	1.07	0.72	MW2439		hypothetical protein, similar to ABC transporter (binding protein)	transport/binding
1.04	0.89	1.19	0.93	1.36	1.10	1.07	1.38	0.75	1.10	0.76	MW2440		hypothetical protein, similar to transcription regulator MarR family	RNA synthesis
0.82	1.20	1.27	1.34	1.25	1.21	0.95	1.05	1.01	1.12	0.71	MW2442		conserved hypothetical protein	
0.76	1.43	1.36	1.41	1.32	1.47	0.94	1.38	1.03	1.07	0.65	MW2443		hypothetical protein, similar to NAD(P)H-flavin oxidoreductase	membrane bioenergetics
0.77	0.92	1.50	1.66	2.05	0.99	1.32	1.08	1.14	1.06	1.13	MW2444	ddh	D-specific D-2-hydroxyacid dehydrogenase	carbohydrate metabolism
0.76	1.09	1.11	1.44	1.36	1.22	0.87	0.88	1.19	1.18	0.77	MW2445		conserved hypothetical protein	
0.64	1.27	1.28	1.11	1.19	1.15	0.83	1.01	1.02	1.06	0.94	MW2446		hypothetical protein, similar to ABC transporter (ATP-binding protein)	transport/binding
1.00	1.04	1.08	0.90	1.10	1.07	1.00	1.08	0.90	1.15	1.21	MW2447		conserved hypothetical protein	
0.85	1.22	1.04	1.26	1.09	1.10	0.91	0.94	0.85	1.17	1.11	MW2448	srtA	sortase	cell wall
0.75	1.09	1.01	1.63	1.14	0.94	0.80	0.65	0.96	1.02	0.96	MW2449		hypothetical protein, similar to N-acetyltransferase	detoxification
0.83	0.83	1.03	1.03	0.98	0.96	0.95	0.93	0.33	1.04	1.19	MW2450		hypothetical protein	
0.86	1.10	1.19	1.48	1.24	1.24	0.86	0.84	1.23	1.16	0.77	MW2451		hypothetical protein, similar to L-serine dehydratase	aminoacid metabolism
0.78	1.53	1.13	1.10	1.14	1.38	0.87	1.41	1.07	1.08	0.81	MW2452		hypothetical protein, similar to beta-subunit of L-serine dehydratas	aminoacid metabolism
0.86	1.10	1.35	1.24	0.96	1.21	1.08	1.15	1.00	1.17	0.84	MW2453		hypothetical protein, similar to regulatory protein pfoR	RNA synthesis
0.76	0.89	1.02	1.04	0.95	1.07	0.75	1.02	0.96	1.11	1.04	MW2454		hypothetical protein	
0.78	0.93	1.09	1.37	1.04	1.19	0.87	0.94	0.98	1.08	1.25	MW2455		conserved hypothetical protein	
0.81	1.26	1.10	1.50	1.08	1.34	0.82	0.95	1.03	1.07	0.93	MW2456		conserved hypothetical protein	pathogenic factor
0.70	1.00	1.04	1.29	1.05	1.04	0.90	1.03	0.88	1.10	1.15	MW2457		hypothetical protein, similar to thioredoxin	membrane bioenergetics
0.84	0.91	0.90	1.15	0.88	0.99	0.83	1.02	0.77	1.03	0.82	MW2458		conserved hypothetical protein	
0.60	1.18	0.65	0.91	0.77	1.11	0.82	1.59	0.89	0.88	0.54	MW2459	ptsG	PTS system glucose-specific IIABC component	transport/binding
0.69	0.93	0.77	0.76	0.99	1.19	0.79	1.88	0.64	0.97	0.57	MW2459n	ptsG	PTS system, glucose-specific IIABC component	transport/binding
0.62	0.84	0.52	0.68	0.76	2.65	0.92	1.25	0.59	0.90	2.39	MW2460		hypothetical protein, similar to pyruvate oxidase	carbohydrate metabolism
0.67	1.11	0.55	1.00	0.75	3.11	1.00	1.12	0.68	0.91	2.20	MW2461		conserved hypothetical protein	
0.63	0.87	0.53	0.97	0.75	0.82	0.51	0.70	0.50	0.78	2.42	MW2462		conserved hypothetical protein	
0.72	1.08	0.83	1.36	0.90	1.23	0.81	0.94	1.05	0.94	1.01	MW2463		hypothetical protein, similar to transcription regulator	RNA synthesis
1.08	0.38	0.74	0.97	0.64	0.27	0.61	0.57	0.83	1.20	0.52	MW2464		hypothetical protein	
1.08	0.95	1.00	1.06	0.95	0.94	1.06	0.84	0.94	1.06	1.03	MW2465		hypothetical protein, similar to secretory antigen precursor SsaA	pathogenic factor
0.87	0.40	0.82	0.58	0.62	0.77	0.96	0.88	0.92	0.99	0.76	MW2466	mvaA	hydroxymethylglutaryl-CoA reductase	lipid metabolism
0.87	0.96	0.69	0.82	0.83	1.10	1.27	1.19	1.08	0.78	0.73	MW2467	mvaS	3-hydroxy-3-methylglutaryl CoA synthase	lipid metabolism
1.19	0.89	0.77	1.07	0.65	1.16	1.28	1.18	0.97	1.00	0.68	MW2468	adaB	probable methylated DNA-protein cysteine methyltransferase	DNA repair or modify
0.94	2.91	0.99	3.16	0.68	16.79	2.81	2.91	1.02	0.97	0.62	MW2469	clpL	ATP-dependent Clp proteinase chain clpL	adaptation to atypical
1.16	1.59	1.04	1.06	0.97	2.83	1.61	1.42	1.05	0.93	0.92	MW2470		hypothetical protein	
0.97	1.26	0.91	0.76	1.28	1.87	1.61	1.45	0.99	0.94	1.04	MW2470n		hypothetical protein	
0.75	1.20	0.93	1.11	0.72	1.82	1.64	1.63	1.01	1.01	1.03	MW2471	feoB	ferrous iron transport protein B homolog	transport/binding
0.90	1.24	1.10	1.02	0.97	1.44	1.35	1.53	0.72	1.09	0.95	MW2472		hypothetical protein	
0.71	0.97	1.14	0.82	0.69	1.46	1.59	1.51	0.71	1.17	1.13	MW2473		hypothetical protein, similar to antibiotic transport-associated protein	transport/binding
0.82	0.90	0.85	0.96	0.95	1.09	1.30	1.06	0.86	0.78	0.83	MW2474		hypothetical protein, similar to transcriptional regulator tetR-family	RNA synthesis
0.85	1.31	1.33	1.57	1.03	1.23	0.96	1.07	1.00	1.18	1.00	MW2474n		hypothetical protein, similar to transcriptional regulator tetR-family	RNA synthesis
0.80	1.48	1.18	0.94	1.12	2.47	1.31	1.55	0.92	1.22	1.02	MW2475	rocA	1-pyrroline-5-carboxylate dehydrogenase	aminoacid metabolism
0.84	1.47	1.22	1.19	1.16	1.82	1.24	1.66	0.86	1.09	1.08	MW2476		hypothetical protein, similar to O-acetyltransferase	carbohydrate metabolism
1.04	1.01	1.07	0.81	0.76	0.89	1.75	1.12	0.93	1.03	0.82	MW2477		hypothetical protein	
1.15	1.15	1.07	0.90	1.04	1.36	1.49	1.54	0.79	0.95	0.90	MW2477n		hypothetical protein	
0.81	1.19	0.94	0.91	1.02	1.34	1.12	1.39	0.75	1.18	1.77	MW2478	copA	copper-transporting ATPase copA	transport/binding
1.10	1.19	0.93	0.80	0.97	1.30	0.94	1.07	0.82	0.92	1.57	MW2479		hypothetical protein, similar to mercuric ion-binding protein	transport/binding
0.77	0.75	1.02	0.98	1.11	1.00	1.10	0.66	1.02	1.04	0.98	MW2480		hypothetical protein, similar to D-specific D-2-hydroxyacid dehydrogenase ddh hor	carbohydrate metabolism
0.85	1.20	0.90	0.85	1.04	1.82	0.85	1.37	0.72	0.97	1.23	MW2481		hypothetical protein, similar to aspartate aminotransferase	aminoacid metabolism
0.84	1.29	0.99	1.04	1.00	2.58	1.58	1.14	0.94	1.15	0.84	MW2482	crtN	squalene desaturase	lipid metabolism
0.79	1.69	0.96	1.20	1.01	4.62	1.56	1.57	0.97	1.06	0.82	MW2483	crtM	squalene synthase	lipid metabolism
0.76	1.30	1.08	1.58	1.00	3.90	1.33	1.22	1.01	1.07	0.80	MW2484	crtQ	conserved hypothetical protein	
0.80	1.21	1.08	0.82	0.98	2.69	1.67	1.76	0.74	1.12	0.72	MW2485	crtP	hypothetical protein, similar to phytoene dehydrogenase	lipid metabolism
0.76	1.72	1.08	1.05	0.98	2.07	1.28	1.11	1.02	1.01	0.76	MW2486	crtO	hypothetical protein	
1.37	1.20	0.96	0.96	1.13	1.23	1.05	1.37	0.90	0.97	0.95	MW2487		hypothetical protein, similar to secretory antigen precursor SsaA	pathogenic factor
0.98	1.12	1.06	0.95	1.06	1.11	0.85	0.91	1.00	1.14	1.15	MW2487n		hypothetical protein, similar to secretory antigen precursor SsaA	pathogenic factor
0.80	1.30	1.09	1.09	1.11	1.03	0.86	0.78	1.19	0.90	1.00	MW2488		hypothetical protein, similar to acyltransferase	cell wall
0.95	1.11	0.96	0.81	1.04	0.74	0.86	1.07	0.80	0.82	0.71	MW2489		conserved hypothetical protein	
1.05	1.33	1.11	1.27	1.34	0.56	0.87	0.67	1.04	0.95	0.49	MW2490	isaA	immunodominant antigen A	pathogenic factor
1.01	0.59	0.48	0.61	0.77	0.32	0.73	0.36	0.73	1.14	0.85	MW2491		hypothetical protein, similar to regulatory protein (pfoS/R)	RNA synthesis
0.80	1.01	0.82	0.83	0.94	0.83	0.76	0.83	0.67	0.96	1.04	MW2492		hypothetical protein, similar to transcriptional regulator (TetR/AcrR family)	RNA synthesis
0.87	1.04	1.03	0.90	0.97	0.95	0.91	0.91	0.75	1.11	1.05	MW2493		hypothetical protein	
0.87	0.99	0.94	1.16	0.97	0.90	0.88	0.79	0.86	1.04	1.11	MW2494		conserved hypothetical protein	
0.76	1.14	0.98	1.05	1.05	1.11	1.03	1.18	1.00	1.20	0.97	MW2495		conserved hypothetical protein	
0.77	1.19	1.28	1.16	1.03	1.26	1.10	1.14	0.94	1.06	0.96	MW2496		conserved hypothetical protein	
0.78	0.83	1.03	1.51	0.95	1.14	0.97	0.82	0.86	1.12	1.32	MW2497		hypothetical protein	
0.56	1.29	1.13	1.25	1.00	1.48	0.85	1.08	1.22	1.02	0.86	MW2498		hypothetical protein, similar to transcription regulator acrR	RNA synthesis

0.79	1.40	1.18	1.36	1.02	1.59	1.01	1.21	1.00	1.12	0.83	MW2499		hypothetical protein, similar to short chain oxidoreductase	
0.76	1.48	1.27	1.39	1.05	2.19	1.18	1.26	1.13	1.15	0.77	MW2500		conserved hypothetical protein	
0.77	1.01	1.15	1.75	1.07	2.08	1.09	1.04	1.02	1.11	0.70	MW2501		conserevd hypothetical protein	
0.65	1.37	1.24	1.39	1.14	1.90	1.05	1.20	1.15	1.11	0.43	MW2502		hypothetical protein, similar to cobalamin synthesis related protein CobW	aminoacid metabolism
0.79	1.17	1.28	1.37	1.04	1.75	1.08	1.24	1.09	1.15	0.38	MW2503		hypothetical protein, similar to ferrous iron transporter protein B	transport/binding
0.66	1.47	1.48	1.52	1.09	1.69	1.01	1.28	1.13	1.19	0.36	MW2504		conserved hypothetical protein	
0.74	1.00	1.02	0.61	0.81	1.05	1.09	1.34	0.86	1.11	0.83	MW2505		conserved hypothetical protein	
0.90	1.04	1.15	1.18	1.03	1.29	1.22	1.42	1.22	1.14	0.77	MW2506		hypothetical protein	
0.97	1.26	1.24	1.75	1.00	3.10	1.99	1.67	1.34	1.09	0.59	MW2508		conserved hypothetical protein	
0.78	1.13	1.45	4.47	1.08	1.26	1.03	1.52	1.42	1.02	0.33	MW2509		hypothetical protein, similar to dihydroorotate dehydrogenase	[illegible]
1.09	0.82	1.29	2.81	1.05	0.91	1.02	1.33	1.44	0.91	0.46	MW2510		hypothetical protein	
0.89	1.19	1.25	1.58	1.03	1.16	1.06	1.26	1.36	1.05	1.04	MW2511		conserved hypothetical protein	
0.84	1.17	1.35	1.32	0.93	1.07	1.24	1.23	1.16	1.15	0.86	MW2512		conserved hypothetical protein	
0.89	1.43	1.16	1.22	0.98	1.07	1.01	1.20	1.01	1.00	0.96	MW2513		hypothetical protein, similar to transcriptional regulator tetR-famil	RNA synthesis
0.92	0.39	0.89	0.59	0.68	0.87	1.10	0.98	0.85	0.85	0.91	MW2513n		hypothetical protein, similar to transcriptional regulator tetR-family	RNA synthesis
0.87	0.54	0.60	0.68	0.63	0.71	0.99	1.02	0.76	0.78	1.04	MW2514		conserved hypothetical protein	
0.81	0.98	0.87	0.89	0.80	0.82	1.04	0.99	1.05	0.78	1.07	MW2515		hypothetical protein	
1.12	1.12	0.92	0.83	1.11	0.87	0.88	0.91	0.81	0.79	1.52	MW2516	panD	aspartate 1-decarboxylase	coenzyme metabolism
1.01	0.61	0.59	0.73	0.73	0.62	1.03	0.70	0.88	0.72	1.40	MW2516n	panD	aspartate 1-decarboxylase	coenzyme metabolism
0.89	0.61	0.81	0.85	0.76	0.60	1.12	0.84	0.90	0.78	1.07	MW2518	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	coenzyme metabolism
0.96	1.05	0.98	1.19	1.03	0.81	0.87	0.91	0.92	0.96	1.04	MW2519		hypothetical protein, similar to 2-dehydropantoate 2-reductase	coenzyme metabolism
1.08	0.73	0.88	0.96	0.87	0.89	0.80	1.16	0.70	0.89	1.13	MW2520		hypothetical protein, similar to alpha-acetolactate decarboxylase	carbohydrate metabolism
0.88	0.84	0.86	1.25	0.83	0.78	0.74	0.79	0.78	0.92	0.95	MW2520n		hypothetical protein, similar to alpha-acetolactate decarboxylase	carbohydrate metabolism
0.79	0.72	0.85	2.04	1.10	1.07	0.77	2.59	0.73	0.79	1.41	MW2521	ldh	L-lactate dehydrogenase	carbohydrate metabolism
0.81	0.48	0.83	0.85	0.69	0.39	0.57	0.52	0.48	1.51	1.27	MW2522		hypothetical protein, similar to amino acid transporter	transport/binding
0.85	0.75	0.63	0.52	0.59	0.47	0.41	0.50	0.49	0.97	0.92	MW2523		hypothetical protein, similar to pyridoxal-phosphate dependent aminotransfera	aminoacid metabolism
0.92	0.86	0.72	0.79	0.78	0.99	0.73	0.85	0.73	0.87	1.05	MW2524		hypothetical protein	
0.77	1.07	1.05	1.32	0.69	1.41	0.94	2.06	0.84	0.89	1.82	MW2525		fructose-bisphosphate aldolase homolog	carbohydrate metabolism
0.95	0.86	0.85	1.21	1.17	0.66	0.79	1.14	0.78	0.99	1.52	MW2526	mqo2	malate:quinone oxidoreductase	carbohydrate metabolism
1.19	0.92	0.97	1.15	1.02	1.08	0.87	1.09	0.83	0.87	1.05	MW2527		hypothetical protein	
0.92	0.94	0.89	0.87	1.02	1.07	0.81	0.65	1.09	0.89	0.90	MW2527n		hypothetical protein	
0.73	1.00	0.79	0.98	0.90	1.20	0.74	0.94	0.83	0.92	1.43	MW2528		acetate-CoA ligase	carbohydrate metabolism
0.69	1.12	0.95	0.84	0.84	1.69	0.92	1.16	0.76	0.92	0.92	MW2529		conserved hypothetical protein	
0.90	0.94	1.11	0.84	0.90	1.14	0.94	1.14	0.73	1.04	0.97	MW2530		hypothetical protein	
0.66	1.19	1.10	0.88	0.97	1.00	0.91	0.95	0.85	1.10	0.86	MW2531	betA	choline dehydrogenase	adaptation to atypical
0.58	1.36	1.11	1.06	1.11	1.10	0.76	1.00	0.97	1.04	0.90	MW2532	gbsA	glycine betaine aldehyde dehydrogenase gbsA	adaptation to atypical
0.84	0.87	1.10	1.15	0.99	0.76	0.94	0.67	0.84	0.99	1.08	MW2533		conserved hypothetical protein	
0.76	1.23	1.24	1.00	1.03	0.90	0.84	0.87	0.92	1.05	0.92	MW2534		hypothetical protein	
0.72	1.15	1.08	0.87	1.13	0.73	0.77	1.14	0.81	1.21	0.75	MW2535	cudT	choline transporter	transport/binding
0.81	1.05	0.73	0.83	0.93	0.33	0.59	0.22	0.77	1.14	0.45	MW2536		hypothetical protein, similar to anaerobic ribonucleotide reductase activator pro	nucleic acid metabolism
0.97	0.87	0.72	0.69	0.86	0.32	0.56	0.27	0.74	0.83	0.31	MW2537	nrdD	anaerobic ribonucleoside-triphosphate reductase	nucleic acid metabolism
0.67	1.13	1.07	1.33	1.06	0.79	0.82	0.67	1.06	1.05	0.79	MW2538		hypothetical protein, similar to magnesium citrate secondary transporter	transport/binding
0.75	1.19	1.02	1.06	0.99	0.86	1.11	0.79	0.98	0.94	0.83	MW2539		hypothetical protein; similar to uroporphyrin-III C-methyltransferase	coenzyme metabolism
0.66	1.10	1.10	1.26	1.04	1.03	1.06	0.84	0.86	1.11	0.95	MW2540	cysJ	sulfite reductase flavoprotein	sulfur metabolism
0.80	1.31	1.14	1.19	1.10	1.15	0.90	0.94	0.97	1.02	1.04	MW2541		hypothetical protein, similar to glutathione peroxidase	adaptation to atypical
0.79	1.33	1.21	1.10	1.09	1.09	0.96	1.10	0.81	1.11	1.05	MW2542		hypothetical protein, similar to ABC transporter (permease)	transport/binding
0.79	1.33	1.29	0.67	0.83	1.16	1.00	1.38	0.82	1.00	1.44	MW2543		hypothetical protein, similar to ABC transporter (ATP-binding protein)	transport/binding
0.86	0.91	1.07	1.49	0.97	0.95	0.99	0.82	1.10	1.03	0.99	MW2544		hypothetical protein, similar to two-component sensor histidine kinase	sensor
0.82	1.35	1.21	1.30	1.12	1.30	0.89	1.03	1.23	1.03	1.02	MW2545		hypothetical protein, similar to two-component response regulator	RNA synthesis
1.09	1.27	1.19	1.34	0.93	1.40	0.96	1.00	1.18	1.10	1.04	MW2546		hypothetical protein	
1.00	1.24	1.41	1.42	1.07	1.19	1.04	1.17	1.11	1.23	0.99	MW2547	phoB	alkaline phosphatase III precursor	phosphate metabolism
1.49	0.47	0.90	0.90	0.97	1.08	0.99	0.66	0.95	0.99	1.22	MW2548		hypothetical protein	
0.92	0.91	0.96	1.49	1.05	0.92	0.92	0.65	1.08	1.01	0.90	MW2549		hypothetical protein, similar to transcriptional regulator	RNA synthesis
0.78	1.19	1.24	1.42	1.04	1.21	0.81	0.84	1.11	1.09	0.91	MW2550		hypothetical protein, similar to tributyrin esterase	lipid metabolism
1.10	0.87	1.03	0.72	0.93	0.61	0.95	0.87	0.85	1.55	1.67	MW2551	clfB	Clumping factor B	pathogenic factor
1.02	1.20	1.21	0.97	1.02	0.88	1.22	1.40	0.74	1.58	1.68	MW2551a	clfB	Clumping factor B	pathogenic factor
0.67	3.65	1.71	1.51	1.18	1.52	1.09	1.21	1.17	1.33	0.94	MW2552		hypothetical protein, similar to transcription regulator Crp/Fnr family protein	RNA synthesis
0.83	2.28	1.29	0.84	1.06	1.34	1.10	1.11	0.98	1.29	0.85	MW2553	arcC	carbamate kinase	aminoacid metabolism
0.80	2.32	1.54	1.11	1.22	1.69	1.15	1.37	1.25	1.19	0.83	MW2554	arcD	arginine/oirnithine antiporter	transport/binding
0.72	2.07	1.50	1.39	1.13	1.61	1.07	1.12	0.95	1.27	0.77	MW2555	arcB	ornithine transcarbamoylase	aminoacid metabolism
0.81	2.58	1.72	1.36	1.17	1.90	1.42	1.31	1.32	1.31	0.79	MW2556	arcA	arginine deiminase	aminoacid metabolism
0.79	1.38	1.25	0.92	0.98	1.28	0.96	1.42	1.16	1.23	1.00	MW2557		hypothetical protein, similar to arginine repressor	RNA synthesis
0.75	1.39	1.44	1.25	1.22	1.60	1.04	1.36	1.25	1.14	0.84	MW2558	aur	zinc metalloproteinase aureolysin	pathogenic factor
0.89	1.38	1.11	1.43	0.96	2.73	1.01	1.34	1.29	1.06	0.58	MW2559	isaB	immunodominant antigen B	pathogenic factor
1.02	0.98	1.17	1.28	1.04	1.21	1.14	0.91	1.25	1.11	0.74	MW2560		conserved hypothetical protein	
0.87	0.55	0.78	0.26	0.66	0.92	1.12	1.35	0.71	1.01	0.82	MW2561		hypothetical protein, similar to transcription antiterminator BglG family	RNA synthesis
1.01	0.68	0.54	0.70	0.79	0.77	1.03	1.07	0.94	1.05	1.45	MW2562		fructose phosphotransferase system enzyme fruA homolog	transport/binding
0.96	0.94	0.89	0.99	1.00	0.82	0.76	0.99	1.07	1.19	1.39	MW2563	pml	mannose-6-phosphate isomerase	carbohydrate metabolism
1.10	0.48	0.70	0.53	0.64	0.58	1.16	1.11	0.86	0.91	1.34	MW2564		hypothetical protein, similar to phage infection protein	phage-related
1.37	0.88	0.71	0.68	0.87	0.70	1.13	0.95	0.95	0.81	1.13	MW2565		hypothetical protein, similar to autolysin precursor	cell wall
1.05	1.07	1.14	1.25	1.11	1.21	0.91	0.89	1.03	0.99	0.87	MW2566		hypothetical protein, similar to N-Carbamoylsarcosine Amidohydrolase	coenzyme metabolism
1.05	1.14	1.17	1.12	0.99	1.17	1.08	1.22	1.27	1.03	1.24	MW2567		conserved hypothetical protein	
0.92	1.17	1.32	1.01	0.96	1.01	1.15	1.15	1.13	1.16	1.00	MW2568		hypothetical protein	
0.98	1.48	1.36	0.95	1.09	1.30	1.13	1.37	0.95	1.01	1.04	MW2569		hypothetical protein, similar to lipopolysaccharide biosynthesis protein	cell wall
1.00	1.39	1.25	0.76	1.45	1.65	1.11	1.56	0.90	0.89	1.09	MW2570		preprotein translocase secA homolog	protein secretion
0.95	1.69	1.38	1.01	1.47	1.57	1.14	1.80	0.97	0.95	1.15	MW2571		hypothetical protein	
0.98	1.61	1.35	1.05	1.41	1.61	1.04	2.21	0.80	1.03	1.03	MW2572		hypothetical protein	
0.97	1.89	1.53	1.06	1.45	1.71	1.07	1.98	1.32	1.05	1.11	MW2573		hypothetical protein	
1.16	1.75	1.47	0.90	1.43	1.82	1.39	1.87	1.19	1.04	1.16	MW2574		hypothetical protein, similar to preprotein translocase secY	protein secretion
1.37	1.58	1.53	1.08	1.90	1.59	1.30	2.51	1.44	1.04	1.24	MW2575		hypothetical protein, similar to streptococcal hemagglutinin protein	pathogenic factor
1.11	1.38	1.60	1.06	1.53	1.63	1.24	2.18	0.90	1.01	0.88	MW2576		conserved hypothetical protein	
0.87	2.19	1.71	1.41	1.58	2.27	1.16	1.94	1.19	1.13	0.99	MW2577		hypothetical protein	
0.96	1.37	1.12	1.12	1.04	1.52	1.21	1.18	1.03	1.17	0.99	MW2578		hypothetical protein	
0.79	1.69	1.46	1.38	1.24	1.75	1.25	1.62	1.22	1.16	0.97	MW2579		conserved hypothetical protein	
0.86	1.24	1.27	1.36	1.18	1.55	1.19	1.36	1.20	1.15	1.18	MW2580		hypothetical protein, similar to peptide methionine sulfoxide reductase	protein modification
0.77	1.79	1.42	1.52	1.15	1.74	1.09	1.60	1.00	1.08	0.96	MW2581		conserved hypothetical protein	
0.77	2.07	1.54	1.17	1.28	1.70	1.07	1.83	0.98	1.18	0.90	MW2582	capC	capsular polysaccharide biosynthesis, capC	adaptation to atypical
0.95	1.40	1.38	0.95	1.32	1.41	1.35	2.00	0.65	1.19	0.98	MW2583	capB	capsular polysaccharide biosynthesis, capB	adaptation to atypical
0.71	1.58	1.26	1.24	0.98	1.36	0.95	1.26	0.98	1.11	0.97	MW2584	capA	capsular polysaccharide biosynthesis, capA	adaptation to atypical
0.94	1.04	1.21	1.17	1.13	1.20	0.99	1.06	1.10	1.20	1.11	MW2585	icaR	ica operon transcriptional regulator IcaR	RNA synthesis
0.79	1.53	1.38	1.23	1.12	1.54	1.04	1.16	0.82	1.26	1.07	MW2586	icaA	intercellular adhesion protein A	pathogenic factor
0.81	1.11	1.30	1.00	1.33	1.08	1.06	1.11	0.87	1.15	1.06	MW2587	icaD	intercellular adhesion protein D	pathogenic factor
0.75	1.43	1.33	1.51	1.19	1.42	0.97	1.26	1.23	1.26	1.10	MW2588	icaB	intercellular adhesion protein B	pathogenic factor
0.73	1.29	1.20	0.95	1.08	1.48	1.02	1.31	0.95	1.19	1.26	MW2589	icaC	intercellular adhesion protein C	pathogenic factor
0.70	1.19	1.32	1.23	1.14	1.24	0.84	1.20	1.02	1.26	0.95	MW2590	lip	triacylglycerol lipase precursor	pathogenic factor
0.70	1.00	1.09	1.09	1.00	1.19	0.86	0.81	1.01	1.20	0.96	MW2591	hisI	histidine biosynthesis bifunctional protein HisIE	aminoacid metabolism
0.82	1.24	1.33	1.24	0.98	1.56	0.92	1.04	0.99	1.18	0.90	MW2592	hisF	cyclase-like protein hisF	aminoacid metabolism

0.78	1.32	1.32	1.32	1.11	1.37	0.95	0.98	1.11	1.21	0.86	MW2593		thetical protein, similar to phosphoribosylformimino-5-aminoimidazole carboxamide ribo	aminoacid metabolism
0.72	1.05	1.40	1.12	1.11	1.19	1.04	1.12	0.91	1.41	0.97	MW2594	hisH	amidotransferase hisH	aminoacid metabolism
0.72	0.95	1.24	1.16	1.06	1.31	0.83	0.90	0.83	1.19	0.96	MW2595	hisB	imidazoleglycerol-phosphate dehydratase	aminoacid metabolism
0.67	1.44	1.34	1.35	1.05	1.57	0.80	1.05	0.98	1.14	1.05	MW2596		hypothetical protein, similar to histidinol-phosphate transaminase	aminoacid metabolism
0.66	1.56	1.36	1.27	1.03	1.37	0.83	1.03	1.08	1.26	0.84	MW2597		hypothetical protein, similar to histidinol dehydrogenase	aminoacid metabolism
0.75	1.24	1.29	1.43	1.11	1.47	1.06	0.94	0.99	1.19	0.85	MW2598	hisG	ATP phosphoribosyltransferase	aminoacid metabolism
0.60	1.18	1.14	1.29	0.95	1.27	0.81	0.94	0.95	1.18	0.89	MW2599		hypothetical protein, similar to ATP phosphoribosyltransferase regulatory subu	nucleic acid metabolism
0.77	1.00	1.07	1.29	0.86	1.15	0.83	0.95	1.03	1.17	1.11	MW2600		hypothetical protein	
0.82	1.18	0.95	0.91	0.78	1.03	0.87	1.06	0.83	1.12	1.39	MW2601		conserved hypothetical protein	
0.80	1.63	1.13	0.92	0.71	0.95	0.85	0.99	0.68	1.20	1.40	MW2602		conserved hypothetical protein	transport/binding
0.60	1.54	1.05	1.11	1.03	1.24	0.63	1.22	0.73	1.02	1.13	MW2603		hypothetical protein, similar to cation ABC transporter	transport/binding
0.60	0.90	1.20	1.05	0.97	0.93	0.89	0.92	0.71	1.18	1.09	MW2603n		hypothetical protein, similar to cation ABC transporter (ATP-binding protei)	transport/binding
0.66	1.05	0.87	1.22	0.72	0.97	0.79	0.80	0.80	1.01	1.11	MW2604		conserved hypotehtical protein	
0.76	1.05	0.99	1.10	0.86	1.02	0.79	0.88	0.90	1.09	0.97	MW2605		conserved hypothetical protein	
1.21	1.53	1.50	1.56	0.99	1.17	1.35	1.26	1.33	1.38	1.18	MW2606		conserved hypothetical protein	
0.88	1.07	0.92	0.98	2.64	1.09	1.39	1.14	1.01	0.88	0.97	MW2607		hypothetical protein	
0.80	1.15	1.39	1.54	1.08	1.08	1.11	0.94	1.04	1.24	0.93	MW2608	drp35	Drp35	cell wall
0.71	1.08	1.06	1.29	0.92	0.85	1.18	0.88	1.18	1.05	0.98	MW2609		conserved hypotehtical protein	
0.95	0.86	1.03	1.19	0.87	0.77	1.01	0.84	1.10	1.00	1.00	MW2610	pcp	pyrrolidone-carboxylate peptidase	protein modification
1.20	0.57	1.05	1.80	1.12	0.41	0.93	1.12	0.79	1.30	1.43	MW2612	can	collagen adhesin precursor	pathogenic factor
0.84	0.99	1.22	1.56	0.91	0.85	1.13	1.11	1.29	1.12	1.43	MW2613		2-oxoglutarate/malate translocator homolog	transport/binding
0.83	1.06	0.92	0.85	0.83	1.08	1.23	0.99	0.94	0.90	1.00	MW2616		hypothetical protein	
0.98	1.26	1.19	0.99	1.15	1.35	1.54	1.61	0.83	1.02	1.19	MW2617		hypothetical protein, similar to high-affinity nickel-transport protein	transport/binding
0.92	1.49	1.17	1.12	1.32	1.56	1.04	1.70	0.84	0.95	0.99	MW2618		hypothetical protein, similar to N-hydroxyarylamine O-acetyltransferase	carbohydrate metabolism
0.98	1.15	0.88	0.93	0.61	1.43	1.70	1.20	0.82	0.95	0.90	MW2619		conserved hypothetical protein	
0.87	1.27	1.09	1.20	1.13	1.06	1.08	1.17	0.92	1.07	0.93	MW2620	vraD	hypothetical protein, similar to ABC transporter	transport/binding
0.89	0.83	0.86	0.91	0.94	1.12	1.38	1.15	1.15	0.86	1.03	MW2620n	vraD	hypothetical protein, similar to ABC transporter	transport/binding
0.78	1.91	1.08	1.05	1.04	1.20	1.48	1.86	0.95	1.07	1.56	MW2622		hypothetical protein	
0.74	1.13	1.15	1.16	1.05	1.29	0.94	1.19	0.92	1.06	1.24	MW2622n		hypothetical protein	
1.24	0.51	0.91	0.72	0.66	0.23	1.14	0.45	1.01	1.51	1.17	MW2623	cspB	cold shock protein cspB	adaptation to atypical
1.04	0.79	0.80	1.01	1.12	0.80	1.40	0.98	1.12	0.70	1.14	MW2624		hypothetical protein, similar to hypothetical protein	RNA synthesis
1.02	0.95	0.99	1.14	1.26	1.22	1.30	1.31	0.91	0.87	0.97	MW2625		hypothetical protein	
0.89	0.66	0.67	0.80	0.90	0.77	1.22	0.92	0.92	0.68	0.85	MW2626		hypothetical protein	
0.91	1.03	1.10	1.02	1.05	1.12	1.05	1.05	0.91	1.00	0.96	MW2627		hypothetical protein, similar to DNA-binding protein SpoOJ-like homolog	sporulation
1.11	1.29	1.06	1.21	1.12	1.38	1.03	1.32	0.95	0.89	0.81	MW2628	gidB	glucose inhibited division protein B	cell division
0.95	1.37	1.21	1.05	1.19	1.51	1.01	1.63	0.97	1.02	0.80	MW2629	gidA	glucose inhibited division protein A	cell division
1.24	0.90	1.13	0.77	1.37	1.25	1.17	1.78	0.71	1.05	0.76	MW2630	thdF	possible thiophene and furan oxidation protein	detoxification
0.96	1.31	1.09	1.12	1.04	1.16	0.89	1.11	1.06	0.98	0.84	MW2631	rnpA	ribonuclease P protein component	RNA modification
1.53	0.87	1.00	0.74	1.04	0.30	0.87	0.64	1.04	1.05	0.67	MW2632	rpmH	50S ribosomal protein L34	protein synthesis
1.57	1.00	0.79	0.66	0.98	0.29	0.77	0.58	1.02	1.02	0.63	MW2632n	rpmH	50S ribosomal protein L34	protein synthesis