

functional group/accession	Gene	Product	log2FC		p-value	
			15 min	60 min	15 min	60 min
proline balance						
CDIF630erm_00112	<i>proS1</i>	proline-tRNA ligase	-0,960	0,467	-2,302	0,000
CDIF630erm_00113	<i>proS2</i>	proline-tRNA ligase	-0,446	0,828	-2,866	0,000
ribonucleotide synthesis/ purin/replication						
CDIF630erm_00204	<i>nrdD</i>	anaerobic ribonucleoside triphosphate reductase	1,225	0,171	1,914	0,000
CDIF630erm_00205	<i>nrdG</i>	anaerobic ribonucleoside-triphosphate reductase-activating protein	2,106	0,152	1,580	0,116
CDIF630erm_01905	<i>codB</i>	putative cytosine permease	-0,742	0,586	-1,627	0,002
CDIF630erm_02331	<i>pbuG</i>	adenine / guanine / hypoxanthine permease	-1,834	0,006	-4,027	0,000
CDIF630erm_02839	<i>priA</i>	primosomal protein	3,149	0,000	4,133	0,000
compatible solutes						
CDIF630erm_01020	<i>opuCA</i>	ABC-type transport system glycine betaine / carnitine / choline ATP-binding protein	0,846	0,455	3,148	0,000
CDIF630erm_01021	<i>opuCC</i>	ABC-type transport system glycine betaine / carnitine / choline permease	1,604	0,018	3,710	0,000
CDIF630erm_01161	<i>potB</i>	ABC-type transport system spermidine / putrescine permease	-0,646	0,828	-2,447	0,003
CDIF630erm_01162	<i>potC</i>	ABC-type transport system spermidine / putrescine permease	1,221	0,450	-1,416	0,126
CDIF630erm_01163	<i>potD</i>	ABC-type transport system spermidine / putrescine solute-binding protein	0,276	0,937	-2,052	0,007
CDIF630erm_02052		transcriptional regulator AraC family	-0,449	0,896	1,974	0,002
cell surface/cell wall/ sporulation						
CDIF630erm_01157		putative spore coat protein	1,696	0,551	3,948	0,001
CDIF630erm_01511	<i>cspB</i>	cold shock protein CspB	-1,464	0,006	-2,516	0,000
CDIF630erm_01012	<i>cspA</i>	cold shock protein	0,037	0,989	-1,505	0,001
CDIF630erm_02205	<i>cspC1</i>	major cold shock protein CspC	-0,169	0,947	-2,284	0,000
CDIF630erm_02548	<i>cspD</i>	cold shock protein D	0,167	0,956	-2,670	0,000
CDIF630erm_01803	<i>vanG</i>	D-alanine--D-alanine ligase	0,029	0,996	5,888	0,000
CDIF630erm_01804	<i>vanY1</i>	D-alanyl-D-alanine carboxypeptidase VanY-like	0,289	0,967	4,813	0,000
CDIF630erm_01805	<i>vanTG</i>	alanine racemase	0,501	0,869	4,153	0,000
CDIF630erm_01391	<i>vanZ</i>	teicoplanin resistance protein	1,528	0,096	3,182	0,000
CDIF630erm_02379		putative vancomycin resistance protein vanW family	0,132	0,964	2,470	0,000
CDIF630erm_02361	<i>dxr</i>	1-deoxy-D-xylulose 5-phosphate reductoisomerase	0,226	0,964	2,171	0,004
CDIF630erm_02986		putative polysaccharide deacetylase	3,812	0,000	3,878	0,000
CDIF630erm_02988	<i>glyA1</i>	serine hydroxymethyltransferase	0,101	0,964	1,664	0,000
CDIF630erm_03811	<i>spoVB</i>	stage V sporulation protein B	0,943	0,467	1,580	0,007
CDIF630erm_03889	<i>yabG</i>	sporulation-specific protease	1,574	0,521	2,089	0,044
CDIF630erm_03945	<i>phnA</i>	phosphonoacetate hydrolase	0,101	0,974	1,373	0,023
CDIF630erm_03120	<i>dltA</i>	D-alanine--poly(phosphoribitol) ligase subunit 1	-0,226	0,964	1,793	0,013
CDIF630erm_03122	<i>dltD</i>	putative D-alanine transferase DltD	1,285	0,441	2,906	0,000
C-metabolism/PTS-system/ fermentation						
CDIF630erm_00523	<i>hadA</i>	isocaproenoyl-CoA:2-hydroxyisocaproate CoA-transferase	-0,734	0,513	1,618	0,001
CDIF630erm_00524	<i>hadI</i>	activator of 2-hydroxyisocaproyl-CoA dehydratase	-0,385	0,853	1,560	0,000
CDIF630erm_00525	<i>hadB</i>	2-hydroxyisocaproyl-CoA dehydratase alpha subunit	-0,881	0,284	1,121	0,013
CDIF630erm_00526	<i>hadC</i>	2-hydroxyisocaproyl-CoA dehydratase beta subunit	-0,151	0,947	1,138	0,005
CDIF630erm_00693	<i>gapN</i>	glyceraldehyde-3-phosphate dehydrogenase (NADP+)	-1,665	0,129	-1,819	0,013
CDIF630erm_01194	<i>bcd</i>	butyryl-CoA dehydrogenase catalytic subunit	-0,673	0,494	-1,149	0,006
CDIF630erm_01195	<i>etfB3</i>	butyryl-CoA dehydrogenase electron transfer flavoprotein beta subunit	-0,598	0,606	-1,544	0,000
CDIF630erm_01196	<i>etfA3</i>	butyryl-CoA dehydrogenase electron transfer flavoprotein alpha subunit	-0,875	0,278	-1,137	0,008
CDIF630erm_01197	<i>crt2</i>	short-chain-enoil-CoA hydratase	-0,335	0,903	-1,142	0,045
CDIF630erm_01207	<i>ccpA</i>	transcriptional regulator LacI family	0,155	0,964	1,429	0,018
CDIF630erm_01505	<i>cprA</i>	ABC-type transport system lantibiotic / multidrug-family ATP-binding protein	1,908	0,351	5,585	0,000
CDIF630erm_01506	<i>cprB</i>	ABC-type transport system lantibiotic / multidrug-family permease	1,495	0,547	5,086	0,000
CDIF630erm_01507	<i>cprC</i>	ABC-type transport system lantibiotic / multidrug-family permease	0,094	0,989	3,672	0,001
CDIF630erm_02028	<i>metA</i>	homoserine O-succinyltransferase	0,685	0,899	3,479	0,001
CDIF630erm_02446	<i>cynT</i>	carbonic anhydrase	0,380	0,913	2,065	0,001

CDIF630erm_02581	<i>sucD</i>	succinate-semialdehyde dehydrogenase (acetylating)	-1,418	0,513	-3,635	0,000
CDIF630erm_02583		putative succinate transporter	-0,901	0,627	-1,829	0,007
CDIF630erm_03810	<i>yabN</i>	bifunctional tetrapyrrole methylase / NTP pyrophosphohydrolase	1,214	0,098	1,395	0,005
CDIF630erm_03312	<i>kpsF</i>	arabinose 5-phosphate isomerase	-0,351	0,863	-1,447	0,000
CDIF630erm_03378	<i>bglA3</i>	6-phospho-beta-glucosidase	0,599	0,867	-2,104	0,001
CDIF630erm_03380	<i>bglF2</i>	PTS system beta-glucoside-specific IIBC component bglF2	-0,754	0,789	-2,841	0,000
CDIF630erm_03421	<i>bglA5</i>	6-phospho-beta-glucosidase	-0,672	0,531	-1,850	0,000
CDIF630erm_03422	<i>bglF5</i>	PTS system beta-glucoside-specific IIBC component bglF5	-0,952	0,277	-2,395	0,000
CDIF630erm_03462	<i>eno</i>	enolase	-0,049	0,986	-2,294	0,000
CDIF630erm_03463	<i>gpmI</i>	23-bisphosphoglycerate-independent phosphoglycerate mutase	-0,118	0,967	-3,338	0,000
CDIF630erm_03464	<i>tpi</i>	triosephosphate isomerase	-0,746	0,693	-2,780	0,000
CDIF630erm_03465	<i>pgk</i>	phosphoglycerate kinase	-0,599	0,619	-3,715	0,000
CDIF630erm_03466	<i>gapA</i>	glyceraldehyde-3-phosphate dehydrogenase	-0,169	0,947	-4,210	0,000
CDIF630erm_03467	<i>cggR</i>	transcriptional regulator SorC family	-0,001	1,000	-2,358	0,000
CDIF630erm_03472		xanthine / urate permease	-0,030	0,996	-2,912	0,006
CDIF630erm_03585	<i>pgi</i>	glucose-6-phosphate isomerase	0,550	0,521	1,411	0,000
CDIF630erm_03699	<i>pyk</i>	pyruvate kinase	-0,317	0,828	-2,564	0,000
CDIF630erm_03700	<i>pfkA</i>	ATP-dependent 6-phosphofruktokinase	-0,705	0,253	-2,463	0,000
CDIF630erm_01777		PTS system lactose / cellobiose-family IIB component	-0,633	0,531	-1,704	0,000
CDIF630erm_03311		PTS system arabinose-specific IIA component	-0,743	0,521	-1,966	0,000
CDIF630erm_03314		PTS system arabinose-specific IIBC component	-0,858	0,411	-1,904	0,000
CDIF630erm_00934	<i>bglF1</i>	PTS system beta-glucoside-specific IIBC component bglF1	-0,792	0,755	-1,718	0,029
CDIF630erm_03380	<i>bglF2</i>	PTS system beta-glucoside-specific IIBC component bglF2	-0,754	0,789	-2,841	0,000
CDIF630erm_03422	<i>bglF5</i>	PTS system beta-glucoside-specific IIBC component bglF5	-0,952	0,277	-2,395	0,000
CDIF630erm_02921	<i>ptsG-BC</i>	PTS system glucose-specific IIBC component	-1,031	0,323	-2,576	0,000
CDIF630erm_01777		PTS system lactose / cellobiose-family IIB component	-0,633	0,531	-1,704	0,000
CDIF630erm_02759		PTS system maltose-specific IIBC component	-0,416	0,907	-2,300	0,001
CDIF630erm_03352	<i>xynD</i>	PTS system xyloside-specific IID component	-0,833	0,653	-1,741	0,011

oxidative stress

CDIF630erm_00930		putative universal stress protein A (UspA)	-0,171	0,973	1,975	0,012
CDIF630erm_01508	<i>cprK</i>	two-component sensor histidine kinase	1,784	0,175	3,559	0,000
CDIF630erm_01505	<i>cprA</i>	ABC-type transport system lantibiotic / multidrug-family ATP-binding protein	1,908	0,351	5,585	0,000
CDIF630erm_01506	<i>cprB</i>	ABC-type transport system lantibiotic / multidrug-family permease	1,495	0,547	5,086	0,000
CDIF630erm_01507	<i>cprC</i>	ABC-type transport system lantibiotic / multidrug-family permease	0,094	0,989	3,672	0,001
CDIF630erm_01672		putative thioredoxin	2,874	0,014	3,507	0,000
CDIF630erm_01705	<i>nfnB</i>	NADH-dependent reduced ferredoxin:NADP+ oxidoreductase subunit beta	-0,555	0,531	-1,575	0,000
CDIF630erm_02445		transcriptional regulator MarR family			3,127	0,009
CDIF630erm_02222	<i>effR</i>	transcriptional regulator MarR family	-0,250	0,936	1,935	0,000
CDIF630erm_01875	<i>trxA1</i>	thioredoxin	-1,153	0,054	-1,371	0,001
CDIF630erm_01992		putative oxidoreductase	0,987	0,696	2,886	0,001
CDIF630erm_02074		putative oxidoreductase	1,419	0,521	3,770	0,000
CDIF630erm_02233	<i>ilvD</i>	dihydroxy-acid dehydratase	-0,681	0,828	-1,659	0,020
CDIF630erm_02678	<i>recO</i>	DNA repair protein RecO	0,371	0,943	2,483	0,004

cysteine metabolism

CDIF630erm_01767	<i>cysK</i>	cysteine synthase	0,183	0,964	2,944	0,000
CDIF630erm_01768	<i>cysE</i>	serine O-acetyltransferase	-0,501	0,875	2,712	0,000

thiamin metabolism

CDIF630erm_01891	<i>thiF</i>	sulfur carrier protein ThiS adenyltransferase	0,194	0,943	-1,474	0,004
CDIF630erm_01892	<i>thiG</i>	thiazole synthase	-0,943	0,513	-2,224	0,000

glycine metabolism

CDIF630erm_01931		glycine / sarcosine / betaine reductase complexprotein b alpha / beta subunit	1,067	0,812	2,673	0,004
CDIF630erm_01932		glycine/sarcosine/betaine reductase complexprotein b gamma subunit	0,562	0,907	2,233	0,001
CDIF630erm_02588	<i>grdC</i>	glycine reductase complex component C subunit beta	-0,228	0,947	-1,730	0,001
CDIF630erm_02589	<i>grdB</i>	glycine reductase complex component B gamma subunit (selenocysteine)	-0,342	0,879	-1,242	0,004
CDIF630erm_02592	<i>grdA</i>	glycine reductase complex selenoprotein A (selenocysteine)	-0,189	0,952	-1,486	0,003

CDIF630erm_02594	<i>grdE</i>	glycine reductase complex component B subunits alpha and beta (Selenoproti-	0,495	0,867	-1,607	0,004
CDIF630erm_02596	<i>trxB3</i>	thioredoxin reductase	-1,544	0,327	-2,101	0,000

formylation of methionine

CDIF630erm_02837	<i>fmt</i>	methionyl-tRNA formyltransferase	2,063	0,008	3,060	0,000
CDIF630erm_02838	<i>def2</i>	peptide deformylase	1,394	0,441	3,166	0,000

chaperone / proteases

CDIF630erm_02497	<i>prsA1</i>	peptidyl-prolyl cis-trans isomerase PpiC-type	2,456	0,000	3,217	0,000
CDIF630erm_03584		serine protease HrtA family	6,087	0,000	5,498	0,000

cobalamin biosynthesis

CDIF630erm_03727	<i>hemB</i>	delta-aminolevulinic acid dehydratase	0,411	0,720	-1,822	0,000
CDIF630erm_03730	<i>cbiKP</i>	sirohydrochlorin cobaltochelataase CbiKP	-0,569	0,867	-2,708	0,000

riboflavin

CDIF630erm_00266	<i>ribU</i>	riboflavin transporter	2,802	0,000	1,063	0,203
CDIF630erm_01882	<i>ribH</i>	67-dimethyl-8-ribityllumazine synthase	4,543	0,000	0,132	0,930
CDIF630erm_01883	<i>ribBA</i>	bifunctional 34-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrol	4,275	0,001	1,308	0,375
CDIF630erm_01885	<i>ribD</i>	bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase	4,180	0,000	1,790	0,109
CDIF630erm_01840		cation-transporting ATPase	5,093	0,000	4,553	0,000